

CG/914088

GenCore version 5.1.6  
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Protein - protein search, using sw model

Run on: November 5, 2003, 17:11:03 ; Search time 21 Seconds  
(without alignments)  
41.215 Million cell updates/sec

File: US-09-914-088-1

Perfect score: 47

Sequence: 1 EDQVMEVD 9

Scoring table: R:OSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 759

Minimum DB seq length: 9

Maximum DB seq length: 9

Post processing: Minimum Match 3%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 761\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	36.2	6	2 PT0604	T-cell receptor be
2	17	36.2	6	2 PT0657	T-cell receptor be
3	17	36.2	7	2 PT0543	T-cell receptor be
4	17	36.2	8	2 A28713	thymic humoral fac
5	16	34.0	9	2 A37027	macrophage chemot
6	16	34.0	9	2 A60427	macrophage cytotox
7	14	29.8	4	2 PT0271	Ig heavy chain CRD
8	14	29.8	7	2 S29735	polysphosphate-gluc
9	14	29.8	8	2 PT0537	T-cell receptor be
10	14	29.8	9	2 B39841	dectransucrase (EC
11	14	29.8	9	2 D44787	CalHMramide 13
12	14	29.8	9	2 A56029	N-methylpurine DNA
13	13	27.7	4	2 A41890	protein D - Escher
14	13	27.7	6	2 B35640	cerebellar degener
15	13	27.7	7	2 PC2370	probable H-transp
16	13	27.7	8	2 PT0279	Ig heavy chain CRD
17	13	27.7	8	2 S66296	Na--transporting A
18	13	27.7	9	2 B45796	dihydrofolateamide S
19	13	27.7	9	2 A61230	calsequestrin, car
20	13	27.7	9	2 D48186	ATPase R1 subunit
21	13	27.7	9	2 C60070	gastrin - domestic
22	12	25.5	5	2 B31836	25K protein - Rick
23	12	25.5	5	2 PT0699	T-cell receptor be
24	12	25.5	5	2 PT0703	T-cell receptor be
25	12	25.5	6	2 PC4392	whey glycoprotein
26	12	25.5	6	2 A20186	fatty acid synthas
27	12	25.5	6	2 PT0720	T-cell receptor be
28	12	25.5	6	2 PT0589	T-cell receptor be
29	12	25.5	7	2 S20446	glucanase - Pseudom

30	12	25.5	7	2 B39127	phosphotransferase
31	12	25.5	7	2 PT0611	T-cell receptor be
32	12	25.5	7	2 PT0523	T-cell receptor be
33	12	25.5	7	2 PT0665	T-cell receptor be
34	12	25.5	7	2 PT0567	T-cell receptor be
35	12	25.5	7	2 PT0689	T-cell receptor be
36	12	25.5	7	2 PT0688	T-cell receptor be
37	12	25.5	8	2 E60588	sperm-activating p
38	12	25.5	8	2 G60588	sperm-activating p
39	12	25.5	8	2 XGHUEU	urine glycopeptide
40	12	25.5	8	2 PT0298	Ig heavy chain CRD
41	12	25.5	8	2 PT0613	T-cell receptor be
42	12	25.5	8	2 PT0547	T-cell receptor be
43	12	25.5	8	2 PT0724	T-cell receptor be
44	12	25.5	8	2 PT0725	T-cell receptor be
45	12	25.5	8	2 A25836	L-serine ammonia

ALIGNMENTS

RESULT 1

PT0604

T-cell receptor beta chain V-D-J region (111-1A) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0604

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0604

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 36.2%; Score 17; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGG 4

Db 4 DGG 6

RESULT 2

PT0657

T-cell receptor beta chain V-D-J region (121-1K) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0657

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0657

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FE>

A:Experimental source: day 4 postnatal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 36.2%; Score 17; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DGG 4

Db 4 DGG 6









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SW protein-protein search, using sw model

Run on: November 5, 2003, 17:14:37, server time 11 seconds  
Database: GenCore  
Query: us-09-914-088-1  
Query length: 494 amino acids  
Query start: 1  
Query end: 494  
Query type: protein

Results: 1 hit

Hit: 1

Hit name: ACT\_CARMA

Hit length: 494 amino acids

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit alignment: 100%

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit score: 49.0, Gap: 0.0

Hit description: ACT\_CARMA, 494 amino acids, 49426705 residues

Hit score: 49.0, Gap: 0.0

34 10 21 3 9 1 LITG\_LITAC  
35 10 21 3 9 1 LITG\_PHYC  
36 10 21 3 9 1 MOSH\_CLYJA  
37 10 21 3 9 1 MOSH\_CLYJA  
38 10 21 3 9 1 THA2\_HUMAN  
39 10 21 3 9 1 UPAG\_HUMAN  
40 9 19 1 6 1 C192\_VYTED  
41 9 19 1 7 1 WNA1\_ACEFC  
42 9 19 1 7 1 WNA2\_ACEFC  
43 9 19 1 7 1 WNA3\_ACEFC  
44 9 19 1 8 1 AKIS\_GRYR  
45 9 19 1 8 1 AKIS\_TIBAU

ALIGNMENTS

RESULT 1  
ACT\_CARMA STANDARD: PRT: 8 AA  
ID ACT\_CARMA STANDARD: PRT: 8 AA  
AC P8C709;  
ET 01-OCT-1996 (Rel. 14, Created)  
DT 01-OCT-1996 (Rel. 14, Last sequence update)  
DT 15-JUL-1999 (Rel. 13, Last annotation update)  
DE Actin (fragment)  
OS Carcinus maenas (Common shore crab) (Green crab)  
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
CC Eumalacostraca; Decapoda; Decapoda; Pleocyemata; Brachyura;  
CC Eubrachyura; Portunidae; Portunidae; Carcinus  
CC NCBI TaxID:6759;  
RN [1]  
RP SEQUENCE  
RA Rachaise F., Sore G., Carpenter G., Grapton E., Webster S.,  
RA Rachassarian D.,  
RA "A transaldolase. An enzyme implicated in crab steroidogenesis".  
RL Endocrine 5:23-32 (1996).  
CC - FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED  
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE OBVIOUSLY EXPRESSED  
CC IN ALL EUKARYOTIC CELLS.  
CC - SUBCELLULAR LOCATION: Cytoplasmic.  
CC - MISCELLANEOUS: ON THE 2D GEL, THE DETERMINED PI OF THIS PROTEIN IS:  
CC 5.8. ITS MW IS 46 kDa.  
CC - SIMILARITY: Belongs to the actin family.  
CC InterPro: IPR040001; Actin.  
CC InterPro: IPR040001; Actin-like.  
CC PROSITE: PS00456; ACTINS 1; PARTIAL.  
CC PROSITE: PS00456; ACTINS 2; PARTIAL.  
CC PROSITE: PS00456; ACTINS 3; PARTIAL.  
CC Structural protein  
FT NON TER 1 1  
FT NON TER 5 9  
SQ SEQUENCE 8 AA: 976 MW: 1424005AB2CAAB3 CRC64;

Query Match 14.0% Score 16; DB 1; Length 8;  
Best local similarity 100.0%; Pred No. 1.3e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 DVD 9  
DB 3 DVD 5

RESULT 2  
PLP\_BRANA STANDARD: PRT: 8 AA  
ID PLP\_BRANA STANDARD: PRT: 8 AA  
AC P8707;  
ET 15-JUL-1995 (Rel. 13, Created)  
DT 15-JUL-1995 (Rel. 13, Last sequence update)  
DT 15-JUL-2000 (Rel. 13, Last annotation update)  
DE Plastidial lipid-associated protein (fragment).  
CC Brassica napus (Rapeseed)  
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;







OC Hypocreales: Hypocreales; Hypocreales; Hypocreales.

RA NBI\_TaxID:321

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RX MEDLINE:98121193; PubMed:9461295;

RA Dave H., Johnson A.H., Maestro J. L., Scott A.G., Jaros P.P.,

RA Thorpe A.;

RA "Isolation and identification of multiple neuropeptides of the

RA allatostatin superfamily in the shore crab *Carcinus maenas*."

RL Eur. J. Biochem. 250:727-734 (1997).

CC "FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.

CC "SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

KW Neuropeptide; Allatostatin; Multigene family.

FT MOD.RES 8 8 AMIDATION (POTENTIAL).

SQ SEQUENCE 8 AA; 858 MW; C82B7955AB460865 CRC64;

Query Match 23.4%; Score 11; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQ 4

DB 1

2 GQ 3

Search completed: November 5, 2003, 17:13:17

Job time : 12 secs

OC Hypocreales: Hypocreales; Hypocreales; Hypocreales.

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd  
CM protein: protein search, using sw model  
Run on: November 5, 2003, 17:10:22 / Search time: 11 seconds  
(without alignment)  
70,378 Million cell updates/sec

Title: US-09-914-088-1  
Perfect score: 47  
Sequence: : EDAQVQDVQ 9  
Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5  
Searched: 93526 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 175  
Minimum DB seq length: 0  
Maximum DB seq length: 9  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Summary:  
1: sp:archaea:  
2: sp:bacteria:  
3: sp:fungi:  
4: sp:human:  
5: sp:invertebrate:  
6: sp:mammal:  
7: sp:phage:  
8: sp:organelle:  
9: sp:phage:  
10: sp:plant:  
11: sp:rodent:  
12: sp:virus:  
13: sp:vertebrate:  
14: sp:unclassified:  
15: sp:virus:  
16: sp:bacteriophage:  
17: sp:archaea:  
18: sp:archaea:  
19: sp:bacteria:  
20: sp:fungi:  
21: sp:human:  
22: sp:invertebrate:  
23: sp:mammal:  
24: sp:phage:  
25: sp:organelle:  
26: sp:phage:  
27: sp:plant:  
28: sp:rodent:  
29: sp:virus:  
30: sp:vertebrate:  
31: sp:unclassified:  
32: sp:virus:  
33: sp:bacteriophage:  
34: sp:archaea:  
35: sp:archaea:  
36: sp:bacteria:  
37: sp:fungi:  
38: sp:human:  
39: sp:invertebrate:  
40: sp:mammal:  
41: sp:phage:  
42: sp:organelle:  
43: sp:phage:  
44: sp:plant:  
45: sp:rodent:  
46: sp:virus:  
47: sp:vertebrate:  
48: sp:unclassified:  
49: sp:virus:  
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54: sp:fungi:  
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56: sp:invertebrate:  
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58: sp:phage:  
59: sp:organelle:  
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63: sp:virus:  
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66: sp:virus:  
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78: sp:plant:  
79: sp:rodent:  
80: sp:virus:  
81: sp:vertebrate:  
82: sp:unclassified:  
83: sp:virus:  
84: sp:bacteriophage:  
85: sp:archaea:  
86: sp:archaea:  
87: sp:bacteria:  
88: sp:fungi:  
89: sp:human:  
90: sp:invertebrate:  
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93: sp:organelle:  
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108: sp:mammal:  
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110: sp:organelle:  
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147: sp:rodent:  
148: sp:virus:  
149: sp:vertebrate:  
150: sp:unclassified:  
151: sp:virus:  
152: sp:bacteriophage:  
153: sp:archaea:  
154: sp:archaea:  
155: sp:bacteria:  
156: sp:fungi:  
157: sp:human:  
158: sp:invertebrate:  
159: sp:mammal:  
160: sp:phage:  
161: sp:organelle:  
162: sp:phage:  
163: sp:plant:  
164: sp:rodent:  
165: sp:virus:  
166: sp:vertebrate:  
167: sp:unclassified:  
168: sp:virus:  
169: sp:bacteriophage:  
170: sp:archaea:  
171: sp:archaea:  
172: sp:bacteria:  
173: sp:fungi:  
174: sp:human:  
175: sp:invertebrate:  
176: sp:mammal:  
177: sp:phage:  
178: sp:organelle:  
179: sp:phage:  
180: sp:plant:  
181: sp:rodent:  
182: sp:virus:  
183: sp:vertebrate:  
184: sp:unclassified:  
185: sp:virus:  
186: sp:bacteriophage:  
187: sp:archaea:  
188: sp:archaea:  
189: sp:bacteria:  
190: sp:fungi:  
191: sp:human:  
192: sp:invertebrate:  
193: sp:mammal:  
194: sp:phage:  
195: sp:organelle:  
196: sp:phage:  
197: sp:plant:  
198: sp:rodent:  
199: sp:virus:  
200: sp:vertebrate:  
201: sp:unclassified:  
202: sp:virus:  
203: sp:bacteriophage:  
204: sp:archaea:  
205: sp:archaea:  
206: sp:bacteria:  
207: sp:fungi:  
208: sp:human:  
209: sp:invertebrate:  
210: sp:mammal:  
211: sp:phage:  
212: sp:organelle:  
213: sp:phage:  
214: sp:plant:  
215: sp:rodent:  
216: sp:virus:  
217: sp:vertebrate:  
218: sp:unclassified:  
219: sp:virus:  
220: sp:bacteriophage:  
221: sp:archaea:  
222: sp:archaea:  
223: sp:bacteria:  
224: sp:fungi:  
225: sp:human:  
226: sp:invertebrate:  
227: sp:mammal:  
228: sp:phage:  
229: sp:organelle:  
230: sp:phage:  
231: sp:plant:  
232: sp:rodent:  
233: sp:virus:  
234: sp:vertebrate:  
235: sp:unclassified:  
236: sp:virus:  
237: sp:bacteriophage:  
238: sp:archaea:  
239: sp:archaea:  
240: sp:bacteria:  
241: sp:fungi:  
242: sp:human:  
243: sp:invertebrate:  
244: sp:mammal:  
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1043: sp:mammal:  
1044: sp:phage:  
1045: sp:organelle:  
1046: sp:phage:  
1047: sp:plant:  
1048: sp:rodent:  
1049: sp:virus:  
1050: sp:vertebrate:  
1051: sp:unclassified:  
1052: sp:virus:  
1053: sp:bacteriophage:  
1054: sp:archaea:  
1055: sp:archaea:  
1056: sp:bacteria:  
1057: sp:fungi:  
1058: sp:human:  
1059: sp:invertebrate:  
1060: sp:mammal:  
1061: sp:phage:  
1062: sp:organelle:  
1063: sp:phage:  
1064: sp:plant:  
1065: sp:rodent:  
1066: sp:virus:  
1067: sp:vertebrate:  
1068: sp:unclassified:  
1069: sp:virus:  
1070: sp:bacteriophage:  
1071: sp:archaea:  
1072: sp:archaea:  
1073: sp:bacteria:  
1074: sp:fungi:  
1075: sp:human:  
1076: sp:invertebrate:  
1077: sp:mammal:  
1078: sp:phage:  
1079: sp:organelle:  
1080: sp:phage:  
1081: sp:plant:  
1082: sp:rodent:  
1083: sp:virus:  
1084: sp:vertebrate:  
1085: sp:unclassified:  
1086: sp:virus:  
1087: sp:bacteriophage:  
1088: sp:archaea:  
1089: sp:archaea:  
1090: sp:bacteria:  
1091: sp:fungi:  
1092: sp:human:  
1093: sp:invertebrate:  
1094: sp:mammal:  
1095: sp:phage:  
1096: sp:organelle:  
1097: sp:phage:  
1098: sp:plant:  
1099: sp:rodent:  
1100: sp:virus:  
1101: sp:vertebrate:<

```

RS Zea mays (Maize).
RC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
RD Spermatophyta; Magnoliophyta; Liliopsida; Poales; Rubrales;
RE PACCAN clade; Ranunculales; Ranunculaceae; Zed.
RF NCBI_TaxID=4577;
RG (1)
RH
RI
RJ
RK
RL
RM
RN
RO
RQ
RSEQUENCE 5 AA: 977 MW: 505541201AAAS CR34.

Query Match 40.4% Score 19 DB 10 Length 7
Best Local Similarity 42.9% Pred. No. 8.3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDG 7
DB 2 KODVNC 8

RESULT 3
CQ9285 PRELIMINARY; PRT; 4 AA.
ID CQ9285
AC CQ9285
DT 01-OCT-2000 (TREMURel: 15, Created:
DT 01-OCT-2000 (TREMURel: 15, Last sequence update:
DT 01-OCT-2000 (TREMURel: 15, Last annotation update:
DE Cloning factor VIII (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Shihara M., Saito M., Morishika S., Yoshida A.,
RT Human cloning factor VIII gene: function regions of the deletion of
RT exon 4 through 7.
RI Submitted (MAR 2000) to the EMBL/GenBank/DBCP databases.
DR EMBL; ABC40872; BAA94312.1
DT NON_TER 1 1
FT NON_TER 4 8
SQ SEQUENCE 8 AA: 866 MW: 101654455DQVLS CR34.

Query Match 36.3% Score 19 DB 10 Length 7
Best Local Similarity 100.0% Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDG 3
DB 4 EDG 4

RESULT 4
CQ9285 PRELIMINARY; PRT; 4 AA.
ID CQ9285
AC CQ9285
DT 01-MAY-2000 (TREMURel: 13, Created:
DT 01-MAY-2000 (TREMURel: 13, Last sequence update:
DT 01-JUN-2002 (TREMURel: 21, Last annotation update:
DE 18 kDa cell growth factor (Fragment)
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Clamata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE
RA
RI
RJ
RK
RL
RM
RN
RO
RQ
RSEQUENCE 920.897% PubMed=1656970;

```

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RA Milner P.G.;
RT "Simian sarcoma virus transformation of normal rat kidney fibroblasts
RT is associated with markedly increased basic fibroblast growth factor
RT expression."
RL Biochem. Biophys. Res. Commun. 190:423-430(1991).
RT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 807 MW: 8787AA06767JAPA CR64;

Query Match 46.2% Score 17 DB 10 Length 8;
Best Local Similarity 100.0% Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDG 3
DB 5 EDG 7

RESULT 5
Q90493 PRELIMINARY; PRT; 8 AA.
ID Q90493
AC Q90493
DT 01-NOV-1996 (TREMURel: 11, Created:
DT 01-NOV-1996 (TREMURel: 11, Last sequence update:
DT 01-NOV-1996 (TREMURel: 11, Last annotation update:
DE Myoglobin (fragment)
OS Mus musculus (House mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Petroicidae; Eopsaltria
OX NCBI_TaxID=44319;
RN (1)
RP SEQUENCE FROM N.A.
RA Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;
RT Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae
RT assessed by temperature gradient Gel electrophoresis.
RL Electrophoresis 14:142-151(1998).
DR EMBL; J40495; AAC50362.1
DT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 921 MW: C6CA82DAF5R0450R CR64;

Query Match 34.0% Score 16 DB 10 Length 8;
Best Local Similarity 50.0% Pred. No. 8.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 QWQVNC 9
DB 2 QVXVNC 7

RESULT 6
Q42452 PRELIMINARY; PRT; 9 AA.
ID Q42452
AC Q42452
DT 01-NOV-1996 (TREMURel: 11, Created:
DT 01-NOV-1996 (TREMURel: 11, Last sequence update:
DT 01-OCT-2002 (TREMURel: 22, Last annotation update:
DE Heat shock protein (Fragment)
OS HSP26.7; OR HSP26.02
OC Triticum aestivum (Wheat)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spelmatoxyla; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Triticeae; Triticeae
OX NCBI_TaxID=4565;
RN (1)
RP SEQUENCE FROM N.A.
RA Coshi C.P., Kiew N., Nguyen H.T.;
RI Submitted (APR 1995) to the EMBL/GenBank/DBCP databases.
DR EMBL; L41844; AAA4972.1
DT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA: 866 MW: 101654455DQVLS CR34.

```

KW Heat shock.  
 PT NON-TER  
 QC SEQUENCE 9 AA; 1084 MW; 46582122CAAA04203 CRC64;

Query March 34.0%; Score 15; DB 10; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 4 QWMDV 8  
 DB 2 KVIDW 6

RESULT 9  
 Q50812 Q9N6M5 PRELIMINARY; PRT; 4 AA;  
 ID Q50812  
 AC Q50812  
 DT 01-NOV-1996 (TRENBLER: 31, Created)  
 DT 01-NOV-1996 (TRENBLER: 31, Last sequence update)  
 DT 01-NOV-1996 (TRENBLER: 31, Last annotation update)  
 DE Intergenic AT-rich DNA sequence (Fragment).  
 OS Methanococcus voltae.  
 CC Archaea; Euryarchaeota; Methanococci; Methanococcoides;  
 CC Methanococcaceae; Methanococcus.  
 NX NCBI\_TaxID:2188;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC BELLINGRUP-85330582; PubMed=4006307;  
 RA Bollingweller C., Kuehn P., Klein A.  
 PT "Non-repetitive AT-rich sequences are found in intergenic regions of  
 Methanococcus voltae DNA".  
 EVBIO J. 4:1805-1810 (1983).  
 EVBL XC2518; CAA26355.1;  
 FT NON-TER 9  
 SQ SEQUENCE 9 AA; 1087 MW; 95ED806DC404412A CRC64;

Query March 31.9%; Score 15; DB 10; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 6 MWDV 9  
 DB 1 MFIN 4

RESULT 9  
 P72149 Q9N6M5 PRELIMINARY; PRT; 4 AA;  
 ID P72149  
 AC P72149  
 DT 01-FEB-1997 (TRENBLER: 32, Created)  
 DT 01-FEB-1997 (TRENBLER: 32, Last sequence update)  
 DT 01-FEB-2001 (TRENBLER: 19, Last annotation update)  
 DE Putative glucokinase (Fragment).  
 OS GLX  
 CC Bacteroides aeruginosa.  
 CC Bacteriia; Proteobacteria; Gammaproteobacteria; Bacteroidales;  
 CC Bacteroidaceae; Bacteroides.  
 NX NCBI\_TaxID:287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN PAO1;  
 RA MEDLINE=96427144; PubMed=8830308;  
 RA Sage A.E., Proctor W.D., Phibbs P.V.  
 PT "A two-component response regulator, BTEF, is required for glucose  
 transport activity in Pseudomonas aeruginosa PAO1".  
 RA J. Bacteriol. 178:6564-6566 (1996).  
 EVBIO US0912; AA:44474.1;  
 EVBL K01010; C10710CAAAC016 CRC64;  
 FT NON-TER 1  
 SQ SEQUENCE 9 AA; 944 MW; C10710CAAAC016 CRC64;

Query March 31.9%; Score 15; DB 10; Length 9;  
 Best Local Similarity 33.3%; Pred. No. 9.3e+05;

Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 CY 4 QWMDV 9  
 DB 3 QALDAE 8

RESULT 9  
 Q9N6M5 Q9N6M5 PRELIMINARY; PRT; 8 AA;  
 ID Q9N6M5  
 AC Q9N6M5  
 DT 01-OCT-2000 (TRENBLER: 15, Created)  
 DT 01-OCT-2000 (TRENBLER: 15, Last sequence update)  
 DT 01-OCT-2000 (TRENBLER: 15, Last annotation update)  
 DE Dihydrofolate reductase (Thymidylate synthase (Fragment)).  
 OS POLI.  
 CC Toxoplasma gondii.  
 CC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimerida; Sarcocystidae;  
 CC Toxoplasma  
 NX NCBI\_TaxID:5811;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RH; COUGAR T031014; SEA OTTER T082801; and BEVERLEY;  
 RA Lehmann C., Blackston C.R., Pamley S.F., Remington J.S., Dubey J.P.  
 PT "Strain Typing of Toxoplasma gondii: Comparison of Antigen-Coding and  
 RT Housekeeping Genes".  
 RA J. Parasitol. 91: 612-620.  
 DR ENBL; AF249695; AAF79153.1;  
 DR ENBL; AF249692; AAF79150.1;  
 DR ENBL; AF249693; AAF79151.1;  
 DR ENBL; AF249694; AAF79152.1;  
 FT NON-TER 8  
 FT NON-TER 9  
 SQ SEQUENCE 8 AA; 1015 MW; 33CAAAAC5B131044 CRC64;

Query March 39.8%; Score 14; DB 5; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 6.3e+05;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

CY 4 QWMDV 8  
 DB 1 RKEID 6

RESULT 10  
 Q42507 Q9N6M5 PRELIMINARY; PRT; 8 AA;  
 ID Q42507  
 AC Q42507  
 DT 01-NOV-1996 (TRENBLER: 33, Created)  
 DT 01-NOV-1996 (TRENBLER: 31, Last sequence update)  
 DT 01-OCT-2002 (TRENBLER: 32, Last annotation update)  
 DE Heat shock protein (Fragment).  
 CC HSP70 OR HSP72A OR HSP70S.  
 OS Triticum aestivum (Wheat).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;  
 CC Triticeae; Triticum.  
 NX NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV MUSTANG;  
 RX MEDLINE=96189275; PubMed=8605112;  
 RA Joshi C.P., Kumar S., Nguyen H.T.  
 PT "Application of modified differential display technique for cloning  
 RT and sequencing of the 3' region from three putative members of wheat  
 HSP70 Gene family".  
 RA Plant Mol. Biol. 30:641-646 (1996).  
 DR ENBL; L41507; AABR2333.1;  
 DR ENBL; L41506; AABR2331.1;  
 DR ENBL; L41506; AABR2332.1;  
 KW Heat shock.  
 FT NON-TER 1  
 SQ SEQUENCE 8 AA; 840 MW; VHBGVH101512766 CRC64;



Query Match 29.8% Score 147 DB 10 Length 81  
 Best Local Similarity 33.3% Pred. NO. 8.3e+05;  
 Matches 27 Conservative 3; Mismatches 1; Indels 0;

QY 4 QNDVD 9  
 DB 3 KNEVD 4

## RESULT 11

Q94953 PRELIMINARY; PRT; 9 AA.  
 AC Q88953;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update;  
 DT 01-NOV-1998 (TrEMBLrel. 06, Last annotation update;  
 DE Scfins (Fragment);  
 GN B13R/SRI-2;  
 OS Vaccinia virus  
 CC Viruses; USNA viruses, no RNA stage, Poxviridae; Orthopoxvirinae;  
 CC Orthopoxvirus  
 CX NCBI TaxID:102457;  
 RN 1;  
 SP SEQUENCE FROM N.A.  
 RX MEDLINE:9531144; PubMed:7431769;  
 FA Kettle S., Blake N.W., Law K.M., Smith G.D.;  
 FT "Vaccinia virus serpins B13R (SPI 2) and B13R (SPI 1) encode with 18.5  
 RT and 40K, intracellular polypeptides that do not affect virus virulence  
 RI in a guinea hiracass model";  
 RL Virology 256:147-147(1995);  
 FR EMBL: S75134; AA:G0736.1;  
 FT NCN TER 9  
 SQ SEQUENCE 9 AA; 138 MW; 9594D00040905A CR664.

Query Match 29.8% Score 147 DB 12 Length 81  
 Best Local Similarity 66.7% Pred. NO. 8.3e+05;  
 Matches 27 Conservative 1; Mismatches 0; Indels 0;

QY 6 QNDV 8  
 DB 1 MOI 3

## RESULT 12

Q1594 PRELIMINARY; PRT; 8 AA.  
 AC Q1594;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update;  
 DT 01-FEB-2001 (TrEMBLrel. 19, Last annotation update;  
 DE VOPR protein (Fragment);  
 GN Escherichia coli;  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Escherichia;  
 CX NCBI TaxID 562;  
 RN 1;  
 SP SEQUENCE FROM N.A.  
 RX MEDLINE:8623322; PubMed:2423502;  
 FA Weber P.C., Palcaudhuri S.;  
 FT "Incompatibility repressor in a *topA* like replication of the *trfA*;  
 RT Plasmid COV2-K94";  
 RL J. Bacteriol. 166:1116-112(1984);  
 FR EMBL: M13472; AA:Q1194.1;  
 FT NCN TER 1  
 SQ SEQUENCE 8 AA; 998 MW; 0F3705AA 64707 CR664.

Query Match 27.7% Score 147 DB 21 Length 81  
 Best Local Similarity 40.0% Pred. NO. 8.3e+05;  
 Matches 27 Conservative 2; Mismatches 1; Indels 0;

QY 4 QNDV 8  
 DB 2 QRLD1 6

## RESULT 13

Q9UB13 PRELIMINARY; PRT; 8 AA.  
 AC Q9UB13;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update;  
 DE Calmodulin (Fragment);  
 OS Aibinaria hippolyti;  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 CC Sigmurethra; Clausilioides; Clausiliidae; Alopinae; Aibinaria;  
 CX NCBI TaxID:69418;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RA Schilthuisen M., Houkstra W.P., Gittenberger E.;  
 RT "Selective maintenance of a rare haplotype in a land snail hybrid  
 zone";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 266:218-2185(1999);  
 DR EMBL: AF132316; AA:Q3486.1;  
 FT NCN TER 1  
 FT NCN TER 5  
 SQ SEQUENCE 8 AA; 406 MW; FVADIA83CH144356 CR664.

Query Match 27.7% Score 147 DB 5 Length 81  
 Best Local Similarity 40.0% Pred. NO. 8.3e+05;  
 Matches 27 Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 VQVD 4  
 DB 2 INEVD 6

## RESULT 14

Q94695 PRELIMINARY; PRT; 8 AA.  
 AC Q94695;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update;  
 DE Actin (Fragment);  
 GN ARDC;  
 OS Physarum polycephalum (slime mold);  
 CC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;  
 CC Physarum;  
 CX NCBI TaxID 5731;  
 RN 1;  
 PP SEQUENCE FROM N.A.  
 RX MEDLINE:9618218; PubMed:8622700;  
 RA Beard M., Lagna G., Pallotta D., Pierron G.;  
 RT "Mapping of a replication origin within the promoter region of two  
 RT unlinked, abundantly transcribed actin genes of Physarum  
 RT polycephalum";  
 RL Mol. Cell. Biol. 15:968-976(1996);  
 DR EMBL: M73459; AA:Q3706.1;  
 FT NCN TER 8  
 SQ SEQUENCE 8 AA; 978 MW; F4C6C2CAAB197B16 CR664.

Query Match 27.7% Score 147 DB 5 Length 81  
 Best Local Similarity 75.0% Pred. NO. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDO 4  
 DB 4 EDVQ 2

## RESULT 15

Q51765

```
ID C51765 PRELIMINARY; PRT; 9 AA.
AC
AG 05-765.
CI NOV-1996 (TREVBLREL_01, Created)
CC C1-NOV-1996 (TREVBLREL_01, Last sequence update)
CU C1-DEC-2001 (TREVBLREL_19, Last annotation update)
FE Unknown ORF (fragment).
GI Pseudomonas fluorescens
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
CX NCBI_TaxID:2947
IL
PN
PP SEQUENCE FROM N.A.
PX MEDLINE:9013284; Pubmed:2515251.
RA Benen J.A., Van Belkai W.J., Van Dongen W.M., Miller P., De Ruk A.;
RI "Molecular cloning and sequence determination of the 17d gene encoding
RI 1-epicamide dehydrogenase from Pseudomonas fluorescens";
RL J. Gen. Microbiol. 135:1787-1797(1989).
DR EVRI: M28156; AAA9233.1
RT NCN_188
SQ SEQUENCE 9 AA; 101 MW; 269ENV272734CDS1 (P064).

Query Match 27.71; Score 13; DB 2; Length 9.
Best local similarity 50.08; Pred. NC: 9.3e-05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 5 VMDV 9
CG 4 LLDV 9

Search completed: November 5, 2003, 17:14:04
CPU time : 16 sec
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

Query protein: protein search, using sw model

Run on: November 5, 2003, 17:53:52 : Search time 41 seconds  
(without alignments)  
34,842 Million cell updates/sec

Title: US 09 324-088-1

Perfect score: 49

Sequence: 1 EFGGMDVD 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 110783 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 176625

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Genes7 19Jun03.\*

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24	/SID1/gcgdata/geneseq/geneseqp-emb/AA1982.DAT*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	9	21	Immunoglobulin E
2	47	100.0	9	21	zeta C-reson-2 do
3	47	100.0	9	22	peptide-P1 derived
4	47	100.0	9	22	the peptide #1, M
5	47	100.0	9	23	Human IgE immunoge
6	47	100.0	9	23	Human immunoglobul
7	47	100.0	9	23	Human immunoglobul
8	47	100.0	9	23	Human immunoglobul
9	47	100.0	9	23	Human immunoglobul

10	30	63.8	9	24	AAE35076
11	28	59.6	7	23	AAE14481
12	28	59.6	9	23	ABJ12821
13	26	55.3	9	24	AAE35101
14	25	53.2	9	23	ABG67564
15	25	53.2	9	24	AAE35082
16	23	48.9	8	17	AAE8589
17	23	48.9	9	13	AAE29631
18	23	48.9	9	13	AAE35433
19	23	48.9	9	13	AAE28886
20	22	46.6	6	20	AAE42592
21	22	46.6	7	21	AAE61729
22	22	46.6	7	23	AAU91643
23	22	46.6	8	21	AAE61785
24	22	46.6	9	20	AAE48666
25	22	46.6	9	20	AAE00372
26	22	46.6	9	21	AAE61798
27	22	46.6	9	23	ABJ13116
28	22	46.6	9	23	ABJ13116
29	22	46.6	9	24	ABJ20192
30	21	44.7	7	19	AAE63724
31	21	44.7	8	23	AAE25317
32	21	44.7	9	18	AAW15176
33	21	44.7	9	19	AAW0838
34	21	44.7	9	20	AAE30292
35	21	44.7	9	21	AAE33468
36	21	44.7	9	22	AEJ53963
37	21	44.7	9	22	AAJ71987
38	21	44.7	9	22	AAE11010
39	21	44.7	9	22	AAE43428
40	21	44.7	9	22	AAE24564
41	21	44.7	9	22	AAE24549
42	21	44.7	9	22	AAE24760
43	21	44.7	9	22	AAE24341
44	21	44.7	9	22	AAE24361
45	21	44.7	9	22	AAE25563

#### ALIGNMENTS

RESULT 1  
AAB23867  
ID AAB23867 standard; peptide; 9 AA.  
XX AAB23867; AC  
XX C1-JAN-2001 (first entry)  
XX  
XX  
XX Immunoglobulin E epitope immunogenic peptide SEQ ID NO:5.  
XX Immunoglobulin E IgE, immunogenic; immunogen; Protein D, carrier;  
KW prostate cancer; Haemophilus influenzae; vaccine; infectious disease;  
KW malaria; cytostatic; anti-allergy; C; noctropic; neuroprotective;  
KW protozoicide; Alzheimer's disease; allergy.  
XX  
XX Homo sapiens  
XX  
XX WC200505077-A1.  
XX  
XX 31-AUG-2000.  
XX  
XX 22-FEB-2000; 2000WG EP01457.  
XX  
XX 25-FEB-1999; 99GB-2004425.  
XX 25-FEB-1999; 99GB-2004428.  
XX 25-FEB-1999; 99GB-2004412.  
XX 13-AUG-1999; 99GB-0019260.  
XX  
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
XX Coste M, Lobet Y, Van Mechelen NP, Verriest G;



IR WPI: 2001-521967/57.  
 XX A linkage comprising an immunogenic conjugate useful for treatment of IGE  
 PT mediated diseases.  
 XX  
 XX Example 4; Page 21; 49pp; English.  
 XX The present invention relates to linkage methodology for use in the  
 XX conjugation of compounds (e.g. peptides) to carrier vehicles  
 XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 XX biological and immunological constructs. The invention provides a  
 XX method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 XX protein) for use in a pharmaceutical composition or a vaccine. The  
 XX invention describes peptides derived from or mimotopes of the  
 XX Cepsillon2, Cepsillon3 or Cepsillon4 regions of human immunoglobulin E  
 XX (IgE) which are used to produce conjugated compounds. The compounds or  
 XX conjugations of the invention are useful in the manufacture of a  
 XX medicament for the treatment of IGE-mediated diseases. The invention  
 XX allows for controlled conjugation of a peptide epitope designed to a  
 XX protein so as to form an immunogenic conjugate which may be able to  
 XX raise a protective antibody response in an animal or human patient.  
 XX AA016632-AA016913 represent peptides derived from or mimotopes of  
 XX the Cepsillon2/Cepsillon3/Cepsillon4 region of human IgE.  
 XX  
 XX Sequence 9 AA:  
 XX  
 XX Query Match 100.0%; Score 47; DB 22; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 EDGQVMQVD 9  
 XX | | | | |  
 XX Db 1 EDGQVMQVD 9  
 XX  
 XX RESULT 4  
 XX AA051023  
 XX ID AA051023 standard; Peptide: 9 AA.  
 XX AC AA051023;  
 XX  
 XX DT 21-MAR-2001 (first entry)  
 XX  
 XX DE IGE peptide #1.  
 XX  
 XX KW Vaccine; immunoglobulin E; IgE; anti-allergy.  
 XX  
 XX OS Mammalia  
 XX  
 XX PN WC00004716 AA.  
 XX  
 XX FD 14-DEC-2000.  
 XX  
 XX FF 06-JUN-2000; 2000WO-EP05164.  
 XX  
 XX TP 08-JUN-1999; 93JP-0013327.  
 XX  
 XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 XX PT Priority 3;  
 XX  
 XX DR WPI: 2001-031150/10.  
 XX  
 XX PT New vaccine comprising allergy peptides linked by an inert carrier,  
 XX useful for boosting an anti-allergy immune response in an individual  
 XX susceptible to an allergic response.  
 XX  
 XX PS Claim 5; Page 20; 26pp; English.  
 XX  
 XX CC The present invention relates to a conjugation comprising allergy  
 XX peptides linked by an inert carrier. The allergy peptides are derived  
 XX from immunoglobulin E (IgE) or IgE receptor. The present peptide is one  
 XX such peptide from IgE. The composition is useful as a vaccine or for

CC manufacturing a medicament for the prophylaxis or treatment of allergy.  
 CC In particular, for boosting an anti-allergy immune response in an  
 CC individual susceptible to an allergic response.  
 XX  
 XX Sequence 9 AA:  
 XX  
 XX Query Match 100.0%; Score 47; DB 22; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 EDGQVMQVD 9  
 XX | | | | |  
 XX Db 1 EDGQVMQVD 9  
 XX  
 XX RESULT 5  
 XX ABJ00217  
 XX ID ABJ00217 standard; Peptide: 9 AA.  
 XX AC ABJ00217;  
 XX  
 XX DT 02-SEP-2002 (first entry)  
 XX  
 XX DE Human IgE immunogenic peptide SEQ ID NO: 1.  
 XX  
 XX KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 XX vaccine; anti-allergic.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PN WC000216409 AA.  
 XX  
 XX FD 28-FEB-2002.  
 XX  
 XX FF 17-AUG-2001; 2001WO-EP09376.  
 XX  
 XX ER 22-AUG-2000; 2000GB-0020117.  
 XX  
 XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 XX PI Friede M, Nason S, Turnell WG, Vinals Bassols YC;  
 XX  
 XX DR WPI: 2002-489648/52.  
 XX  
 XX PT Conjugate for use in vaccine for treatment of allergy, comprises  
 XX disulfide bridge cyclized peptide and immunogenic carrier.  
 XX  
 XX PS Claim 4; Page 9; 45pp; English.  
 XX  
 XX CC The present invention relates to conjugates suitable for use in vaccines,  
 XX where the conjugate comprises a disulphide bridge cyclized peptide and an  
 XX immunogenic carrier. The vaccines can be used in the treatment of  
 XX allergies. The present sequence is a peptide immunogen derived from human  
 XX immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
 XX  
 XX Sequence 9 AA:  
 XX  
 XX Query Match 100.0%; Score 47; DB 23; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 EDGQVMQVD 9  
 XX | | | | |  
 XX Db 1 EDGQVMQVD 9  
 XX  
 XX RESULT 6  
 XX AAE35091  
 XX ID AAE35091 standard; peptide: 9 AA.  
 XX AC AAE35091;  
 XX  
 XX

DT 28-MAY-2003 (first entry)  
 XX Human immunoglobulin E (IgE) HLA A2 peptide motif #23.  
 XX  
 XX Cytotoxic T lymphocytes; CTLs; tumour; antigen presenting cells; allergy;  
 XX lupus; autoimmune disease; rheumatoid arthritis; autoimmune hepatitis;  
 XX psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever;  
 XX inflammatory bowel disease; insulin dependent diabetes; cell therapy;  
 XX Crohn's disease; allergic rhinitis; graft versus host disease; asthma;  
 XX transplant rejection; human; immunoglobulin E; IgE.  
 XX  
 XX Homo sapiens  
 XX  
 XX WO200232773 A2.  
 XX  
 XX 21-NOV-2002  
 XX  
 XX 13-MAY-2002; 2002WC US5341.  
 XX  
 XX 15 MAY 2001; 2001US-29130P.  
 XX  
 XX (ORIGIN: ORTHO-MONOCILL PHARM INC.  
 XX  
 XX Cat Z, Jackson MR, Peterson PA, Shi W, Kono Y, Degraw G  
 XX  
 XX WPI; 2002 125671/11.  
 XX  
 XX Producing cytotoxic T lymphocytes for treating auto-immune  
 XX diseases, comprises culturing CD8+ T cells with antigen presenting  
 XX cells to activate precursor CD8+ T cells specific for T cell  
 XX epitopes  
 XX  
 XX Example 3; Colburn 48, 49pp; English.  
 XX  
 XX The invention relates to a method of producing cytotoxic T lymphocytes  
 XX (CTLs) specific for one or more non-tumour self antigen T cell epitopes.  
 XX The method involves loading antigen presenting cells (APCs) having class  
 XX II major histocompatibility complex molecules with the T cell epitopes,  
 XX and culturing the CD8+ T cells with the APCs to activate precursor CD8+  
 XX T cells specific for the T cell epitopes. The invention is useful for  
 XX treating autoimmune disease including rheumatoid arthritis, psoriasis,  
 XX lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,  
 XX insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
 XX graft versus host disease and transplant rejection and/or allergic  
 XX disease such as food allergy, hay fever, allergic rhinitis, allergic  
 XX asthma and venom allergy. The invention is also useful in cell therapy.  
 XX The present sequence is human immunoglobulin E (IgE) HLA A2 peptide  
 XX motif. This peptide is used in the exemplification of the invention.  
 XX  
 XX Sequence 9 AA:  
 XX  
 XX Query Match 66.0%; Score 11; DB 04; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY : EDGQXX #  
 XX | | | | |  
 XX Db 4 EDGQXX 4  
 XX  
 XX RESULT 7  
 XX AAB25923  
 XX ID AAB25923 standard; Peptide: 7 AA.  
 XX  
 XX AC AAB25923;  
 XX  
 XX 05-JUN-2001 (first entry)  
 XX  
 XX F1 mimotope peptide P15s SEQ ID NO:17.  
 XX  
 XX Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;  
 XX allergic disease; immunoprecipitation; immunotherapy; anti-allergic;  
 XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;

KW allergy; atopy.  
 XX  
 XX OS  
 XX Homo sapiens.  
 XX  
 XX WO2002050460 A1.  
 XX  
 XX 31 AUG-2000.  
 XX  
 XX 22-FEB-2000; 2000WO-EP01455.  
 XX  
 XX 25-FEB-1999; 99GB-0004405.  
 XX  
 XX 23-MAR-1999; 99GB-0007151.  
 XX  
 XX 07-MAY-1999; 99GB-0010537.  
 XX  
 XX 07-MAY-1999; 99GB-0010538.  
 XX  
 XX 07-AUG-1999; 99GB-0018594.  
 XX  
 XX 07-AUG-1999; 99GB-0018603.  
 XX  
 XX 07-SEP-1999; 99GB-0021046.  
 XX  
 XX 07-SEP-1999; 99GB-0021047.  
 XX  
 XX 29-OCT-1999; 99GB-0025619.  
 XX  
 XX 23-NOV-1999; 99GB-0027698.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 XX Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;  
 XX Randall F, Turnell WG, Van Mechelen MP, Vinals De Bassols YC;  
 XX  
 XX WPI; 2002-572073/53.  
 XX  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 XX diseases, comprising an isolated surface exposed group of a specific  
 XX domain from immunoglobulin E -  
 XX  
 XX Example 7; Page 35; 129pp; English.  
 XX  
 XX The present invention describes a peptide (I), comprising an isolated  
 XX surface exposed group/epitope (a) of C-epsilon-2 domain (D) of  
 XX immunoglobulin E (IgE), or its mimotope. Also described are: (i) an  
 XX immunogen (ii) for treating allergy comprising (i); (2) a vaccine (iii)  
 XX for treating allergies comprising (ii); (3) a ligand (iv) capable of  
 XX recognising E1; (4) a pharmaceutical composition (v) comprising (i);  
 XX (5) a peptide (ia) capable of being recognised by (iv); (6) an immunogen  
 XX (ila) comprising (ia), and (7) producing (iii) by producing (ii). (7)  
 XX can have anti-allergic and immunosuppressive activities, and can be used  
 XX as a vaccine and histamine release inhibitor. (ii), (iii) and (iv) are  
 XX useful in medicine and in the manufacture of medicaments for treating  
 XX and preventing allergies. (iv) is useful for identifying mimotopes of E1.  
 XX in medicine and also in manufacturing medicaments for treating  
 XX allergies. (ii) is useful in diagnostics and in the affinity purification  
 XX of circulating anti-IgE antibodies from blood. (ii), (iii) and (iv) are  
 XX useful for treating a patient susceptible to or suffering from allergies.  
 XX (iv) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
 XX peptide sequences which are used in the exemplification of the present  
 XX invention.  
 XX  
 XX Sequence 7 AA.  
 XX  
 XX Query Match 63.0%; Score 10; DB 21; Length 7;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 4 QVMEVD 9  
 XX | | | | |  
 XX Db 1 QVMEVD 6  
 XX  
 XX RESULT 8  
 XX AAU16648  
 XX ID AAU16648 standard; Peptide: 7 AA.  
 XX  
 XX AC AAU16648;  
 XX  
 XX 07-NOV-2001 (first entry)

XX DE Peptide P115 derived as mimotope of Cepsilon2 region of human IgE.  
 XX KW Human linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX CS Homo sapiens  
 OS Synthetic.  
 XX PN WO200145745 A2.  
 XX PD 24 JUN-2002.  
 XX PF 21-DEC-2000; 2000WG-GR04935.  
 XX FR 21-FEB-1999; 93GB 0032233.  
 XX PR 22 FEB-2000; 2000GB-0004098.  
 XX FR 22 AUG-2000; 2000GB-0020707.  
 XX FR 22 AUG-2000; 2000GB-0003708.  
 XX PA ACAM-1 ACAM-1 RES LTD.  
 XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX PI Flynn N, Johnson T;  
 XX WI WIPI; 2001-521767/57.  
 XX PT A linkage comprising an immunogenic conjugate useful treatment of IgE mediated diseases.  
 XX PS Example 4; Page 21; 48pp; English.  
 XX CC The present invention relates to linkage methodology for use in the conjugation of compounds (e.g. peptides) to carrier vehicles (e.g. macromolecules, polymers, dendrimers, proteins) to produce biological and immunological constructs. The invention provides a method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition or a vaccine. The invention describes peptides derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E (IgE) which are used to produce conjugated compounds. The compounds or compositions of the invention are useful in the manufacture of a medicament for the treatment of IgE mediated diseases. The invention allows for controlled conjugation of a peptide epitope (antigen) to a protein so as to form an immunogenic conjugate which may be able to raise a protective antibody response in an animal or human patient. AA016632 (AA01691) represent peptides derived from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX SQ Sequence 7 AA;  
 Query Match 63.8%; Score 30; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 QVMDVD 9  
 Db |||||  
 : QVMDVD 6  
 RESULT 9  
 ABC02227  
 ID ABJ00227 standard; Peptide; 7 AA.  
 AC ARJ00227;  
 XX ARJ00227;  
 CC 02-SEP-2002 (first entry)  
 XX Human IgE immunogenic peptide SEQ ID NO: 11  
 DE Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 KW vaccine; anti-allergic.

XX OS Homo sapiens.  
 XX PN WO200216409 A2.  
 XX PD 28-FEB-2002.  
 XX PF 17-AUG-2001; 2001WG-EP09576.  
 XX PR 22-AUG-2000; 2000GB-0020717.  
 XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX PA (EPIT-) PEPTIDE THERAPEUTICS LTD.  
 XX PI Friede M, Mason S, Tutwell WG, Vinals Bassols YC;  
 XX WI WIPI; 2002-489648/52.  
 XX CC Conjugate for use in vaccine for treatment of allergy, comprises disulfide bridge cyclized peptide and immunogenic carrier.  
 XX PS Claim 4; Page 9; 48pp; English.  
 XX CC The present invention relates to conjugates suitable for use in vaccines, where the conjugate comprises a disulfide bridge cyclised peptide and an immunogenic carrier. The vaccines can be used in the treatment of allergies. The present sequence is a peptide immunogen derived from human immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
 XX SQ Sequence 7 AA;  
 Query Match 63.8%; Score 30; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 QVMDVD 9  
 Db |||||  
 : QVMDVD 6  
 RESULT 10  
 AA035076  
 ID AA035076 standard; peptide; 9 AA.  
 AC AA035076;  
 XX 28-MAY-2003 (first entry)  
 XX Human immunoglobulin E (IgE) HLA-A2 peptide motif #14.  
 KW Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy; lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis; psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever; inflammatory bowel disease; insulin dependent diabetes; cell therapy; Crohn's disease; allergic rhinitis; graft versus host disease; asthma; transplant rejection; human; immunoglobulin E; IgE.  
 XX OS Homo sapiens.  
 XX PN WO200292773-A2.  
 XX PD 21-NOV-2002.  
 XX PF 13-MAY-2002; 2002WO-US15341.  
 XX PR 15-MAY-2001; 2001US-291300P.  
 XX PA (ORTH) ORTHO-MCNEIL PHARM INC.  
 XX PI Cai Z, Jackson MP, Peterson PA, Shi W, Korg Y, Degraw C;  
 XX WI WIPI; 2003-120673/11.  
 XX

PT Producing cytotoxic T lymphocytes for treating e.g. autoimmune  
 PT diseases, comprises culturing CD8<sup>+</sup> T cells with antigen presenting  
 PT cells to activate precursor CD8<sup>+</sup> T cells specific for T cell  
 PT epitopes  
 PS Example 3; Column 47; 49pp; English.  
 XX The invention relates to a method of producing cytotoxic T lymphocytes  
 CC (CTLs) specific for one or more non-tumor self antigen T cell epitopes.  
 CC The method involves loading antigen presenting cells (APCs) having class  
 CC I major histocompatibility complex molecules with the T cell epitopes.  
 CC and culturing the CD8<sup>+</sup> T cells with the APCs to activate precursor CD8<sup>+</sup>  
 CC T cells specific for the T cell epitopes. The invention is useful for  
 CC treating autoimmune disease including rheumatoid arthritis, psoriasis,  
 CC lupus, autoimmune hepatitis, multiple sclerosis, autoimmune thyroiditis,  
 CC insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
 CC graft versus host disease and transplant rejection and/or allergic  
 CC disease such as food allergy, hay fever, allergic rhinitis, allergic  
 CC asthma and venom allergy. The invention is also useful in cell therapy.  
 CC The present sequence is human immunoglobulin E (IgE) HcA-A2 peptide  
 CC motif. This peptide is used in the exemplification of the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 63.8%; Score 30; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 QYQVMD 9  
 QV QVQVMD 9  
 DB 1 QYQVMD 9  
 RESULT 11  
 AAE1448;  
 ID AAE:4481 standard; Peptide; 7 AA  
 XX  
 AC AAE:4481;  
 DT 26-MAR-2002 (first entry);  
 XX  
 DE Ophiophorus gracilirostris luciferase 35 kDa subunit peptide.  
 XX  
 KW luciferase; deep sea luminous shrimp; decapoda; reporter enzyme;  
 KW 35 kDa subunit; photoprotein.  
 XX  
 OS Ophiophorus gracilirostris.  
 XX  
 PN EP1156:03 A2.  
 XX  
 PD 21 NOV-2001.  
 XX  
 PF 25-APR-2001; 2001EP-0109479.  
 XX  
 PP 26-APR-2000; 2000JP-0125053.  
 XX  
 PA (CHCC) CHISSO CORP.  
 XX  
 FI Inouye S;  
 XX  
 UR WPI; 2002 084319/12.  
 XX  
 PT Novel secretional luciferase derived from the deep sea luminous  
 PT shrimp Ophiophorus gracilirostris consists of 19kDa and 35 kDa subunits  
 PT and is useful as a reporter enzyme.  
 XX  
 PS Example 4; Page 11; 35pp; English.  
 XX The invention relates to polynucleotide encoding secretional luciferase  
 CC derived from deep sea luminous shrimp (Ophiophorus gracilirostris). The  
 CC luciferase protein is composed of 19 and 35 kDa proteins and  
 CC is useful as a reporter enzyme. Antibodies against luciferase and  
 CC oligonucleotides derived from luciferase polynucleotides are useful for

CC identification of novel luciferase or photoproteins from related  
 CC species. The present sequence is a peptide from 35 kDa  
 CC subunit of Ophiophorus gracilirostris luciferase.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 59.6%; Score 28; DB 23; Length 7;  
 Best Local Similarity 71.4%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 QYQVMD 9  
 QV QVQVMD 9  
 DB 1 QYQVMD 9  
 RESULT 12  
 ABJ1282;  
 ID ABJ1282; standard; Peptide; 9 AA.  
 XX  
 AC ABJ1282;  
 DT 10-DEC-2002 (first entry);  
 XX  
 DE Human 125P5C8 epitope #1447.  
 XX  
 KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;  
 KW bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200272785-A2.  
 XX  
 PD 19-SEP-2002.  
 XX  
 PF 13-MAR-2002; 2002WO-US07855.  
 XX  
 PP 14-MAR-2001; 2001US-CR09635.  
 XX  
 PA (AGEN) AGENSYS INC.  
 XX  
 PI Faris M, Chailita eld PM, Hubert RS, Afar DEH, Raitano AB, Ge W;  
 PI Morrison RK, Morrison K, Jakobovits A;  
 XX  
 DR WPI; 2002-713510/77.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 125P5C8 gene or a molecule that is modulated by 125P5C8. Useful for  
 PT treating or preventing cancer that expresses or over expresses 125P5C8  
 PT .  
 XX  
 PS Disclosure; Page 163; 274pp; English.  
 XX  
 CC The present invention relates to compositions comprising a substance that  
 CC modulates the status of 125P5C8 or a molecule that is modulated by  
 CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The  
 CC composition is useful for treating cancer, particularly prostate,  
 CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein  
 CC and/or a nucleotide sequence encoding the protein is useful for  
 CC immunising a mammal against cancer. The present sequence is a 125P5C8  
 CC epitope shown in the exemplification of the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 59.6%; Score 28; DB 23; Length 9;  
 Best Local Similarity 55.6%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 EGGQVMD 9  
 QV EGGQVMD 9  
 DB 1 EGGQVMD 9  
 RESULT 13



AAE5101:  
ID AAE5101 standard; peptide; 9 AA.  
XX  
XX  
XX AAE5101:  
XX  
XX 28-MAY-2003 (first entry)  
XX  
XX Human immunoglobulin E (IgE) HLA-A2 peptide motif #19.  
XX  
XX Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;  
XX Lupus; autoimmune disease; rheumatoid arthritis; autoimmune hepatitis;  
XX psoriasis; AIC; multiple sclerosis; autoimmune lymphocitis; hay fever;  
XX inflammatory bowel disease; insulin dependent diabetes mellitus therapy;  
XX Crohn's disease; allergic rhinitis; graft versus host disease; asthma;  
XX transplant rejection; human; immunoglobulin E; IgE  
XX  
XX Homo sapiens.  
XX  
XX WO200202773 A2.  
XX  
XX 21-NOV 2002.  
XX  
XX 15-MAY-2002; 2002WC-US15341.  
XX  
XX 15 MAY 2002; 2002US-291300P.  
XX  
XX (ORTH) ORTHO MCNEIL PHARM INC.  
XX  
XX Gal Z, Jackson KR, Peterson PA, Shi W, Kong Y, Deitrow J,  
XX WPI; 2003-120693/11.  
XX  
XX Producing cytotoxic T lymphocytes for treating e.g. autoimmune  
XX diseases, comprises culturing CD8+ T cells with antigen presenting  
XX cells to activate precursor CD8+ T cells specific for T cell  
XX epitopes.  
XX  
XX Example 3; Column 49; 49pp; English.  
XX  
XX The invention relates to a method of producing cytotoxic T lymphocytes  
XX which are specific for one or more tumour self antigen T cell epitopes.  
XX The method involves loading antigen presenting cells (APCs) having class  
XX I major histocompatibility complex molecules with the T cell epitopes,  
XX and culturing the CD8+ T cells with the APCs to activate precursor CD8+  
XX T cells specific for the T cell epitopes. The invention is useful for  
XX treating autoimmune disease including rheumatoid arthritis, psoriasis,  
XX lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,  
XX insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
XX graft versus host disease and transplant rejection and/or allergic  
XX disease such as food allergy, hay fever, allergic rhinitis, allergic  
XX asthma and venom allergy. The invention is also useful in cell therapy.  
XX The present sequence is human immunoglobulin E (IgE) HLA A2 peptide  
XX motif. This peptide is used in the exemplification of the invention.  
XX  
XX Sequence 9 AA:  
XX  
Query Match 55.1%; Score 24; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX : EGGGV 5  
XX 5 EGGGV 9  
XX  
XX  
XX RESULT 14  
XX AEG67564  
XX ID AEG67564 standard; Peptide; 9 AA.  
XX  
XX AEG67564:  
XX  
XX 07-DEC-2002 (first entry)  
XX  
XX

DE Human ADPI tryptic digest peptide #273.  
XX  
XX Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;  
XX Alzheimer's disease-associated feature; neuroprotective;  
XX Alzheimer's disease-associated protein isoform; neotropic;  
XX ADPI tryptic digest peptide.  
XX  
XX Homo sapiens.  
XX  
XX WO200246767-A2.  
XX  
XX 11-JUN-2002.  
XX  
XX 29-NOV-2001; 2001WP-GR05289.  
XX  
XX 08-DEC-2000; 2000WJ 254411F  
XX  
XX (OXFO) OXFORD GLYCOSCIENCES UK LTD.  
XX  
XX Herath HMAc, Parakk RB, Rohlf C;  
XX  
XX WPI; 2002-508575/54.  
XX  
XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
XX comprises detecting Alzheimer's disease-associated features or  
XX Alzheimer's disease associated protein isoforms in brain tissue  
XX from the subject.  
XX  
XX Claim 7; Page 59; 427pp; English.  
XX  
XX The present invention relates to methods and compositions for the  
XX screening, diagnosis or prognosis of Alzheimer's disease (AD) in  
XX a subject. The method comprises analysing a sample of brain tissue  
XX from a subject by 2D electrophoresis to generate a 2D array of  
XX Alzheimer's disease-associated features (ADFs), whose relative  
XX abundance correlates with the presence, absence, stage or severity of  
XX AD and comparing the abundance of each feature with the abundance of  
XX that chosen feature in brain tissue from persons free from AD. The  
XX invention also describes Alzheimer's disease associated protein  
XX isoforms (ADPIs) detectable in brain tissue. The methods and  
XX compositions of the invention are useful for the screening, diagnosis  
XX or prognosis of AD in a subject, for determining the stage or severity  
XX of AD in a subject, for identifying a subject at risk of developing AD,  
XX or for monitoring the effect of therapy administered to a subject  
XX having AD. Antibodies capable of binding to ADPIs are useful for  
XX treating or preventing AD, and for determining the efficacy of a given  
XX treatment regime. An agent that modulates the activity of ADPI is  
XX useful in the manufacture of a medicament for the treatment or  
XX prevention of AD in a subject. AEG67292-AEG68038 represent human ADPI  
XX tryptic digest peptides.  
XX  
XX Sequence 9 AA:  
XX  
Query Match 51.2%; Score 25; DB 23; Length 9;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 3 GQVMDV 8  
XX 1 GQVMDV 6  
XX  
XX  
XX RESULT 15  
XX AAE35082  
XX ID AAE35082 standard; peptide; 9 AA.  
XX  
XX AAE35082:  
XX  
XX 28-MAY-2003 (first entry)  
XX  
XX Human immunoglobulin E (IgE) HLA-A2 peptide motif #20.  
XX  
XX Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;  
XX



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

SW: protein - protein search, using sw model

Run on: November 5, 2003, 17:14:14 / Search time: 29 seconds  
Without alignments:  
53,182 Million cell updates/sec

Title: US-09-914-088-1

Perfect score: 47  
Sequence: 1 EDGQWMDV 9

Scoring table: BLOSUM62

Sapop 12.0, Gapext 2.5

Searched: 644070 seqs, 171749282 residues

Total number of hits satisfying chosen parameters: 6127

Minimum DB seq length: 9

Maximum DB seq length: 9

Post-processing: Minimum Match 3%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications, AA\*

- 1: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 2: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 3: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 4: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 5: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 6: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 7: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 8: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 9: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 10: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 11: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 12: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 13: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 14: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 15: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 16: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 17: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.
- 18: /sgn2\_6/prodata/2/pubaa/US09\_PUBCOMB pep.

Prod. No. is the number of results produced by database search. A score greater than or equal to the score of the best hit is printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Match	Length	DB ID	Description
1	47	100.0	9	12	US-10-082-014-273
2	47	100.0	9	12	US-10-082-014-273
3	28	59.6	7	10	US-09-920-174-41
4	23	48.9	8	12	US-10-082-014-273
5	22	46.8	7	10	US-09-935-384-535
6	22	46.8	7	15	US-09-935-384-535
7	22	46.8	8	15	US-10-082-014-273
8	22	46.8	9	12	US-10-082-014-273
9	22	46.8	9	15	US-09-935-384-535
10	22	46.8	9	15	US-10-082-014-273
11	21	44.7	9	10	US-09-935-384-535
12	21	44.7	9	10	US-09-935-384-535
13	21	44.7	9	10	US-09-935-384-535
14	21	44.7	9	10	US-09-935-384-535
15	21	44.7	9	10	US-09-935-384-535

16	21	44.7	9	10	US-09-780-053-454
17	21	44.7	9	10	US-09-780-053-454
18	21	44.7	9	10	US-09-920-174-41
19	21	44.7	9	10	US-09-920-174-41
20	20	42.6	6	11	US-09-935-384-535
21	20	42.6	6	12	US-09-935-384-535
22	20	42.6	6	12	US-09-935-384-535
23	20	42.6	6	12	US-09-935-384-535
24	20	42.6	6	12	US-09-935-384-535
25	20	42.6	6	12	US-09-935-384-535
26	20	42.6	6	12	US-09-935-384-535
27	20	42.6	6	12	US-09-935-384-535
28	20	42.6	6	12	US-09-935-384-535
29	19	40.4	6	12	US-09-935-384-535
30	19	40.4	6	12	US-09-935-384-535
31	19	40.4	6	12	US-09-935-384-535
32	19	40.4	6	12	US-09-935-384-535
33	19	40.4	6	12	US-09-935-384-535
34	19	40.4	6	12	US-09-935-384-535
35	19	40.4	6	12	US-09-935-384-535
36	19	40.4	6	12	US-09-935-384-535
37	19	40.4	6	12	US-09-935-384-535
38	19	40.4	6	12	US-09-935-384-535
39	19	40.4	6	12	US-09-935-384-535
40	19	40.4	6	12	US-09-935-384-535
41	19	40.4	6	12	US-09-935-384-535
42	19	40.4	6	12	US-09-935-384-535
43	19	40.4	6	12	US-09-935-384-535
44	19	40.4	6	12	US-09-935-384-535
45	19	40.4	6	12	US-09-935-384-535

ALIGNMENTS

RESULT 1  
US-10-082-014-273  
; Sequence 273, Application US-10082014  
; Publication No. US200318588A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL C  
; FILE REFERENCE: ICC-130.0 4564/75124  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; PRIOR FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/930,315  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 273  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-273

Query Match 100.0% Score 47 DB 12 Length 9  
Best Local Similarity 100.0% Prod. No. 5.8e+05  
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0

Qy 1 EDGQWMDV 9  
Db 1 EDGQWMDV 9

RESULT 2  
US-10-372-076-127  
; Sequence 127, Application US-10372076  
; Publication No. US2003198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS

FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/372,046  
PRIOR FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/080,249  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 306  
SOFTWARE: Patent in version 3.2  
SEQ ID NO: 127  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US 10 102-074-129

Query Match 100.0% Score 478 DB 147 Length 9  
Best Local Similarity 100.0% Pred No 5.8e+05  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EQQWMD 9  
DB 1 EQQWMD 9

RESULT 3  
US-09-842-164-12  
Sequence 12, Application US/09842154  
Publication No. US2002010567A1  
GENERAL INFORMATION:  
APPLICANT: INOYE, Satoshi  
TITLE OF INVENTION: Luciferase and Photoprotein  
FILE REFERENCE: 206457US0  
CURRENT APPLICATION NUMBER: US/09/84-1164  
CURRENT FILING DATE: 2001-04-26  
PRIOR APPLICATION NUMBER: JAPAN 2000-139053  
PRIOR FILING DATE: 2000-04-26  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patent in version 3.1  
SEQ ID NO: 12  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Ophiophorus gracilirostris  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: 111-171  
OTHER INFORMATION: PRT, 35 kDa protein, partial  
US 09-842 164-12

Query Match 55.8% Score 478 DB 147 Length 9  
Best Local Similarity 51.4% Pred No 5.8e+05  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EQQWMD 9  
DB 1 EQQWMD 9

RESULT 4  
US-10 147 140-47  
Sequence 47, Application US/10/47140  
Publication No. US20030153730A1  
GENERAL INFORMATION:  
APPLICANT: STRACKE, VARY  
APPLICANT: LIOTTA, LANCE  
APPLICANT: SCHIFFMAN, ELLIOTT  
APPLICANT: KRUTZ, HENRY  
APPLICANT: MURRAY, JON

TITLE OF INVENTION: MOTILITY STIMULATING PEPTIDE USEFUL IN  
CANCER DIAGNOSIS AND THERAPY  
FILE REFERENCE: 2026.4149US4  
CURRENT APPLICATION NUMBER: US/10/147,140  
CURRENT FILING DATE: 2002-05-15  
PRIOR APPLICATION NUMBER: 07/822,044

PRIOR FILING DATE: 1992-01-17  
PRIOR APPLICATION NUMBER: 08/249,192  
PRIOR FILING DATE: 1994-05-25  
PRIOR APPLICATION NUMBER: 08/346,455  
PRIOR FILING DATE: 1994-11-28  
PRIOR APPLICATION NUMBER: 08/977,221  
PRIOR FILING DATE: 1997-11-24  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patent in Ver. 3.1  
SEQ ID NO: 47  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-147 140-47

Query Match 48.9% Score 237 DB 12 Length 8  
Best Local Similarity 80.0% Pred No 5.8e+05  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQWMD 7  
DB 3 GQWMD 7

RESULT 5  
US-09-884-767A-110  
Sequence 110, Application US/09884767A  
Publication No. US20020192799A1  
GENERAL INFORMATION:  
APPLICANT: DYAX Corp.  
APPLICANT: Leneau, Christopher J.  
APPLICANT: Ladner, Robert C.  
TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES  
FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT  
CURRENT APPLICATION NUMBER: US/09/884,767A  
CURRENT FILING DATE: 2001-06-19  
PRIOR APPLICATION NUMBER: US 09/597,321  
PRIOR FILING DATE: 2000-06-19  
NUMBER OF SEQ ID NOS: 217  
SOFTWARE: Patent in version 3.1  
SEQ ID NO: 110  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic enterokinase cleavage sequence  
US 09 884 767A 110

Query Match 46.8% Score 227 DB 10 Length 7  
Best Local Similarity 60.0% Pred No 5.8e+05  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQWMD 7  
DB 1 GQWMD 5

RESULT 6  
US-10-006-869-1617  
Sequence 1617, Application US/10006869  
Publication No. US20030082166A1  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W  
APPLICANT: SYNGENE, James Matthew  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
CACHERIN-MEDIATED FUNCTIONS  
FILE REFERENCE: 100066, 407C7  
CURRENT APPLICATION NUMBER: US/10/006,869

? CURRENT FILING DATE: 2001-12-03  
 ? NUMBER OF SEQ ID NOS: 4052  
 ? SOFTWARE: Patent In Ver. 2.0  
 ? SEQ ID NO 1617

? LENGTH: 7  
 ? TYPE: PRT

? ORGANISM: Artificial Sequence

? FEATURE:

? OTHER INFORMATION: Representative cyclic modulating agent based on

? OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence

US-10-006 869-1623

Query Match 46.8%; Score 22; DB 15; Length 7;

Best Local Similarity 66.7%; Pred. No. 5.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QINQVD 9

DB 2 QINQVD 7

RESULT 7

US-10-006 869-1623

? Sequence 1623, Application US/10006869

? Publication No. US20010092166A1

? GENERAL INFORMATION:

? APPLICANT: Blaschuk, Crest W.

? APPLICANT: Symonds, James Matthew

? APPLICANT: Court, Barbara J.

? TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NEUROLOGICAL

? TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

? FILE REFERENCE: 100066-407C7

? CURRENT APPLICATION NUMBER: US/10/006 869

? CURRENT FILING DATE: 2001-12-03

? NUMBER OF SEQ ID NOS: 4052

? SOFTWARE: Patent In Ver. 2.0

? SEQ ID NO 1623

? LENGTH: 8

? TYPE: PRT

? ORGANISM: Artificial Sequence

? FEATURE:

? OTHER INFORMATION: Representative cyclic modulating agent based on

? OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence

US-10-006 869-1623

Query Match 46.8%; Score 22; DB 15; Length 8;

Best Local Similarity 66.7%; Pred. No. 5.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QINQVD 9

DB 2 QINQVD 4

RESULT 8

US-10-160-162-263

? Sequence 263, Application US/10160162

? Publication No. US20030166541A1

? GENERAL INFORMATION:

? APPLICANT: Ruben et al.

? TITLE OF INVENTION: 83 Human Secreted Proteins

? FILE REFERENCE: P2012P2

? CURRENT APPLICATION NUMBER: US/10/160,162

? CURRENT FILING DATE: 2002-06-04

? PRIOR APPLICATION NUMBER: 60/295,558

? PRIOR FILING DATE: 2001-06-05

? PRIOR APPLICATION NUMBER: 09/236,557

? PRIOR FILING DATE: 1999-01-26

? PRIOR APPLICATION NUMBER: PCT/US99/15949

? PRIOR FILING DATE: 1998-07-29

? PRIOR APPLICATION NUMBER: 60/054,212

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,234

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,234

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,218

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,214

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,236

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,215

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,211

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,217

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,113

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/055,968

? PRIOR FILING DATE: 1997-08-18

? PRIOR APPLICATION NUMBER: 60/055,969

? PRIOR FILING DATE: 1997-08-18

? PRIOR APPLICATION NUMBER: 60/055,972

? PRIOR FILING DATE: 1997-08-18

? PRIOR APPLICATION NUMBER: 60/056,561

? PRIOR FILING DATE: 1997-08-19

? PRIOR APPLICATION NUMBER: 60/056,534

? PRIOR FILING DATE: 1997-08-19

? PRIOR APPLICATION NUMBER: 60/056,729

? PRIOR FILING DATE: 1997-08-19

? PRIOR APPLICATION NUMBER: 60/056,543

? PRIOR FILING DATE: 1997-08-19

? PRIOR APPLICATION NUMBER: 60/056,727

? PRIOR FILING DATE: 1997-08-19

? PRIOR APPLICATION NUMBER: 60/056,554

? PRIOR FILING DATE: 1997-08-19

? PRIOR APPLICATION NUMBER: 60/056,730

? PRIOR FILING DATE: 1997-08-19

? NUMBER OF SEQ ID NOS: 353

? SOFTWARE: Patent In Ver. 2.0

? SEQ ID NO 263

? LENGTH: 9

? TYPE: PRT

? ORGANISM: Homo sapiens

? US-10-160-162-263

Query Match 46.8%; Score 22; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 5.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQ 4

DB 5 EDGQ 8

RESULT 9

US-03-820-649-263

? Sequence 263, Application US/09820649

? Publication No. US20030199683A1

? GENERAL INFORMATION:

? APPLICANT: Ruben et al.

? TITLE OF INVENTION: 83 Human Secreted Proteins

? FILE REFERENCE: P2012P1

? CURRENT APPLICATION NUMBER: US/09/820,649

? CURRENT FILING DATE: 2001-03-30

? PRIOR APPLICATION NUMBER: US/09/236,557

? PRIOR FILING DATE: 1999-01-26

? PRIOR APPLICATION NUMBER: PCT/US98/15949

? PRIOR FILING DATE: 1998-07-29

? PRIOR APPLICATION NUMBER: 60/054,212

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,209

? PRIOR FILING DATE: 1997-07-30

? PRIOR APPLICATION NUMBER: 60/054,234

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1 PRIOR FILING DATE: 1997-07-30
2 PRIOR APPLICATION NUMBER: 60/054,218
3 PRIOR FILING DATE: 1997-07-30
4 PRIOR APPLICATION NUMBER: 60/054,214
5 PRIOR FILING DATE: 1997-07-30
6 PRIOR APPLICATION NUMBER: 60/054,214
7 PRIOR FILING DATE: 1997-07-30
8 PRIOR APPLICATION NUMBER: 60/054,214
9 PRIOR FILING DATE: 1997-07-30
10 PRIOR APPLICATION NUMBER: 60/054,214
11 PRIOR FILING DATE: 1997-07-30
12 PRIOR APPLICATION NUMBER: 60/054,211
13 PRIOR FILING DATE: 1997-07-30
14 REMAINING PRIOR APPLICATION DATA REMOVED See File Wrapper on PAM.
15 NUMBER OF SEQ ID NOS: 353
16 SOFTWARE: Patent in Ver. 2.0
17 SEQ ID NO: 263
18 LENGTH: 9
19 TYPE: PRT
20 ORGANISM: Homo sapiens
21 US-09-820-649-263

Query Match 46.8%; Score 22; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : EGGQ 4
DB : 5 EGGQ 8

RESULT 10
US-09-806-649-1626
Sequence 1626, Application US/10002866
Publication No. US200203082166A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gehr, Barbara C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CELLULAR
FILE REFERENCE: 1626B6.407C7
CURRENT APPLICATION NUMBER: US/10002866B6
PRIOR FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO: 1626
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative of a family of related compounds
OTHER INFORMATION: Caderin 8 cell surface and binding domain
US-09-806-649-1626

Query Match 46.8%; Score 22; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.8e-05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QGVVD 3
DB 4 QGVVD 9

RESULT 11
US-09-993-180-28
Sequence 28, Application US/09993180
Publication No. US20030054445A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN PERTIN SECRETED FROM LIVER
FILE REFERENCE: C22S, LSI-11
CURRENT APPLICATION NUMBER: US/09993180
PRIOR FILING DATE: 2001-11-14

Query Match 44.7%; Score 21; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DQGV 5
DB 3 DQGV 6

RESULT 13
US-09-780-053-142
Sequence 142, Application US/09780053
Publication No. US20020102642A1
GENERAL INFORMATION:
APPLICANT: Rene S. Hubert
APPLICANT: Daniel E.H. Afar
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Mary Faris
APPLICANT: Eliana Levin
APPLICANT: Steve Chappel Mitchell
APPLICANT: Aya Laskovits
TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
FILE REFERENCE: 129.505J1
CURRENT APPLICATION NUMBER: US/09780053
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 716
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 57
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-780-053-57

Query Match 44.7%; Score 21; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DQGV 5
DB 3 DQGV 6

RESULT 13
US-09-780-053-142
Sequence 142, Application US/09780053
Publication No. US20020102642A1
GENERAL INFORMATION:
APPLICANT: Rene S. Hubert
APPLICANT: Daniel E.H. Afar
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Mary Faris
APPLICANT: Eliana Levin
APPLICANT: Steve Chappel Mitchell
APPLICANT: Aya Laskovits
TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
FILE REFERENCE: 129.505J1
CURRENT APPLICATION NUMBER: US/09780053
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 716
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 57
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-780-053-57

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; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-914-088-1-434

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Query Match 44.7%; Score 21; PR 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 DGGV 5
DB 6 DGGV 9

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## RESULT 14

```

; Sequence 253, Application US/09780053
; Patent No. US2002102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paros
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83PSG4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-914-088-1-253

```

```

Query Match 44.7%; Score 21; PR 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 DGGV 5
DB 6 DGGV 9

```

## RESULT 15

```

; Sequence 434, Application US/09780053
; Patent No. US2002102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paros
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83PSG4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1

```

```

; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 434
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-914-088-1-434

```

```

Query Match 44.7%; Score 21; PR 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 DGGV 5
DB 1 DGGV 4

```

```

Search completed: November 5, 2003, 17:19:16
Job time : 30 secs

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GenCore version 5.1.6  
Copyright (c) 1993 2003 Comugen Ltd.

OK protein: protein search, using sw model:

Run on: November 5, 2003, 17:12:09 / search time 21 seconds  
(without alignments)  
18,133 Million cell updates/sec

Title: US-39 914-088-1

Perfect score: 47

Sequence: 1 EQQWMD 9

Scoring table: 51OSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 4230958 residues

Total number of hits satisfying chosen parameters: 17

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1 Issued Patents AA:

- 1: /cgn2\_6/prodata/1/aa/1A-QVX pep:
- 2: /cgn2\_6/prodata/1/aa/1A-QVX pep:
- 3: /cgn2\_6/prodata/1/aa/1A-QVX pep:
- 4: /cgn2\_6/prodata/1/aa/1A-QVX pep:
- 5: /cgn2\_6/prodata/1/aa/1A-QVX pep:
- 6: /cgn2\_6/prodata/1/aa/1A-QVX pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	28	59.6	7	4	US-09-842-164A-12
2	23	48.9	8	1	US-08-346-455B-47
3	23	48.9	8	3	US-08-346-455B-47
4	23	48.9	8	4	US-09-439-542B-1623
5	23	48.9	8	5	PCT-US-09-439-542B-1623
6	22	46.8	8	1	US-08-346-455B-47
7	22	46.8	8	2	US-08-346-455B-47
8	22	46.8	8	3	US-09-439-542B-1623
9	22	46.8	8	4	US-09-439-542B-1623
10	22	46.8	8	5	PCT-US-09-439-542B-1623
11	22	46.8	8	1	US-08-346-455B-47
12	22	46.8	8	2	US-08-346-455B-47
13	22	46.8	8	3	US-09-439-542B-1623
14	22	46.8	8	4	US-09-439-542B-1623
15	22	46.8	8	5	PCT-US-09-439-542B-1623
16	22	46.8	8	1	US-08-346-455B-47
17	22	46.8	8	2	US-08-346-455B-47
18	22	46.8	8	3	US-09-439-542B-1623
19	22	46.8	8	4	US-09-439-542B-1623
20	22	46.8	8	5	PCT-US-09-439-542B-1623
21	21	44.7	7	4	US-09-439-542B-1623
22	21	44.7	8	1	US-08-346-455B-47
23	21	44.7	8	2	US-08-346-455B-47
24	21	44.7	8	3	US-09-439-542B-1623
25	21	44.7	8	4	US-09-439-542B-1623
26	21	44.7	8	5	PCT-US-09-439-542B-1623
27	20	42.6	6	5	PCT-US-09-439-542B-1623
28	20	42.6	8	2	US-08-346-455B-47

Sequence 16, Appl  
Sequence 13, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 2455, Ap  
Sequence 30, Appl  
Sequence 30, Appl  
Sequence 6, Appl  
Sequence 30, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Patent No 5284931  
Sequence 46, Appl

## ALIGNMENTS

RESULT 1  
US-09-842-164A-12  
; Sequence 12, Application US/09942164A  
; Patent No. 6544754  
; GENERAL INFORMATION:  
; APPLICANT: INQVUE, SATOSHI  
; TITLE OF INVENTION: LUCIFERASE AND PHOTOPROTEIN  
; CURRENT APPLICATION NUMBER: US/09/842,164A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: JP 2000 125053  
; PRIOR FILING DATE: 2000-04-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Coptophorus graciliorostris  
US-09-842-164A-12

Query Match 59.6%; Score 28; DB 4; Length 7;  
Best Local Similarity 71.4%; Pred. No. 2.5e-05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 QQQWMD 9  
Db 1 QQQWMD 7

RESULT 2  
US-08-346-455B-47  
; Sequence 47, Application US/08346455B  
; Patent No. 5731167  
; GENERAL INFORMATION:  
; APPLICANT: UNITED STATES OF AMERICA; DEPT.  
; APPLICANT: OF HEALTH AND HUMAN SERVICES  
; TITLE OF INVENTION: MOTILITY STIMULATING  
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND  
; TITLE OF INVENTION: THERAPY  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEMAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC compatible



```

1 OPERATING SYSTEM: PC-DOS/MS-DOS
2 SOFTWARE: WordPerfect 5.1
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/09/346,455B
5 FILING DATE: 28-NOV-1994
6 CLASSIFICATION: 53C
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: PCT/US95/756e13
9 FILING DATE: 24-MAY-1995
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: 08/249,182
12 FILING DATE: 25-MAY-1994
13 APPLICATION NUMBER: 07/822,043
14 FILING DATE: 17-JAN-1992
15 NAME: DOROTHY R. AUTH
16 REGISTRATION NUMBER: 36,434
17 REFERENCE/DOCKET NUMBER: 2026 4145PCT
18 TELEPHONE: 1212 758-4800
19 TELEFAX: 1212 751-6849
20 INFORMATION FOR SEQ ID NO: 47:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 8
23 TYPE: amino acids
24 STRANDEDNESS: single
25 TOPOLOGY: linear
26 MOLECULE TYPE:
27 DESCRIPTION: Peptide
28 HYPOTHEetical: NO
29 FEATURE:
30 NAME/KEY: ATX 216
31 LOCATION:
32 IDENTIFICATION METHOD:
33 OTHER INFORMATION:
34 US 08-146-455B-47

```

```

Query Match 48.9% Score 23; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 QQVMD 7
   |||
Db 3 QQLMD 7

```

```

1 RESULT 1
2 US 09-914-088-1
3 Sequence 47, Application US/09/346,455B
4 Patent No. 6417318
5 GENERAL INFORMATION:
6 APPLICANT: UNITED STATES OF AMERICA, DEPT
7 APPLICANT: OF HEALTH AND HUMAN SERVICES
8 TITLE OF INVENTION: MOTILITY STIMULATING
9 TITLE OF INVENTION: MOTILITY STIMULATING
10 TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
11 NUMBER OF SEQUENCES: 69
12 CORRESPONDENCE ADDRESS:
13 ADDRESS: MORGAN & FINNEGAN
14 STREET: 345 PARK AVENUE
15 CITY: NEW YORK
16 STATE: NEW YORK
17 COUNTRY: U.S.A.
18 ZIP: 10154
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy Disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: WordPerfect 5.1
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/977,221
26 FILING DATE:

```

```

1 CLASSIFICATION:
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: 08/346,455
4 FILING DATE: 28-NOV-1994
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 08/249,182
7 FILING DATE: 25-MAY-1994
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: 07/822,043
10 FILING DATE: 17-JAN-1992
11 ATTORNEY/AGENT INFORMATION:
12 NAME: DOROTHY R. AUTH
13 REGISTRATION NUMBER: 36,434
14 REFERENCE/DOCKET NUMBER: 2026-4149US3
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: 1212 758-4800
17 TELEFAX: 1212 751-6849
18 INFORMATION FOR SEQ ID NO: 47:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 8
21 TYPE: amino acids
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE:
25 DESCRIPTION: Peptide
26 HYPOTHEtical: NO
27 FEATURE:
28 NAME/KEY: ATX 216
29 LOCATION:
30 IDENTIFICATION METHOD:
31 OTHER INFORMATION:
32 US-08-977-221-47

```

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Query Match 48.9% Score 23; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 QQVMD 7
   |||
Db 3 QQLMD 7

```

```

1 RESULT 4
2 US 09-463 831B-47
3 Sequence 47, Application US/09463831B
4 Patent No. 6417318
5 GENERAL INFORMATION:
6 APPLICANT: STRACK, VARY
7 APPLICANT: LIOTTA, DANCE
8 APPLICANT: SCHIFFMANN, ELICIT
9 APPLICANT: KRUTZER, HENRY
10 APPLICANT: MURATA, JUN
11 TITLE OF INVENTION: AUTOTAXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
12 TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
13 FILE REFERENCE: 2026 4149US4
14 CURRENT APPLICATION NUMBER: US/09/463,831B
15 CURRENT FILING DATE: 2000-01-17
16 PRIOR APPLICATION NUMBER: 07/822,043
17 PRIOR FILING DATE: 1992-01-17
18 PRIOR APPLICATION NUMBER: 08/249,182
19 PRIOR FILING DATE: 1994-05-25
20 PRIOR APPLICATION NUMBER: 08/346,455
21 PRIOR FILING DATE: 1994-11-28
22 PRIOR APPLICATION NUMBER: 08/977,221
23 PRIOR FILING DATE: 1997-11-24
24 NUMBER OF SEQ ID NOS: 70
25 SOFTWARE: Patent Ver. 2.1
26 SEQ ID NO 47
27 LENGTH: 8
28 TYPE: PR
29 ORGANISM: Artificial Sequence
30 FEATURE:
31 OTHER INFORMATION: Description of Artificial Sequence: Synthetic

```

## OTHER INFORMATION: Peptide

US-09 483-831R-47

Query Match 49.98; Score 22; DB 1; Length 4;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQVND 7  
|||  
Db 3 GQLMD 7

## RESULT 5

PC7/US95-06613-47  
; Sequence 47, Application PC7/US9506613  
; GENERAL INFORMATION:  
; APPLICANT: STRACKE, VARY; LIOTTA, LANCE;  
; APPLICANT: SCHIFFMANN, ELLICOTT; KRUTZSCH,  
; APPLICANT: HENRY; MURATA, JUN  
; TITLE OF INVENTION: MOTILITY STIMULATING  
; TITLE OF INVENTION: PROTEIN USED IN CANCER DIAGNOSIS AND  
; TITLE OF INVENTION: THERAPY  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PC7/US95-06613  
FILING DATE: 24-MAY-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/346,455  
FILING DATE: 28-NOV-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/249,182  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/822,041  
FILING DATE: 17-JAN-1992

ATTORNEY/AGENT INFORMATION:  
NAME: DOROTHY P. RUTH  
REGISTRATION NUMBER: 36,434  
REFERENCE/DOCKET NUMBER: 2026 474-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:

LENGTH: 8  
TYPE: amino acids  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: peptide  
HYPOTHETICAL: No  
FEATURE:  
NAME/KEY: ATX-216  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PT/US95-06613-47

Query Match 48.98; Score 21; DB 1; Length 4;  
Best Local Similarity 80.0%; Pred. No. 1.5e+05;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQVND 7  
|||  
Db 3 GQLMD 7

## RESULT 6

US-08-447-010-26  
; Sequence 26, Application US/08447010  
; Patent No. 5703718  
; GENERAL INFORMATION:  
; APPLICANT: MOFFATT, BARBARA  
; TITLE OF INVENTION: GENE FOR APRT FROM PLANT TISSUE  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 310 University Avenue, Suite 701  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/447,010  
FILING DATE: 22-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/230,695  
FILING DATE: 21-APR-1994

CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/888,132  
FILING DATE: 26-MAY-1992  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: STEWART, MICHAEL I

REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 181 181 XIS:V9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
TELEX: 065-24567 SIMBAS  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acids  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-447-010-26

Query Match 46.88; Score 22; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQ 4  
||  
Db 1 EDGQ 4

## RESULT 7

US-08-421-155-8  
; Sequence 8, Application US/08421155  
; Patent No. 5703057  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Michael A.  
; APPLICANT: Gal, Wayne C.  
; APPLICANT: Johnston, Stephen A.

```

1 TITLE OF INVENTION: Expression Library Immunization
2 NUMBER OF SEQUENCES: 8
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: Arnold, White & Durkee
5 STREET: P.O. Box 4433
6 CITY: Houston
7 STATE: Texas
8 COUNTRY: United States of America
9 ZIP: 77210
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patent In Release #1.0, Version #1.39
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/421,155
17 FILING DATE:
18 CLASSIFICATION: 424
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Kitchell, Barbara S.
21 REGISTRATION NUMBER: 33,928
22 REFERENCE/DOCKET NUMBER: JTXD-411,817
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (512) 418-3000
25 TELEFAX: (713) 789-2679
26 TELEX: 79 0924
27 INFORMATION FOR SEQ ID NO: 9:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 6 amino acids
30 TYPE: amino acid
31 STRANDEDNESS: linear
32 TOPOLOGY: linear
33 MOLECULE TYPE: peptide
34 US 08 421,155 8

```

```

Query Match 46.8% Score 22: 18 1: Length 6:
Best Local Similarity 60.0% Pred. No. 2.5e+05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

CY 3 EGGQ 7
DB 2 EGGQ 6

```

```

1 RESULT 9
2 US-08-232-5390-26
3 Sequence 26, Application US/08/232,539
4 Patent No. 5965769
5 GENERAL INFORMATION:
6 APPLICANT: Fresco, Leonard G.
7 ADDRESSEE: Cardillo, Paula M.
8 TITLE OF INVENTION: IGB Antagonists
9 NUMBER OF SEQUENCES: 60
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Genentech, Inc.
12 STREET: 1 DNA Way
13 CITY: South San Francisco
14 STATE: California
15 COUNTRY: USA
16 ZIP: 94080
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: WinPatIn (Genentech)
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/232,539
24 FILING DATE: 21-Apr-1994
25 CLASSIFICATION: 530
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 08/178563
28 FILING DATE: 07-JAN-1994
29 PRIOR APPLICATION DATA:

```

```

1 APPLICATION NUMBER: 07/744768
2 FILING DATE: 14-AUG-1991
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Svoboda, Craig G.
5 REGISTRATION NUMBER: 39,044
6 REFERENCE/DOCKET NUMBER: PC7-8P3
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: 650/225-1469
9 TELEFAX: 650/295-9881
10 INFORMATION FOR SEQ ID NO: 26:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 6 amino acids
13 TYPE: Amino Acid
14 TOPOLOGY: Linear
15 US-08-232-5390-26
16 Query Match 46.8% Score 22: DB 2: Length 6:
17 Best Local Similarity 100.0% Pred. No. 2.5e+05;
18 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
19
20 CY 1 EGGQ 4
21 DB 3 EGGQ 6
22
23 RESULT 9
24 US-09-001-157-8
25 Sequence 8, Application US/09001157
26 Patent No. 5989553
27 GENERAL INFORMATION:
28 APPLICANT: Johnston, Stephen A.
29 APPLICANT: Barry, Michael A.
30 APPLICANT: Lai, Wayne C.
31 TITLE OF INVENTION: EXPRESSION LIBRARY IMMUNIZATION
32 NUMBER OF SEQUENCES: 8
33 CORRESPONDENCE ADDRESS:
34 ADDRESSEE: Arnold, White & Durkee
35 STREET: P.O. Box 4433
36 CITY: Houston
37 STATE: Texas
38 COUNTRY: USA
39 ZIP: 77210
40 COMPUTER READABLE FORM:
41 MEDIUM TYPE: Floppy disk
42 COMPUTER: IBM PC compatible
43 OPERATING SYSTEM: PC-DOS/MS-DOS
44 SOFTWARE: Patent In Release #1.0, Version #1.30
45 CURRENT APPLICATION DATA:
46 APPLICATION NUMBER: US/09/001,157
47 FILING DATE: Concurrently Herewith.
48 CLASSIFICATION:
49 PRIOR APPLICATION DATA:
50 APPLICATION NUMBER: US 09/421,155
51 FILING DATE: 07-APR 1995
52 ATTORNEY/AGENT INFORMATION:
53 NAME: Kitchell, Barbara S.
54 REGISTRATION NUMBER: 33,928
55 REFERENCE/DOCKET NUMBER: JTXD-529
56 TELECOMMUNICATION INFORMATION:
57 TELEPHONE: 512/418-3000
58 TELEFAX: 512/474 7577
59 INFORMATION FOR SEQ ID NO: 8:
60 SEQUENCE CHARACTERISTICS:
61 LENGTH: 6 amino acids
62 TYPE: amino acid
63 STRANDEDNESS:
64 TOPOLOGY: linear
65 US-09-001-157-8

```

```

Query Match 46.8% Score 22: DB 2: Length 6:
Best Local Similarity 60.0% Pred. No. 2.5e+05;
Matches 3: Conservative 2: Mismatches 0: Indels 0: Gaps 0:

```

QY 3 QGVND 7  
1111  
DB 2 QQLLD 6

RESULT 10  
US-09-147-859-1617  
; Sequence 1617, Application US/09187869A  
; Patent No. 6159320  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Grest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING N-METHYL-D-ASPARTATE  
; FILE REFERENCE: 132986.40701  
; CURRENT APPLICATION NUMBER: US/09/147,869A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4552  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO: 1617  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence  
US-09-147-859-1617

Query Match 46.8%, Score 22; DB 4; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QGVND 9  
1111  
DB 2 QGVND 7

RESULT 11  
US-09-914-088-1617  
; Sequence 1617, Application US/09187869A  
; Patent No. 6569996  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Grest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING N-METHYL-D-ASPARTATE  
; FILE REFERENCE: 132986.40701  
; CURRENT APPLICATION NUMBER: US/09/147,869A  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 4552  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO: 1617  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence  
US-09-914-088-1617

Query Match 46.8%, Score 22; DB 4; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QGVND 9  
1111  
DB 2 QGVND 7

RESULT 12  
US-09-421-155-6  
; Sequence 6, Application US/09421155

Patent No. 5763057  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Michael A.  
; APPLICANT: Hall, Wayne C.  
; APPLICANT: Johnston, Stephen A.  
; TITLE OF INVENTION: Expression Library Immunization  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.10  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/421,155  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: UTSD:411/KIT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 389-2679  
; TELEX: 79-0924  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-421-155-6

Query Match 46.8%, Score 22; DB 1; Length 8;  
Best Local Similarity 60.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QGVND 7  
1111  
DB 2 QQLLD 6

RESULT 13  
US-09-571-485-24  
; Sequence 20, Application US/09571485  
; Patent No. 5783557  
; GENERAL INFORMATION:  
; APPLICANT: Burstein, Vigal  
; APPLICANT: Trainor, Nathan  
; APPLICANT: Rykus, Avigail  
; TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical  
; TITLE OF INVENTION: Compositions Comprising Them  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kohn & Associates  
; STREET: 13500 No. 575357th Western Hwy., Suite 410  
; CITY: Farmington Hills  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48334  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/571,985  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: IL 106214  
 FILING DATE: 01-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kahn, Kenneth  
 REGISTRATION NUMBER: 30,955  
 REFERENCE/DOCKET NUMBER: 2163 00049  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (910) 539-5050  
 TELEFAX: (910) 539-5055  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US 09 571-995 20

Query Match 46.8%; Score 22; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQ 4  
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 DB 2 EDGQ 5

RESULT 14  
 US 08-487-860 60  
 Sequence 60, Application US/08487860  
 Patent No. 5792456  
 GENERAL INFORMATION:  
 APPLICANT: Yellon, Dale  
 APPLICANT: Glaser, Scott  
 APPLICANT: Huse, William  
 APPLICANT: Kosak, Mae J.  
 TITLE OF INVENTION: No. 5792456-2 Mutant ERK4 Antibodies and  
 Functional Equivalents Reactive With Human Carcinomas  
 NUMBER OF SEQUENCES: 62  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merchant & Gould  
 STREET: 11150 Santa Monica Blvd., Suite 400  
 CITY: Los Angeles  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 90025 1975  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/487,860  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Adriano, Sarah B.  
 REGISTRATION NUMBER: 34,410  
 REFERENCE/DOCKET NUMBER: 30456 14771  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 310-445-1140  
 TELEFAX: 310-445-9031  
 INFORMATION FOR SEQ ID NO: 60:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US 08-487-860-60

Query Match 46.8%; Score 22; DB 1; Length 8;  
 Best Local Similarity 42.9%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQWD 7  
 |||  
 DB 2 QCGDITD 5

RESULT 15  
 US-09 116-766-20  
 Sequence 20, Application US/09116766  
 Patent No. 5968898  
 GENERAL INFORMATION:  
 APPLICANT: Burstein, Yigal  
 APPLICANT: Trainin, Nathan  
 APPLICANT: Ryssak, Avigail  
 TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical  
 Compositions Comprising Them  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Kahn & Associates  
 STREET: 30500 No. 5968898th Western Hwy., Suite 410  
 CITY: Farmington Hills  
 STATE: Michigan  
 COUNTRY: USA  
 ZIP: 48334  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/116,766  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: IL 106214  
 FILING DATE: 01-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Montgomery, Ilene N.  
 REGISTRATION NUMBER: 38,972  
 REFERENCE/DOCKET NUMBER: 2163 00050  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (248) 539-5050  
 TELEFAX: (248) 539-5055  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09 116-766-20

Query Match 46.8%; Score 22; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQ 4  
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 DB 2 EDGQ 5

Search completed: November 5, 2003, 17:15:10  
 Job time : 22 secs

GenCore version 5.1.15  
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CM protein - protein search, using sw model

Run on: November 5, 2003, 15:18:51 / Search time 8.0475 seconds  
(without alignments)  
47,141 Million cell updates/sec

Title: US-09-914-088-1

Perfect score: 47

Sequence: 1 EQVMVDVC 9

Scoring table: BLOSUM62

Gap: 10.0, Gapext 2.5

Search: 318717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 18711

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 6%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Parents AA:  
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2: /cgn2\_6/ptodata/1/aa/5B\_CMB.pep.  
3: /cgn2\_6/ptodata/1/aa/5A\_CMB.pep.  
4: /cgn2\_6/ptodata/1/aa/5B\_CMB.pep.  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	70.2	462	US-09-914-088-1	Sequence 7128, Ap
2	33	70.2	468	US-09-914-088-1	Sequence 17208, A
3	33	70.2	948	US-09-914-088-1	Sequence 6123, Ap
4	33	70.2	1119	US-09-914-088-1	Sequence 3, Appl
5	32	68.1	273	US-09-914-088-1	Sequence 121, Appl
6	32	68.1	293	US-09-914-088-1	Sequence 2215, A
7	32	68.1	394	US-09-914-088-1	Sequence 21, Appl
8	32	68.1	422	US-09-914-088-1	Sequence 3, Appl
9	32	68.1	426	US-09-914-088-1	Sequence 7, Appl
10	32	68.1	478	US-09-914-088-1	Sequence 9, Appl
11	32	68.1	508	US-09-914-088-1	Sequence 1, Appl
12	32	68.1	1357	US-09-914-088-1	Sequence 21306, A
13	31.5	67.0	90	US-09-914-088-1	Sequence 615, App
14	31.5	67.0	232	US-09-914-088-1	Sequence 1, Appl
15	31.5	67.0	232	US-09-914-088-1	Sequence 7, Appl
16	31.5	67.0	160	US-09-914-088-1	Sequence 7, Appl
17	31	66.0	160	US-09-914-088-1	Sequence 7, Appl
18	31	66.0	160	US-09-914-088-1	Sequence 7, Appl
19	31	66.0	160	US-09-914-088-1	Sequence 7, Appl
20	31	66.0	160	US-09-914-088-1	Sequence 7, Appl
21	31	66.0	247	US-09-914-088-1	Sequence 44, Appl
22	31	66.0	294	US-09-914-088-1	Sequence 22068, A
23	31	66.0	294	US-09-914-088-1	Sequence 168, Ap
24	31	66.0	303	US-09-914-088-1	Sequence 6113, Ap
25	31	66.0	332	US-09-914-088-1	Sequence 3193, Ap
26	31	66.0	410	US-09-914-088-1	Sequence 22340, A
27	31	66.0	411	US-09-914-088-1	Sequence 2, Appl

28	31	66.0	411	3	US-09-914-088-1	Sequence 2, Appl
29	31	66.0	411	4	US-09-914-088-1	Sequence 2, Appl
30	31	66.0	414	4	US-09-914-088-1	Sequence 7057, Ap
31	31	66.0	517	4	US-09-914-088-1	Sequence 3115, A
32	31	66.0	520	2	US-09-914-088-1	Sequence 2, Appl
33	31	66.0	520	4	US-09-914-088-1	Sequence 2, Appl
34	31	66.0	604	4	US-09-914-088-1	Sequence 6437, Ap
35	31	66.0	735	4	US-09-914-088-1	Sequence 3440, Ap
36	30	63.8	29	4	US-09-914-088-1	Sequence 6, Appl
37	30	63.8	115	4	US-09-914-088-1	Sequence 6466, Ap
38	30	63.8	226	4	US-09-914-088-1	Sequence 5486, Ap
39	30	63.8	233	4	US-09-914-088-1	Sequence 36, Appl
40	30	63.8	237	4	US-09-914-088-1	Sequence 12496, A
41	30	63.8	240	4	US-09-914-088-1	Sequence 30, Appl
42	30	63.8	247	4	US-09-914-088-1	Sequence 46, Appl
43	30	63.8	252	4	US-09-914-088-1	Sequence 14, Appl
44	30	63.8	280	4	US-09-914-088-1	Sequence 323, App
45	30	63.8	283	4	US-09-914-088-1	Sequence 6278, Ap

## ALIGNMENTS

RESULT 1  
US-09-914-088-1:2128  
; Sequence 7128, Application US/09128352  
; Patent No. 6562959  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09128,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8452  
; SEQ ID NO 7128  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-914-088-1:2128

Query Match: 70.2%, Score 33; DB 4; Length 462;  
Best Local Similarity: 65.7%; Pred. No: 1.2e+02;  
Matches: 6; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 3 GQVMVDVC  
DB 188 GQVMVDVC

RESULT 2  
US-09-914-088-1:17208  
; Sequence 17208, Application US/09128352  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09128,352  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/374,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/394,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 17208  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-914-088-1:17208

Query Match: 70.2%, Score 33; DB 4; Length 468;

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Best Local Similarity 85.78; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DGGQWMD 9
DB 194 GQLMVD 200

RESULT 3
US-09-396-6518 6123
; Sequence 6123, Application US/09329452
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: G059-03PA
; CURRENT APPLICATION NUMBER: US/09/728,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 9252
; SEQ ID NO 6123
; LENGTH: 848
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-396-6518 6123

Query Match 70.2%; Score 33; DB 4; Length 848;
Best Local Similarity 50.0%; Pred. No. 1.0e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGQWMD 9
DB 186 GQLMVD 193

RESULT 4
US-09-396-6518 2
; Sequence 2, Application US/093966518
; Patent No. 6225076
; GENERAL INFORMATION:
; APPLICANT: Carst, Seth A
; APPLICANT: Zhao, Gengyi
; APPLICANT: Campbell, Elizabeth
; APPLICANT: Minakiri, Leonid
; APPLICANT: Svetlov, Konstantin
; TITLE OF INVENTION: A CRYSTAL OF BACTERIAL PROTEIN COVERAGE AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 6001258
; CURRENT APPLICATION NUMBER: US/09/006,611P
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Thermus aquaticus
; FEATURE: SITE
; NAME/KEY: 16960
; LOCATION: 16957..16960
; OTHER INFORMATION: Any amino acids can be at these two positions.
US-09-396-6518 2

Query Match 70.2%; Score 33; DB 4; Length 119;
Best Local Similarity 66.7%; Pred. No. 1.0e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGQWMD 9
DB 599 DGGQWMD 607

RESULT 5
US-09-427-700 12
; Sequence 12, Application US/09427700
; Patent No. 6372489
; GENERAL INFORMATION:
; APPLICANT: Articanter
; APPLICANT: Zhao, Ming
; TITLE OF INVENTION: METHOD AND MODEL FOR HAIR PIGMENTATION
; FILE REFERENCE: 31276-20017 C0
; CURRENT APPLICATION NUMBER: US/09/427,700
; CURRENT FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 65/105,725
; PRIOR FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reduced amino acid sequence of SEQ ID NO:11
US-09-427-700 12

Query Match 68.1%; Score 32; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 1e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGQWMD 7
DB 112 DGGQWMD 117

RESULT 6
US-09-252-991A-22215
; Sequence 22215, Application US/99252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Ruberfeld et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 101361136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 39142
; SEQ ID NO 22215
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22215

Query Match 68.1%; Score 32; DB 4; Length 293;
Best Local Similarity 66.7%; Pred. No. 1.1e-02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGQWMD 9
DB 233 PFAEALVD 241

RESULT 7
US-08-705-771-21
; Sequence 21, Application US/08705771
; Patent No. 6554289
; GENERAL INFORMATION:
; APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
; APPLICANT: Jian Ni and Jing-Shan Hu
; TITLE OF INVENTION: Human Genes, Sequences and
; TITLE OF INVENTION: Expression Products
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CABELLA, BYRNE, RAIN, GILFILLAN,
```

```
Best Local Similarity 85.78; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 DGGQWMD 9
DB 194 GQLMVD 200

RESULT 3
US-09-396-6518 6123
; Sequence 6123, Application US/09329452
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: G059-03PA
; CURRENT APPLICATION NUMBER: US/09/728,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 9252
; SEQ ID NO 6123
; LENGTH: 848
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-396-6518 6123

Query Match 70.2%; Score 33; DB 4; Length 848;
Best Local Similarity 50.0%; Pred. No. 1.0e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGQWMD 9
DB 186 GQLMVD 193

RESULT 4
US-09-396-6518 2
; Sequence 2, Application US/093966518
; Patent No. 6225076
; GENERAL INFORMATION:
; APPLICANT: Carst, Seth A
; APPLICANT: Zhao, Gengyi
; APPLICANT: Campbell, Elizabeth
; APPLICANT: Minakiri, Leonid
; APPLICANT: Svetlov, Konstantin
; TITLE OF INVENTION: A CRYSTAL OF BACTERIAL PROTEIN COVERAGE AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 6001258
; CURRENT APPLICATION NUMBER: US/09/006,611P
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Thermus aquaticus
; FEATURE: SITE
; NAME/KEY: 16960
; LOCATION: 16957..16960
; OTHER INFORMATION: Any amino acids can be at these two positions.
US-09-396-6518 2

Query Match 70.2%; Score 33; DB 4; Length 119;
Best Local Similarity 66.7%; Pred. No. 1.0e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGQWMD 9
DB 599 DGGQWMD 607

RESULT 5
US-09-427-700 12
; Sequence 12, Application US/09427700
; Patent No. 6372489
; GENERAL INFORMATION:
; APPLICANT: Articanter
; APPLICANT: Zhao, Ming
; TITLE OF INVENTION: METHOD AND MODEL FOR HAIR PIGMENTATION
; FILE REFERENCE: 31276-20017 C0
; CURRENT APPLICATION NUMBER: US/09/427,700
; CURRENT FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 65/105,725
; PRIOR FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reduced amino acid sequence of SEQ ID NO:11
US-09-427-700 12

Query Match 68.1%; Score 32; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 1e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGQWMD 7
DB 112 DGGQWMD 117

RESULT 6
US-09-252-991A-22215
; Sequence 22215, Application US/99252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Ruberfeld et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 101361136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 39142
; SEQ ID NO 22215
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22215

Query Match 68.1%; Score 32; DB 4; Length 293;
Best Local Similarity 66.7%; Pred. No. 1.1e-02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGQWMD 9
DB 233 PFAEALVD 241

RESULT 7
US-08-705-771-21
; Sequence 21, Application US/08705771
; Patent No. 6554289
; GENERAL INFORMATION:
; APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
; APPLICANT: Jian Ni and Jing-Shan Hu
; TITLE OF INVENTION: Human Genes, Sequences and
; TITLE OF INVENTION: Expression Products
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CABELLA, BYRNE, RAIN, GILFILLAN,
```

ADDRESSEE: CECCHI, STEWART & OLSTEIN  
 STREET: 6 BECKER FARM ROAD  
 CITY: ROSELAND  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 INCH DISKETTE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WORD PERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/725,071  
 FILING DATE: August 10, 1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MULLINS, J.G.  
 REGISTRATION NUMBER: 33,073  
 REFERENCE/DOCKET NUMBER: 32581-344 (HF136)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 973-994-1720  
 TELEFAX: 973-994-1744  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 394 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-914-088-1

Query Match 68.1%; Score 32; DB 1; Length 394;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDQGVWD 9  
 |||||  
 DB 9 EDQGVWD 17

RESULT 8  
 US-08-152-483B-3  
 Sequence 3, Application US/08152483B  
 Patent No. 5529909  
 GENERAL INFORMATION:  
 APPLICANT: Della Cioppa, Guy  
 APPLICANT: Kumagai, Monto  
 TITLE OF INVENTION: TYROSINASE-ACTIVATOR  
 TITLE OF INVENTION: PROTEIN FUSION ENZYME  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pecore & Edmunds  
 STREET: 2730 Sand Hill Road  
 CITY: Menlo Park  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 94025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0,  
 SOFTWARE: Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/152,483B  
 FILING DATE: No. 5529909eember 12, 1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 7/857,602  
 FILING DATE: March 30, 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 923,692  
 FILING DATE: July 31, 1992  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 600,244  
 FILING DATE: October 22, 1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 641,617  
 FILING DATE: January 16, 1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 737,899  
 FILING DATE: July 26, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hattis, Albert P.  
 REGISTRATION NUMBER: 25,227  
 REFERENCE/DOCKET NUMBER: BIOG-20240/8129 040  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 854 3660  
 TELEFAX: (415) 854 3694  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 422  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE:  
 DESCRIPTION: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGIN: SOURCE:  
 ORGANISM:  
 IMMEDIATE SOURCE:  
 CLONE:  
 FEATURE:  
 US-08-152-483B-3

Query Match 68.1%; Score 32; DB 1; Length 422;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DQGVWD 7  
 |||||  
 DB 112 DQGVWD 117

RESULT 9  
 US-08-152-483B-7  
 Sequence 7, Application US/08152483B  
 Patent No. 5529909  
 GENERAL INFORMATION:  
 APPLICANT: Della Cioppa, Guy  
 APPLICANT: Kumagai, Monto  
 TITLE OF INVENTION: TYROSINASE-ACTIVATOR  
 TITLE OF INVENTION: PROTEIN FUSION ENZYME  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pecore & Edmunds  
 STREET: 2730 Sand Hill Road  
 CITY: Menlo Park  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 94025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0,  
 SOFTWARE: Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/152,483B  
 FILING DATE: No. 5529909eember 12, 1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 7/857,602  
 FILING DATE: March 30, 1992  
 PRIOR APPLICATION DATA:



1 APPLICATION NUMBER: 923,692  
2 FILING DATE: July 31, 1992  
3 PRIOR APPLICATION DATA:  
4 APPLICATION NUMBER: 600,244  
5 FILING DATE: October 22, 1990  
6 PRIOR APPLICATION DATA:  
7 APPLICATION NUMBER: 641,617  
8 FILING DATE: January 16, 1991  
9 PRIOR APPLICATION DATA:  
10 APPLICATION NUMBER: 737,899  
11 FILING DATE: July 26, 1991  
12 ATTORNEY/AGENT INFORMATION:  
13 NAME: Halling, Albert F.  
14 REGISTRATION NUMBER: 25,227  
15 REFERENCE/DOCKET NUMBER: BIOG 20240/8123-040  
16 TELECOMMUNICATION INFORMATION:  
17 TELEPHONE: (415) 854-3660  
18 TELEX: 66141 PENNIE  
19 INFORMATION FOR SEQ ID NO: 1:  
20 SEQUENCE CHARACTERISTICS:  
21 LENGTH: 426  
22 TYPE: amino acid  
23 STRANDEDNESS: Circular  
24 TOPOLOGY: Circular  
25 MOLECULE TYPE: Protein  
26 DESCRIPTION: Protein  
27 HYPOTHEetical: NO  
28 ANTI-SENSE: NO  
29 ORIGINAL SOURCE:  
30 ORGANISM:  
31 IMMEDIATE SOURCE:  
32 CLONE:  
33 FEATURE:  
34 US-09-152-483B-9

Query Match: 68.18; Score 12; DB 1; Length 478;  
Best Local Similarity 100.0%; Prod. No. 19e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DQVMD 7  
DB 264 DQVMD 269

RESULT 1:  
US-09-152-483B-9  
Sequence 1, Application: US/2415-483B  
Patent No. 5523706  
GENERAL INFORMATION:  
APPLICANT: Cellucloppa, Gary  
APPLICANT: Kumbal, Monte  
TITLE OF INVENTION: TYROSINASE ACTIVATOR  
TITLE OF INVENTION: PROTEIN FUSION ENZYME  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pernie & Edmonds  
STREET: 2030 Sand Hill Road  
CITY: Menlo Park  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/152-481B  
FILING DATE: No. 552990e-be: 12, 1991  
CORRESPONDENCE ADDRESS:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/724-281  
FILING DATE: 01 OCT-1996

1 APPLICATION NUMBER: 7/857,602  
2 FILING DATE: March 30, 1992  
3 PRIOR APPLICATION DATA:  
4 APPLICATION NUMBER: 923,692  
5 FILING DATE: July 31, 1992  
6 PRIOR APPLICATION DATA:  
7 APPLICATION NUMBER: 600,244  
8 FILING DATE: October 22, 1990  
9 PRIOR APPLICATION DATA:  
10 APPLICATION NUMBER: 641,617  
11 FILING DATE: January 16, 1991  
12 ATTORNEY/AGENT INFORMATION:  
13 NAME: Halling, Albert F.  
14 REGISTRATION NUMBER: 25,227  
15 REFERENCE/DOCKET NUMBER: BIOG 20240/8123-040  
16 TELECOMMUNICATION INFORMATION:  
17 TELEPHONE: (415) 854-3660  
18 TELEX: 66141 PENNIE  
19 INFORMATION FOR SEQ ID NO: 2:  
20 SEQUENCE CHARACTERISTICS:  
21 LENGTH: 478  
22 TYPE: amino acid  
23 STRANDEDNESS: Single  
24 TOPOLOGY: Linear  
25 MOLECULE TYPE: DNA  
26 DESCRIPTION: DNA  
27 HYPOTHEtical: NO  
28 ANTI-SENSE: NO  
29 ORIGINAL SOURCE:  
30 ORGANISM:  
31 IMMEDIATE SOURCE:  
32 CLONE:  
33 FEATURE:  
34 US-08-152-483B-9

Query Match: 69.18; Score 12; DB 1; Length 478;  
Best Local Similarity 100.0%; Prod. No. 19e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DQVMD 7  
DB 316 DQVMD 301

RESULT 1:  
US-08-152-483B-9  
Sequence 1, Application: US/04-04281  
Patent No. 584089  
GENERAL INFORMATION:  
APPLICANT: SCHLEGEL, C. Richard  
APPLICANT: JENSEN, A. Bennett  
TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724-281  
FILING DATE: 01 OCT-1996

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1 CLASSIFICATION: 424
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: US 60/004,691
4 FILING DATE: 02-OCT-1995
5 ATTORNEY/AGENT INFORMATION:
6 NAME: Teskin, Robin L.
7 REGISTRATION NUMBER: 35,030
8 REFERENCE/DOCKET NUMBER: C10091-015
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: (703) 836-6620
11 TELEFAX: (703) 836-2021
12 INFORMATION FOR SEQ ID NO: 1:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 508 amino acids
15 TYPE: amino acid
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 MOLECULE TYPE: protein
19 US-09-914-281.1

Query Match 68.1%; Score 32; DB 2; Length 508;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQVMQV 8
DB 200 EDSQVMDI 207

RESULT 13
US-09-252-991A-21308
; Sequence 21308, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubinfeld et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ABRUGINCSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,901A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 3142
; SEQ ID NO 21308
; LENGTH: 1357
; TYPE: PPT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21308

Query Match 68.1%; Score 32; DB 4; Length 1357;
Best Local Similarity 85.7%; Pred. No. 6.1e+22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQVMDVD 9
DB 603 GQVMDVD 609

RESULT 14
US-09-227-157-635
; Sequence 635, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P201291
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,503
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,911
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08

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1	EARLIER APPLICATION NUMBER: 60/051,915	
2	EARLIER FILING DATE: 1997-07-08	
3	EARLIER APPLICATION NUMBER: 60/051,920	
4	EARLIER FILING DATE: 1997-07-28	
5	EARLIER APPLICATION NUMBER: 60/052,133	
6	EARLIER FILING DATE: 1997-07-28	
7	EARLIER APPLICATION NUMBER: 60/052,195	
8	EARLIER FILING DATE: 1997-07-28	
9	EARLIER APPLICATION NUMBER: 65/051,419	
10	EARLIER FILING DATE: 1997-07-28	
11	EARLIER APPLICATION NUMBER: 65/051,428	
12	EARLIER FILING DATE: 1997-07-28	
13	EARLIER APPLICATION NUMBER: 65/051,422	
14	EARLIER FILING DATE: 1997-08-18	
15	EARLIER APPLICATION NUMBER: 65/051,423	
16	EARLIER FILING DATE: 1997-08-18	
17	EARLIER APPLICATION NUMBER: 60/055,448	
18	EARLIER FILING DATE: 1997-08-18	
19	EARLIER APPLICATION NUMBER: 60/055,449	
20	EARLIER FILING DATE: 1997-08-18	
21	EARLIER APPLICATION NUMBER: 60/055,453	
22	EARLIER FILING DATE: 1997-08-19	
23	EARLIER APPLICATION NUMBER: 60/055,950	
24	EARLIER FILING DATE: 1997-08-18	
25	EARLIER APPLICATION NUMBER: 60/055,947	
26	EARLIER FILING DATE: 1997-08-18	
27	EARLIER APPLICATION NUMBER: 60/055,964	
28	EARLIER FILING DATE: 1997-08-18	
29	EARLIER APPLICATION NUMBER: 60/056,460	
30	EARLIER FILING DATE: 1997-08-18	
31	EARLIER APPLICATION NUMBER: 65/055,484	
32	EARLIER FILING DATE: 1997-08-18	
33	EARLIER APPLICATION NUMBER: 65/055,484	
34	EARLIER FILING DATE: 1997-08-18	
35	EARLIER APPLICATION NUMBER: 60/056,464	
36	EARLIER FILING DATE: 1997-08-18	
37	EARLIER APPLICATION NUMBER: 60/056,464	
38	EARLIER FILING DATE: 1997-08-18	
39	EARLIER APPLICATION NUMBER: 60/056,485	
40	EARLIER FILING DATE: 1997-09-12	
41	EARLIER APPLICATION NUMBER: 60/056,484	
42	EARLIER FILING DATE: 1997-09-12	
43	NUMBER OF SEQ ID NOS: 672	
44	SOFTWARE: Patent In War. 2.3	
45	SEQ ID NO: 635	
46	LENGTH: 95	
47	TYPE: FMT	
48	ORGANISM: Homo Sapiens	
49	CS: 207,397,435	

Cy	1	EDGGV	DVD	9
		11	11	11
Op	22	EDGGIMFVDE		31

RESULT 14  
 US 59 779 910 1  
 7 Sequence 1, Application US/5977910  
 7 Patent No. 5847291  
 7 GENERAL INFORMATION:  
 7 APPLICANT: Baraban, Olga  
 7 APPLICANT: Golik, Surya K.  
 7 APPLICANT: Hillman, Jennifer L.  
 7 TIME OF INVENTION: NOVEL HUMAN ACETONIS BEN  
 7 TIME OF INVENTION: ULATOR  
 7 NUMBER OF SEQUENCES: 3  
 7 CORRESPONDENCE ADDRESS:

GenCore version 5.1.6  
Copyright (c) 1993 2003 CompuGen Ltd.

OM protein - protein search, using sw moduli

Run on: November 5, 2003, 15:48:11 / Search time 7.14376 seconds  
(without alignments)  
121.147 Million cell updates/sec

Title: US-09-914-088-1

Perfect score: 47

Sequence: 1 EGGQVMDV 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 223308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 281304

Minimum DB seq length: 3

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR061\*

1: Pir1\*

2: Pir2\*

3: Pir3\*

4: Pir4\*

Prod No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	47	100.0	426	2	136948		Ig epsilon chain - chimpanzee (fragment)
2	47	100.0	428	2	EHU		Ig epsilon chain - human
3	38	80.8	118	2	G84147		probable transcrip
4	36	76.6	480	2	T46304		hypothetical prote
5	36	76.6	655	2	G87374		probable transcrip
6	35	74.5	198	2	E87391		hypothetical prote
7	35	74.5	265	2	E69160		hypothetical prote
8	35	74.5	846	2	A12134		hypothetical prote
9	35	74.5	1275	2	T49163		hypothetical prote
10	35	74.5	1355	2	T16580		hypothetical prote
11	34	72.3	203	2	C95882		probable transcrip
12	34	72.3	210	2	D96531		hypothetical prote
13	34	72.3	264	2	B95335		hypothetical prote
14	34	72.3	286	2	D63272		hypothetical prote
15	34	72.3	561	2	G84244		DNA ligase (import
16	34	72.3	677	2	A69217		sensory transduct
17	34	72.3	841	2	JQ0647		proprotein transla
18	34	72.3	1379	2	S64603		YTA7 protein - yea
19	33	70.2	189	2	P23036		hnaf protein - Syn
20	33	70.2	287	2	JC5550		hnaf protein - Syn
21	33	70.2	314	2	T13517		hypothetical prote
22	33	70.2	347	2	H84270		betanyleucanin dip
23	33	70.2	448	2	F83628		beta-alanine-pyruv
24	33	70.2	503	2	A95359		putative ABC trans
25	33	70.2	634	2	T30732		hypothetical prote
26	33	70.2	725	2	T13514		probable kinase/ph
27	33	70.2	860	2	S76534		hypothetical prote
28	33	70.2	1155	2	B96761		probable protein k
29	33	70.2	1491	2	T28048		hypothetical prote

ALIGNMENTS

RESULT: 1

136948

Ig epsilon chain - chimpanzee (fragment)

C:Species: Pan troglodytes (chimpanzee)

C:Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jan-2000

C:Accession: I36948

R:Sakoyama, Y.; Hong, K.

Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987

A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangut

A:Reference number: I36948; MUI:87147196; PMID:3103123

A:Accession: I36948

A:Status: preliminary; translated from GB/EMBL/DBE

A:Molecule type: DNA

A:Residues: 1-426 <RES>

A:Cross-references: GR:M1398; NID:G176797; PIR:AAA35416.1; PID:G176798

C:Genetics:

A:Introns: 103/1; 209/1; 317/1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:336-405/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 47; DB 2; Length 426;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGGQVMDV 9

DB 149 EGGQVMDV 157

RESULT 2

EHU

Ig epsilon chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1981 #sequence\_revision 13-Jun-1983 #text\_change 16-Jul-1999

C:Accession: A22771; A21195; PH12.4; A9491; A90824; A94418; B93933; SC2438; A53116; C4

R:Flanagan, J.G.; Rabbitts, T.H.

EMBO J. 1, 655-660, 1982

A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region ger

A:Reference number: A22771; MUI:84236029; PMID:6234164

A:Accession: A22771

A:Molecule type: DNA

A:Residues: 1-428 <FLA>

A:Cross-references: GB:J00022; GB:V00555; NID:G185035

R:Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.

EMBO J. 1, 1539-1544, 1982

A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudo

A:Reference number: A23195; MUI:84207910; PMID:6327276

A:Accession: A23195

A:Molecule type: DNA

A:Residues: 2-428 <JEU>

A:Cross-references: GB:J00022; NID:G184755

R:Zhang, K.; Saxon, A.; Max, E.H.

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A:Experimental source: B cell myeloma J-266
A:Note: sequence extracted from NCBI Backbone (NCBIP:125299);
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 401-428 <HE3>
A:Cross-references: DB:553497; NID:G263162; PIDN:AAB24855.1; PTD:G263163
A:Experimental source: B cell myeloma J-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483);
C:Genetics:
A:Gene: GBR1GR
A:Cross-references: GDB:119335; CMV:147180
A:Map position: 14932.31-14932.33
A:Introns: 1/1; 104/1; 111/1; 19/1
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (L) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a C-subfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglobulin; immunoglobulin homology <IM>
F:128-195/Domain: immunoglobulin homology <IM2>
F:232-301/Domain: immunoglobulin homology <IM3>
F:339-407/Domain: immunoglobulin homology <IM4>
F:4/Disulfide bonds: interchain (to light chain); #status: predicted
F:108-295/Disulfide bonds: interchain (to heavy chain); #status: predicted
F:21-49/99:146,252,275/Binding site: carbohydrate (ASN) (covalent) #status: experimental
F:21,209/Disulfide bonds: interchain (to heavy chain); #status: predicted
Query Match 100.0%; Score 47; DB 1; Length 428;
Best Local Similarity 100.0%; Pred No. 0.26; 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY : EGGQWMDVC 9
|||
DB 151 EGGQWMDVC 159

RESULT 3
GB4322
50S ribosomal protein L24P (imported); - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: GB4322
R:NG, M.V.; Kennedy, S.P.; Makrides, G.G.; Perquist, B.; Pan, M.; Shukla, H.D.; Lasky, J.; Leibauser, B.; Kellert, K.; Cruz, R.; Datsun, M.; Hough, D.W.; Maddocks, D.G.; Jachung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hsu, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebnhardt, N.; Lowe, T.M.; Jachung, K.H.; Alam, M.; Freitas, T.
A:Title: Genomic sequence of Halobacterium species NRC-1.
A:Reference number: A94460; X110:2053483; YN16110:16950
A:Accession: GB4322
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <STG>
A:Cross-references: GB:AE004437; NID:gl0561170; PIDN:AAG19947.1; GSPDB:GK00138
C:Genetics:
A:Gene: rpl24P
C:Superfamily: 3a: ribosomal protein L26
Query Match 92.9%; Score 38; DB 2; Length 118;
Best Local Similarity 77.8%; Pred No. 3.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EGGQWMDVC 9
|||
DB 59 EGGQWMDVC 59

RESULT 4
T46047
Hypothetical protein T46047.160 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
A:Accession: T46047

```

R. Ringert, N. Gabel, C. Mueller-Auer, S. Schaner, M. Zipp, M. Xewes, H.W. Jemke, submitted to the Protein Sequence Database, January 2003  
 A:Reference number: 223015  
 A:Accession: T46047  
 A>Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1480 <R>  
 A:Cross-references: EMBL:AL132965  
 A:Experimental source: cultivar Columbia; EAC clone T46-  
 C:Genetics:  
 A:Map position: 3  
 A:Title: NS: 420/24 4513  
 A:Note: T46K5.166

Query Match 76.6% Score 36.75 DB 2 Length 480  
 Best Local Similarity 75.0% Pred. No. 40  
 Matches 6 Conservative 2 Mismatches 0 Indels 0 Gaps 0

QY 2 EDSQWMDVD 9  
 |||||  
 DB 40 EDSQVLDLD 27

RESULT 5  
 581306  
 hypothetical protein (imported) - Caulobacter crescentus  
 C:Species: Caulobacter crescentus  
 C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
 C:Accession: G81306  
 R:Neiman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.R.; Eisen, J.A.; Heidelberg, J.B.; Laub, M.T.; Deasy, R.T.; Dodson, R.N.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, M.J.; Trevisan, V.; White, O.; Salzberg, S.L.; Shapiro, P.; Venter, A.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A:Title: Complete Genome Sequence of Caulobacter crescentus  
 A:Reference number: A87249; NCID:21173498; PMID:11259647  
 A:Accession: G87306  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1465 <S>  
 A:Cross-references: GB:AE005673; NID:01142170; PIRN:AAR4451.1; GSPT:GN00148  
 C:Genetics:  
 A:Gene: 500454  
 C:Superfamily: hcr-dsRNA ligase

Query Match 76.6% Score 36.75 DB 2 Length 480  
 Best Local Similarity 75.0% Pred. No. 56  
 Matches 6 Conservative 2 Mismatches 0 Indels 0 Gaps 0

QY 2 EDSQWMDVD 9  
 |||||  
 DB 41 EDSQVLDLD 49

RESULT 6  
 581391  
 Probable transcription regulator C10466 (imported) - Caulobacter jejuni strain NCYC 1  
 C:Species: Caulobacter jejuni  
 C:Date: 31-Mar-2000 #sequence\_revision 11-Mar-2000 #text\_change 03-Jun-2002  
 C:Accession: E81391  
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kell, D.; M. O'Connor, C.; Basham, D.; Chilling, N.W.; Quail, M.; Rajandream, M.A.; Krumholz, L.; Venter, A.; Whitehead, S.; Barrett, Nature 403, 665-668, 2000  
 A:Title: The genome sequence of the food-borne pathogen, *Caulobacter jejuni* reveals hyp  
 A:Reference number: A81250; NCID:20150912; PMID:10568524  
 A:Accession: E81391  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1198 <P>  
 A:Cross-references: GB:AL139075; GB:AL131187; NCIC:000000.1; PIRN:AE-8104.1; PIR:G696793  
 A:Experimental source: serotype O2, strain NCTC 11637  
 C:Genetics:  
 A:Gene: C10466

Query Match 74.5% Score 35; DB 2 Length 198;  
 Best Local Similarity 44.4% Pred. No. 23;  
 Matches 4 Conservative 5 Mismatches 0 Indels 0 Gaps 0

QY 1 EDSQWMDVD 9  
 |||||  
 DB 83 EDSQVLDLD 91

RESULT 7  
 569160  
 hypothetical protein MTH462 - Methanobacterium thermoautotrophicum (strain Delta H)  
 C:Species: Methanobacterium thermoautotrophicum  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
 C:Accession: E69160  
 R:Smith, D.R.; Doucette-Stamm, L.A.; DeGugliery, C.; Lee, H.; Dubois, C.; Aldredge, T.; Odu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; S. Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, C.N.; J. Bacteriol. 179, 7115-7155, 1997  
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func  
 A:Reference number: A69300; NCID:38017514; PMID:93711463  
 A:Accession: E69160  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1265 <M>  
 A:Cross-references: GB:AE000830; GB:AE000666; NID:02621523; PIRN:AAR4968.1; PIR:G26215  
 A:Experimental source: strain Delta H  
 C:Genetics:  
 A:Gene: MTH462

Query Match 74.5% Score 35; DB 2 Length 265;  
 Best Local Similarity 55.6% Pred. No. 31;  
 Matches 5 Conservative 4 Mismatches 0 Indels 0 Gaps 0

QY 1 EDSQWMDVD 9  
 |||||  
 DB 155 EDSQVLDLD 163

RESULT 8  
 A12336  
 ribosomal protein N (imported) - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp. strain PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
 C:Accession: A12336  
 R:Kaneko, T.; Nakamura, Y.; Waki, C.; Kurita, T.; Sasamoto, S.; Watanabe, A.; Iriouchi, N.; Nakazaki, M.; Shimada, S.; Sugimoto, M.; Takizawa, M.; Yamada, M.; Tabata, DNA Res. 9, 225-233, 2002  
 A:Title: Complete genomic sequence of the filamentous nitrogen-fixing *Cyanobacterium* An  
 A:Reference number: A12336; NCID:11595451; PMID:11759843  
 A:Accession: A12336  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1846 <R>  
 A:Cross-references: GB:BA00013; NID:BA875947.1; PID:gl7133383; GSFCR:GN00179  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: al14248

Query Match 74.5% Score 35; DB 2 Length 846;  
 Best Local Similarity 66.7% Pred. No. 124+02;  
 Matches 6 Conservative 2 Mismatches 1 Indels 0 Gaps 0

QY 1 EDSQWMDVD 5  
 |||||  
 DB 130 EDSQVLDLD 289

RESULT 9  
 749362  
 hypothetical protein B11160 (imported) - *Neurospora crassa*  
 C:Species: *Neurospora crassa*

C>Date: 22 Jun-2000 #sequence\_revision 02 Jun-2000 #text\_change 02 Jun-2000  
 C/Accession: T49362  
 C/Authors: U. Algr, V. Hohlseil, J. Brandt, P. Fatmann, B. Holland, R. Nyakatura,  
 submitted to the Protein Sequence Database, May 2000  
 A/Title: The complete sequence of the 1,643-kb psym<sup>+</sup> plasmid from the N2-fixing endo  
 A/Reference number: 225022  
 A/Accession: T49362  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-1275 <5'3'>  
 A/Cross-references: EMBL:AL355927; GSI08:GNC0174; NCSP:R10110  
 A/Experimental source: EAC clone 51L1; strain 0874A  
 C/Genetics:  
 A/Genes: NCSP:51L1; fcd  
 A/Map position: 6  
 A/Insertions: 2473

Query Match 74.5% Score 150 DB 2 Length 1275  
 Best Local Similarity 66.7% Pred. No. 36  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 1 EDGQWVVD 9  
 |||||  
 DB 1116 EDGQWVVD 1124

RESULT 10  
 116580  
 Hypothetical protein K07512.1 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 22 Sep 1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C/Accession: 116580  
 A/Title: Submitted to the EMBL Data Library, May 1994  
 A/Reference number: 116580  
 A/Accession: 116580  
 A/Status: preliminary; translated from GB EX024300  
 A/Molecule type: DNA  
 A/Residues: 1-1305 <5'3'>  
 A/Cross-references: EMBL:J02554; NID:948514; FID:948514; IJDA:AAA-0915.1; CESP:K07512  
 A/Experimental source: strain Bristol N2  
 C/Genetics:  
 A/Genes: CESP:K07512.1  
 A/Insertions: 467; 867; 207; 2787; 4307; 8717; 9277; 15557; 15221; 147873  
 1-501473; 425973; 606572; 726673; 789737; 86977; 872573; 88473; 103373; 122347; 1223

Query Match 74.5% Score 150 DB 2 Length 1275  
 Best Local Similarity 66.7% Pred. No. 36  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 1 EDGQWVVD 9  
 |||||  
 DB 1116 EDGQWVVD 1124

RESULT 11  
 09582  
 probable transcription regulator protein (pmsr-1) - Sinorhizobium meliloti (strain 102)  
 C/Species: Sinorhizobium meliloti  
 C/Date: 24-Aug-2001 #sequence\_revision 24 Aug 2001 #text\_change 30-Sep-2001  
 C/Accession: C9582  
 A/Title: N. W. Weidner, S. Wong, K. Khristova, J. J. Dunn, B. Votholter, F. J. Hernan  
 Proc. Natl. Acad. Sci. U.S.A. 98, 9449-9454, 2001  
 A/Reference number: A95842; MUID:2195068; EMBL:114414.1  
 A/Accession: C9582  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-203 <5'3'>  
 A/Cross-references: EMBL:A95842; FID:114414; GSI:GNC0169  
 A/Experimental source: strain 1021, mesoplasmid pSymB  
 R/Galbert, F. J. Dunn, C. M. Long, S. F. Palmer, A. J. Allen, F. J. Parley Butler,  
 P. A. Chain, R. Towse, A. J. Davis, R. W. Drake, S. J. Pedersen, R. A. Fisher, R. F. J.

L. Hyman, R. W. Jones, T.  
 Science 293, 668-672, 2001  
 A/Authors: Kahn, D.; Kahn, M.; Kaimar, S.; Keating, D. H.; Kiss, E.; Komp, C.; Delaure  
 hebaull, P.; Vandenbol, M.; Vornolter, F. J.; Weidner, S.; Wells, D. H.; Wong, K.; Yeh, F.  
 A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
 A/Reference number: A95842; MUID:2136234; PMID:11474104  
 C/Genetics:  
 A/Contents: annotation  
 A/Genes: SMB20317  
 A/Genome: plasmid

Query Match 72.3% Score 34 DB 2 Length 203  
 Best Local Similarity 62.5% Pred. No. 36  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 2 DGGQWVVD 9  
 |||||  
 DB 148 DGGQWVVD 155

RESULT 12  
 D96531  
 Hypothetical protein F13P21.9 (imported) - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 22-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C/Accession: D96531  
 A/Title: Theologis, A.; Ecker, J. R.; Palm, C. C.; Pederspiel, N. A.; Kaul, S.; White, C.; Alonso  
 Chin, C. W.; Chung, M. K.; Conn, A.; Conway, A. B.; Conway, A. R.; Creasy, T. H.; Dewar, K.  
 ansen, N. F.; Hughes, B. J.; Huizar, L.  
 Nature 406, 816-820, 2000  
 A/Authors: Hunter, C.; Jenkins, J.; Johnson Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C. A.; Li, J. H.; Lin, X.; Liu, Z. A.; Luros, C. S.; Maiz, R.; Marziani  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A/Authors: Salzberg, S.; Schwartz, J. P.; Shinn, P.; Southwick, A. M.; Sun, R.; Tallon  
 ker, M.; Wu, F.; Yu, G.; Fraser, C. W.; Venter, J. C.; Davis, R. W.  
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A/Reference number: A86144; MUID:21016719; PMID:1130742  
 A/Accession: D96531  
 A/Status: preliminary  
 A/Molecule type: RNA  
 A/Residues: 1-210 <5'3'>  
 A/Cross-references: GSI:8505173; NID:95430754; PID:AA043154.1; GSPDB:GNC0144  
 A/Genes: F13P21.9  
 A/Map position: 1

Query Match 72.3% Score 34 DB 2 Length 210  
 Best Local Similarity 55.6% Pred. No. 38  
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

CY 1 DGGQWVVD 9  
 |||||  
 DB 136 DGGQWVVD 144

RESULT 13  
 B90535  
 Hypothetical protein MYPU1863 (imported) - Mycoplasma pulmonis (strain UAB CTIP)  
 C/Species: Mycoplasma pulmonis  
 C/Date: 24-May 2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug 2001  
 C/Accession: B90535  
 A/Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pu  
 A/Reference number: A99512; MUID:21267165; PMID:11353084  
 A/Accession: B90535  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-264 <5'3'>  
 A/Cross-references: GSI:AL443566; FID:914089599; PID:GAC13359.1; GSPDB:GNC00153  
 A/Experimental source: strain UAB CTIP  
 C/Genetics:  
 A/Genes: MYPU1860





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QM protein protein search, using sw mode.

Run on: November 5, 2003, 15:44:15 Search time 3.6420 seconds  
without alignment  
115,748 Million cell updates/sec

Title: US 09 914 088 1

Perfect score: 47

Sequence: EDSYKQWD 9

Scoring table: SCSUM62

Searched: 127463 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Testing first 45 summaries

Database: SwissProt\_41\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	428	EPC_HUMAN	P01854 homo sapien
2	37	78.7	980	PYAL_HUMAN	O84004 homo sapien
3	36	76.6	655	SYT_TARTR	O94008 caudo bacter
4	36	76.6	677	BAUS_BAMMO	O94106 bomyx mori
5	34	72.3	561	DNUI_HALWI	O94135 bacteri
6	34	72.3	841	SECA_BAFSC	I24466 bacillus su
7	34	72.3	1379	TBP7_TENAT	I40440 saccharomy
8	33	70.2	287	DNAT_STN7	P50726 synechococ
9	33	70.2	634	NTRP_MVU1	O94169 moluscum c
10	33	70.2	860	GYSA_HUNY	O94134 synechocyst
11	33	70.2	877	PMT1_HANAL	I41193 cardida alb
12	33	70.2	1119	KPOB_TREAU	I40400 thermus aqu
13	32	68.1	95	CH10_BERFE	I44421 bordetella
14	32	68.1	97	RL21_METJA	O84021 methanosarc
15	32	68.1	121	Y408_METJA	O84051 methanococ
16	32	68.1	211	UPPD_PRAAE	O84009 pyrobaculum
17	32	68.1	235	CAAT_PBPBK	I94111 populus kit
18	32	68.1	240	RR40_YEAST	O94125 saccharomy
19	32	68.1	272	TYRO_STEAT	P01824 streptomyce
20	32	68.1	367	GCST_MVCTC	O94136 mycobacteri
21	32	68.1	398	AMPI_AEATH	O94155 arabidopsi
22	32	68.1	501	VLI1_PRAVE	I11126 europaei el
23	32	68.1	508	VLI1_PRAVE	O94159 human papil
24	32	68.1	513	VLI1_PRAVE	O94154 deer papil
25	32	68.1	556	ILV5_THETN	O84135 thermobac
26	32	68.1	602	SYD_TREPA	O84124 tyrocinema p
27	32	68.1	631	NTP1_VACCA	O94114 vaccinia vi
28	32	68.1	631	NTP1_VACCA	O94114 vaccinia vi
29	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
30	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
31	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
32	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
33	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
34	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
35	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
36	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
37	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
38	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
39	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
40	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
41	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
42	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
43	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
44	32	68.1	631	NTP1_VACV	O94114 vaccinia vi
45	32	68.1	631	NTP1_VACV	O94114 vaccinia vi

34	31.5	67.0	218	1	NIPL_MOUSE	Q32217 mus muscula
35	31.5	67.0	219	1	NIPL_HUMAN	O6C236 homo sapien
36	31	66.0	119	1	RJ24_HALWA	P10972 halocaula
37	31	66.0	145	1	RJ13_HALWA	P23198 halocaula
38	31	66.0	171	1	CRIO_MOUSE	P51865 mus muscula
39	31	66.0	180	1	ROC2_AGRRH	P43408 agrobacteri
40	31	66.0	217	1	P85_METJA	P54045 methanococ
41	31	66.0	222	1	YAGY_ECOLI	P71788 escherichia
42	31	66.0	251	1	GJFR_PSEAF	Q51391 pseudomonas
43	31	66.0	258	1	AFGB_SALTY	Q82K17 salmoneilla
44	31	66.0	282	1	PDHD_STRCO	Q92B00 streptomyce
45	31	66.0	290	1	CMFK_SCHPC	Q9USK4 schizosacch

## ALIGNMENTS

### RESULT 1

ID	EPC_HUMAN	STANDARD	PRT	428 AA
AC	PC1854			
DT	21-JUL-1986 (Rel. 0)	Created		
DT	21-JUL-1986 (Rel. 0)	Last sequence update		
DT	15-SEP-2003 (Rel. 42)	Last annotation update		
DE	Ig epsilon chain C region			
GN	IGHF			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo			
OX	NCBI_TaxID=9606			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81168997; PubMed=6300763			
RA	Seno M., Kurokawa T., Oda Y., Onda H., Sasada R., Igarashi K.,			
RA	Kikuchi M., Sugino Y., Nishida Y., Honjo T.			
RT	"Molecular cloning and nucleotide sequencing of human immunoglobulin			
RT	epsilon chain cDNA"			
RL	Nucleic Acids Res. 11:719-726(1983)			
RN	[2]			
RP	SEQUENCE FROM N.A. AND VARIANT IED=359			
RX	MEDLINE=83001945; PubMed=6288268			
RA	Max E.B., Ratley J., Ney R., Kirsch I.R., Leder P.			
RT	"Duplication and deletion in the human immunoglobulin epsilon genes"			
RL	Cell 29:691-699(1982)			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84236029; PubMed=6234164			
RA	Flanagan J.G., Rabbitts T.H.			
RT	"The sequence of a human immunoglobulin epsilon heavy chain constant			
RT	region gene, and evidence for three non allelic genes"			
RL	EMBO J. 1:655-660(1982)			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84207910; PubMed=6127276			
RA	Jeda S., Naka S., Nishida Y., Hisajima H., Honjo T.			
RT	"Long terminal repeat-like elements flank a human immunoglobulin			
RT	epsilon pseudogene that lacks introns"			
RL	EMBO J. 1:1539-1544(1982)			
RN	[5]			
RP	PRELIMINARY SEQUENCE 'MYELOMA PROTEIN ND'			
RA	Bernick H.H., Johansson S.G.O., von Bahr-Lindstrom H.			
RL	(In) Bach M.R. (eds.)			
RT	Immediate hypersensitivity: modern concepts and developments, pp. 1-36,			
RT	Marcel Dekker, New York (1978)			
RN	[6]			
RP	SEQUENCE OF 1,423, 68-114 AND 427-428 FROM N.A.			
RX	MEDLINE=8306233; PubMed=6815656			
RA	Kentel S.H., Molgaard H.V., Houghron M., Derbyshire R.B., Viney J.,			
RA	Beit D.G., Gould H.J.			
RT	"Cloning and sequence determination of the gene for the human			
RT	immunoglobulin epsilon chain expressed in a myeloma cell line"			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982)			
RN	[7]			





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DR EMBL: AB032717; BAB19763.1;  
 DR SP: G00030444; F4Hsp7C protein binding activity; HA.  
 DR InterPro: IPR003103; BAG.  
 DR Pfam: PF02179; BAG; 1.  
 DR SMART: SMCC264; BAG; 1.  
 KW Chaperone; Developmental protein.  
 FT DOMAIN 22 25 POLY QIU.  
 FT DOMAIN 103 141 GLN-RICH.  
 FT DOMAIN 233 380 GLN/RG-RICH.  
 FT DOMAIN 607 643 LYS-RICH.  
 FT DOMAIN 380 457 BAG.  
 SQ SEQUENCE 677 AA; 75979 MW; 308174CAF054FB49 CRC64;

Query Match 76.68; Score 46; DB 1; Length 677;  
 Best Local Similarity 87.58; Prol No. 34;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 EDGQWVDV 9  
 DB 665 DSQWQVDV 672

RESULT 5  
 DNDL HALLM  
 ID DNDL HALLM STANDARD; PRT: 661 AA.  
 AC CSH3A;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28 FEB 2003 (Rel. 41, Last annotation update)  
 DE CNA ligase (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP])  
 GN C3 OR VNGC44G.  
 OS Halobacterium sp. (strain NRC 1 / ATCC 700522 / JCV 115411)  
 CC Archaea; Euryarchaeota; Halobacteria; Halomicrobiales;  
 CC Halobacteriaceae; Halobacterium.  
 OX NCBI TaxID:64091;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2050448; PubMed=1116959;  
 RA Ng W.V., Kennedy S.P., Mahaitas G.J., Verquet R., Hsu M.,  
 RA Shukla H.D., Busky S.R., Hallica M., Thompson T., Hsu M.,  
 RA Swartzel S., Wolf D., Hall J., Hsu M., Mahaitas G.J.,  
 RA DeRubeis P., Folter K., Cruz P., Hsu M., Mahaitas G.J.,  
 RA Maddocks E.G., Halconski P.E., Krebs V., Mahaitas G.J.,  
 RA Isenbarger T.A., Beck R.F., Pohlschmidt M., Stahlhut M.,  
 RA Adam M., Freitas T., Hou S., Daniels T.J., Hsu M.,  
 RA Ehrhardt H., Lowe T.M., Liang P., Riley M., Hsu M.,  
 RA "Genome sequence of Halobacterium species NRC 1".  
 RA Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).  
 CC ! FUNCTION: THIS PROTEIN SEALS DURING DNA REPLICATION. DNA  
 RECOMBINATION AND DNA REPAIR NICKS IN DOUBLE-STRANDED DNA BY  
 SIMILARITY.  
 CC ! CATALYTIC ACTIVITY: ATP + [deoxyribonucleotide] N  
 CC [deoxyribonucleotide] (X) = AMP + diphosphate +  
 CC [deoxyribonucleotide] (N-M).  
 CC ! SIMILARITY: BELONGS TO THE ATP-DEPENDENT DNA LIGASE FAMILY.  
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DR EMBL: AE005027; AAC19323.1;

DR PIR: G84244; G94244.  
 DR HAVAP: MF C0407; 1.  
 DR InterPro: IPR000977; DNA\_ligase.  
 DR Pfam: PF01068; DNA\_ligase; 1.  
 DR Pfam: PF04679; DNA\_ligase\_A\_C; 1.  
 DR Pfam: PF04675; DNA\_ligase\_A\_N; 1.  
 DR TIGRFAMs: TIGR00574; dn1; 1.  
 DR PROSITE: PS00697; DNA\_LIGASE\_A1; 1.  
 DR PROSITE: PS01331; DNA\_LIGASE\_A2; 1.  
 DR PROSITE: PS01601; DNA\_LIGASE\_A3; 1.  
 KW DNA repair; DNA replication; DNA recombination; Cell division; Ligase;  
 KW ATP-binding; Compensate proteome.  
 FT BINDING 255 255 AMP (BY SIMILARITY).  
 SQ SEQUENCE 561 AA; 59639 MW; 5B530D3C1D106D2E CRC64;

Query Match 72.38; Score 34; DB 1; Length 561;  
 Best Local Similarity 55.68; Prol No. 66;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQWVDV 9  
 DB 497 EDGQWVDV 505

RESULT 6  
 SECA BACSU  
 ID SECA BACSU STANDARD; PRT: 841 AA.  
 AC P28366;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Preprotein translocase secA subunit.  
 GN SECA OR DIV.  
 OS Bacillus subtilis  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI TaxID:1423;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168 / Marburg;  
 RX MEDLINE=91192600; PubMed=1301557;  
 RA Sadale Y., Takamatsu H., Nakamura K., Yamae K.;  
 RT "Sequencing reveals similarity of the wild-type div+ gene of Bacillus  
 subtilis to the Escherichia coli secA gene".  
 RL Gene 98131-105 (1991).  
 RN 2;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RA Solde B., Lazarevic V., Marel C., Karamata D.;  
 RT "Sequence of the Bacillus subtilis 168 chromosomal region from 105  
 to 307 degree".  
 RL Submitted (JAN 1979) to the EMBL/GenBank/CCRB databases.  
 RN 3;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9394377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bartoro M.G., Bessieres P., Bolotin A., Borchert S.,  
 RA Bortiss R., Boursier L., Brans A., Braun M., Baignell S.C., Bron S.,  
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
 RA Deniset P., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Enlihan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fura S., Galizzi A., Galleron N.,  
 RA Ghim S.V., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,  
 RA Guiseppe S., Guy R.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Karamata Y., Klier-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,  
 RA Medura N., Mellado R.F., Mizuno M., Mestl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Pourcelot C., Prescott A.M.,



```

KW Chapterone; DNA replication; Heat shock.
FT DOMAIN 4 73 J-DOMAIN.
SQ SEQUENCE 287 AA; 157406 MW; 3102156F87E62E04F CRC64;

Query Match 72.3%; Score 34; DB 1; Length 1379;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQVMVLD 9
DB 57 EDGQVMVLD 65

RESULT 8
DNAB SYNP7 STANDARD; EXT: 287 AA.
AC PS00267;
DT 31-OCT-1996 (Rel. 34, Created);
DT 15-DEC-1999 (Rel. 37, Last sequence update);
DT 16-OCT-2001 (Rel. 40, Last annotation update);
DE Chapterone protein dnab.
GN DNAB
OS Synchococcus sp. strain PCC 7942; (Anacystis nidulans 221).
CC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.
CX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:9738245; PubMed:924046;
RA Ouchii K., Nimura K., Yoshikawa H., Takahashi H.,
RT "Sequence and analysis of a dnab homologue gene in cyanobacterium-
RL Synchococcus sp. PCC7942."
RL Biochem. Biophys. Res. Commun. 236:461-466(1997).
RP SEQUENCE OF 189 FROM N.A.
RX MEDLINE:94271243; PubMed=8003021;
RA Nimura K., Yoshikawa H., Takahashi H.;
RT "Sequence analysis of the third dnab homolog gene in Synchococcus
RL Sp. PCC7942."
RL Biochem. Biophys. Res. Commun. 201:848-854(1994).
RN [1]
RP ERATIM
RX MEDLINE:95110350; PubMed:7811295;
RA Nimura K., Yoshikawa H., Takahashi H.,
RL Biochem. Biophys. Res. Commun. 201:848-854(1994).
CC FUNCTION: ACTS AS A CHAPTERONE-DEPENDENT FACTOR IN DNA REPLICATION.
CC THE ATPASE ACTIVITY OF DNAB IS SIMILAR TO
CC SUBCELLULAR LOCATION: CYTOPLASM; BY SIMILARITY.
CC 1- SIMILARITY: BELONGS TO THE DNAB FAMILY.
CC 2- SIMILARITY: CONTAINS 1 J-DOMAIN.
CC
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CC
CC EMBL: AB003529; AAA21679.1;
CC EXRL: U29968; BAA02315.1;
CC PIR: J05550; J05550.
CC PIR: PC2306; PC2306.
CC HSSP: P23685; 18DJ.
CC InterPro: IPR003939; DnaJ_C.
CC InterPro: IPR01623; DnaJ_N.
CC Pfam: PF0226; DnaJ_1.
CC Pfam: PF01556; DnaJ_C_1.
CC PRINTS: P00625; DNAJ-PROTEIN.
CC SMART: SM00393; DnaJ_1.
CC PROSITE: PS00624; DNAJ_1; 1.
CC PROSITE: PS00624; DNAJ_2; 1.

KW Chapterone; DNA replication; Heat shock.
FT DOMAIN 4 73 J-DOMAIN.
SQ SEQUENCE 287 AA; 157406 MW; 3102156F87E62E04F CRC64;

Query Match 70.2%; Score 33; DB 1; Length 287;
Best Local Similarity 55.6%; Pred. No. 52;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMVLD 9
DB 51 EDGQVMVLD 159

RESULT 9
NTPI MCVI
ID NTPI MCVI STANDARD; PRT: 634 AA.
AC Q98267;
DT 30-MAY-2003 (Rel. 35, Created);
DT 30-MAY-2003 (Rel. 35, Last sequence update);
DT 30-MAY-2003 (Rel. 35, Last annotation update);
DE Nucleoside triphosphatase 1 (NTP 3.6.1.15) (Nucleoside triphosphate
DE phosphohydrolase 1) (NTP 1) (MCI00R).
GN MCI00L.
OS Moluscum contagiosum virus subtype 1 (MCIV1).
CC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
CC Moluscipoxvirus.
CX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:96325459; PubMed=9670425;
RA Senkevich T.G., Sugert J.C., Sisler J.R., Koonin E.V., Darai G.,
RA Moss B.;
RT "Genome sequence of a human tumorigenic poxvirus: prediction of
RT specific host response-evasion genes."
RL Science 273:813-816(1996).
CC FUNCTION: SERVES TWO ROLES IN TRANSCRIPTION: IT ACTS IN CONCERT
CC WITH VIRAL TERMINATION FACTOR/CAPPING ENZYME TO CATALYZE RELEASE
CC OF JUNCTION-CONTAINING NASCENT RNA FROM THE ELONGATION COMPLEX, AND
CC IT ACTS BY ITSELF AS A POLYMERASE ELONGATION FACTOR TO FACILITATE
CC REATHRUGH OF INTRINSIC PAUSE SITES (BY SIMILARITY).
CC 1- CATALYTIC ACTIVITY: NTP + H2O -> NDP + phosphate.
CC 2- SIMILARITY: BELONGS TO THE NPH I SUBFAMILY OF HELICASES.
CC
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CC
CC EMBL: U60315; AAC55228.1;
CC PIR: T30702; T30702.
CC InterPro: IPR001410; DEAD.
CC InterPro: IPR001550; Helicase_C.
CC InterPro: IPR000330; SNF2_N.
CC Pfam: PF00271; Helicase_C_1.
CC Pfam: PF00176; SNF2_N_1.
CC SMART: SM00487; DEXDC_1.
CC SMART: SM00490; HELIC_C_1.
CC Hydroxylase; ATP binding; Transcription.
FT DOMAIN 33 311 SNF2_N.
FT DOMAIN 394 480 HELICASE_C.
FT NP BIND 54 61 ATP (BY SIMILARITY).
FT SITE 140 143 DEXH BOX.
SQ SEQUENCE 634 AA; 72102 MW; B786BFA17E12F56 CRC64;

Query Match 70.2%; Score 33; DB 1; Length 634;
Best Local Similarity 65.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQVMVLD 9
DB 51 EDGQVMVLD 159
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DB      598 EDRVYDAD 606
RESULT 10
CYRA SYN3
ID CYRA SYN3 STANDARD; PRT: 460 AA.
AC Q55738;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2003 (Rel. 40, Last annotation update)
DE DNA GYRASE SUBUNIT A (EC 5.99.1.1)
GN CYRA OR S10417;
OS Synchocystis sp. (strain PCC 6803)
CC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
CC NCBI TaxID:1148;
RN [1]
RH SEQUENCE FROM N.A.
RX MEDLINE:96127523; PubMed:9590279;
RA Kaneko T., Tanaka A., Sato S., Kozani H., Suzuki T., Miyajima N.,
RA Sugiura M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome."
RL DNA Res. 2:133-146(1995).
CC [1] FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE
CC STRANDED DNA IN AN ATP DEPENDENT MANNER AND ALSO CATALYZES THE
CC INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE STRANDED
CC DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS
CC CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC [1] SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA
CC BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE
CC ENZYME FORMS AN A2B2 TETRAMER.
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CC
CC EMBL: S64002; BAA10380.1;
CC F1R: S76534; S76534.
CC RSP: PC9097; 1A84.
CC [1] FUNCTION: TOPISOMERASE; DNA GYRASE.
CC [1] INTERPRO: IPR002425; DNA_TopoisoIV
CC Pfam: PF03989; DNA GyraseA_C7_6
CC Pfam: PF03921; DNA Topoisolv; 1.
CC ProDom: PD000947; DNA_topoisolv; 1.
CC SMART: SM00434; TOP4C7_1.
CC TIGRfam: TIGR01063; GYRA; 1.
CC Isoleucine; Topoisomerase; DNA-binding; Complete protein.
KW Isoleucine; Topoisomerase; DNA CLEAVAGE BY SIMILARITY.
FT ACT SIZE 122 122
FT SEQUENCE 860 AA; 95071 MW; 80448914C589475 CRF4.4.
SQ
Query Match 70.2%; Score 33; DB 1; Length 877;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 2; Gaps 0;
QY 1 EGGQVNDV 9
DB 494 EGGELIDV 502
RESULT 11
PMT1 CANAL
ID PMT1 CANAL STANDARD; PRT: 897 AA.
AC Q74158;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dolichyl (1-phosphate)-mannose-protein mannosyltransferase;

```

```

DB      598 EDRVYDAD 606
RESULT 10
CYRA SYN3
ID CYRA SYN3 STANDARD; PRT: 460 AA.
AC Q55738;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2003 (Rel. 40, Last annotation update)
DE DNA GYRASE SUBUNIT A (EC 5.99.1.1)
GN CYRA OR S10417;
OS Synchocystis sp. (strain PCC 6803)
CC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
CC NCBI TaxID:1148;
RN [1]
RH SEQUENCE FROM N.A.
RX MEDLINE:96127523; PubMed:9590279;
RA Kaneko T., Tanaka A., Sato S., Kozani H., Suzuki T., Miyajima N.,
RA Sugiura M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome."
RL DNA Res. 2:133-146(1995).
CC [1] FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE
CC STRANDED DNA IN AN ATP DEPENDENT MANNER AND ALSO CATALYZES THE
CC INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE STRANDED
CC DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS
CC CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC [1] SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA
CC BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE
CC ENZYME FORMS AN A2B2 TETRAMER.
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CC
CC EMBL: AF000232; AAC31119.1;
CC InterPro: IPR003347; GlycoTrans_39.
CC InterPro: IPR003608; MIR.
CC Pfam: PF02815; MIR; 1.
CC Pfam: PF02366; PMT1; 1.
CC SMART: SW00472; MIR; 3.
CC Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Endoplasmic reticulum; Repeat; Multigene family.
FT TRANSMEM 109 129
FT TRANSMEM 150 170
FT TRANSMEM 196 216
FT TRANSMEM 226 246
FT TRANSMEM 252 272
FT TRANSMEM 291 311
FT TRANSMEM 604 624
FT TRANSMEM 643 664
FT TRANSMEM 666 686
FT TRANSMEM 700 720
FT CARBOHYD 83 83
FT CARBOHYD 195 195
FT CARBOHYD 395 395
FT CARBOHYD 400 400
FT CARBOHYD 721 721
FT SEQUENCE 877 AA; 99935 MW; 3B0F6ED9C96DCC16 CRF64;
SQ
Query Match 70.2%; Score 33; DB 1; Length 877;
Best Local Similarity 77.9%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 3; Gaps 0;
QY 1 EGGQVNDV 9
DB 835 EDQVADV 843
RESULT 12
REOB THEAQ
ID REOB THEAQ STANDARD; PRT: 1119 AA.
AC Q9KJ77;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dolichyl (1-phosphate)-mannose-protein mannosyltransferase;

```





Search completed: November 5, 2003, 15:47:55  
Job time : 4.65625 secs

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CC
CC EXBL: AE013498; AAM32232.1; --
DR HAYAP: XE 05369; -- 1.
DR InterPro: IP020147; Ribosomal_L21e.
DR Pfam: PF01157; Ribosomal_L21e; 1. FALSE NEG.
DR PROSITE: PS0171; RIBOSOMAL_L21E; FALSE NEG.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 97 AA; 11090 MW; 2824EFC06A13E9 CRC64;

Query Match 68.1%; Score 12; E: 1; Length 97.
Best Local Similarity 55.6%; Pred. No: 26;
Matches 5; Conservative 3; Mismatches 2; Gaps 0;

CY 1 EDGQWMDV 9
DB 15 EDGQWMDV 43

RESULT 15
Y408 METTA
ID Y408 METTA STANDARD; PRT: 121 AA.
AC 057851;
DT 02-NOV-1997 (Rel: 35, Created:
DT 02-NOV-1997 (Rel: 35, Last sequence update:
DT 16 Oct 2001 (Rel: 40, Last annotation update:
DE Hypothetical protein MJ0408.
GN M50409.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococaceae; Methanocaldococcus.
CX NCBI_TaxID:2193;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN JALAN / DSM 2661 / ATCC 43047;
RX MEDLINE:96330993; PubMed:8688081;
RA Smith C.J., White G., Olsed G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake C.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Krollavag A.R., Dougherty B.A., Tomb J.F., Adams M.D., Belm C.H.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Mettuck J.M., Gloeck A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Ehrlich J.L., Nguyen D.,
RA Uitterback L.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Clifton M.D., Roberts K.M., Hurst V.A., Kaine B.P., Borodovsky M.,
RA Zank H.P., Fraser C.M., Smith H.C., Woese C.R., Woese J.C.
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii."
PL Science 273:1058-1073(1996).

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CC
CC EXBL: U67493; AAG98198.1;
DR P13: H64350; H64350.
DR TIGR: M20403.
DR Pfam: PF04036; DUF172; 1.
DR Pfam: PF04039; DUF181; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 121 AA; 14181 MW; 28166A6B1616F3 CRC64;

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Query Match 68.1%; Score 12; E: 1; Length 121.
Best Local Similarity 62.5%; Pred. No: 31;
Matches 5; Conservative 3; Mismatches 2; Gaps 0;

CY 2 DGQWMDV 9
DB 32 DGQWMDV 59

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CM protein - protein search, using sw model:  
Run on: November 5, 2003, 15:37:41 Search time 19.466 seconds  
(without alignment)  
119,679 million cell updates/sec

Trailer: US-09-914-088-1  
Perfect score: 47  
Sequence: EUCYMOVD 9

Scoring table: BLOSUM62  
Gap: 10.0, Gapext 0.5

Searched: 91026 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 81525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SPTRXAL\_23:  
1: sp.archaea:  
2: sp.bacteria:  
3: sp.fungi:  
4: sp.human:  
5: sp.invertebrate:  
6: sp.mammal:  
7: sp.mol:  
8: sp.organelle:  
9: sp.phage:  
10: sp.plant:  
11: sp.podent:  
12: sp.virus:  
13: sp.vertebrate:  
14: sp.unclassified:  
15: sp.virus:  
16: sp.bacteriap:  
17: sp.archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	38	80.9	118	17	Q9HPC3		Q9HPC3 Halobacterium
2	37	78.7	344	10	Q92R01		Q92R01 Nicotiana
3	37	78.7	747	9	Q8SP42		Q8SP42 pseudomonas
4	37	78.7	1250	5	Q9NS95		Q9NS95 caenorhabdi
5	36	76.6	448	16	Q8LFR1		Q8LFR1 arabidopsis
6	36	76.6	459	16	Q8NQ21		Q8NQ21 corynebacte
7	36	76.6	480	10	Q9M2X7		Q9M2X7 arabidopsis
8	36	76.6	487	10	Q8W426		Q8W426 oryza sativ
9	36	76.6	569	10	Q8LQ31		Q8LQ31 oryza sativ
10	36	76.6	977	5	P91775		P91775 bacillus
11	35	74.5	198	16	Q9P141		Q9P141 capylobact
12	35	74.5	265	17	Q26562		Q26562 methanobact
13	35	74.5	358	1	Q9P914		Q9P914 Halobacterium
14	35	74.5	574	16	Q856P9		Q856P9 leptospira
15	35	74.5	846	16	Q87P85		Q87P85 arabidopsis
16	35	74.5	1016	16	Q8XJ44		Q8XJ44 caenorhabdi

## ALIGNMENTS

RESULT:

Q9HPC3 PRELIMINARY; PRT: 118 AA.

AC Q9HPC3  
DT C1-MAR-2001 (TrEMBL:rel\_16, Created)  
DT C1-MAR-2001 (TrEMBL:rel\_16, Last sequence update)  
DT C1-MAR-2001 (TrEMBL:rel\_23, Last annotation update)  
DE 55S ribosomal protein L24P.  
GN RPL24P ORF VNG1723.  
OS Halobacterium sp. (strain NRC-1).  
OC Archaea; Euryarchaeota; Halobacterium; Halobacteriales;  
OC Halobacteriaceae; Halobacterium.  
CX MCR:taxid:54091.  
RN 111  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2050483; PubMed=11016950;  
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna C.,  
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,  
RA Leithauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,  
RA Isenberger T.A., Peck R.F., Kohlshroder M., Spudich J.L., Jung K.-H.,  
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.,  
RT "Genome sequence of Halobacterium species NRC-1".  
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
DR EMBL: AE05077; AAG1947.1;  
DR InterPro: IPR005824; K0W.  
DR InterPro: IPR006646; K0W\_sub.  
DR InterPro: IPR005825; Ribosomal\_L24\_26.  
DR Pfam: PFC0467; K0W.  
DR SMART: SM00739; K0W.  
DR PROSITE: PS01108; RIBOSOMA\_L24; 1.  
KW Ribosomal protein, Complete proteome.  
SQ SEQUENCE 118 AA; 13369 MW; 90C2F1C4577190A8 CRC64;

Query Match 80.9%; Score 1d: DB 17; Length 118;  
Best Local Similarity 77.8%; Pred. No: 12;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Q81B14 plasmodium  
Q9P6A4 neurospora  
Q8M08 caenorhabdi  
Q9165 caenorhabdi  
Q8XK4 clostridium  
Q8M219 acanthochei  
Q92W16 rhizobium m  
Q9X1B4 arabidopsis  
Q98124 mycoplasma  
Q30057 archaeoglob  
Q8NU2 oceanobacill  
Q94H06 oryza sativ  
Q9KV28 xanthomoras  
Q9Y750 yarrowia li  
Q8V754 xanthomoras  
Q8R8K6 thermocanaer  
Q26913 methanobact  
Q81GK9 drosophila  
Q8XU7 raietonia s  
Q9VPW8 drosophila  
Q8EG12 shewanella  
Q9ZXD5 bacterioph  
Q566K5 caenorhabdi  
Q8HJ13 halobacteri  
Q9111 arabidopsis  
Q91700 pseudomonas  
Q23644 caenorhabdi  
Q92Y16 rhizobium m  
Q9HJ04 thermoplasm

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QY 1 EDGQWYDVO 9
DB 59 EDGQWYDVO 67

RESULT 2
Q9ZD1 PRELIMINARY; PRT: 344 AA
ID Q9ZD1
AC Q9ZD1
DT 01-MAY-1999 (TRENDEL 16, Created)
DT 01-MAY-1999 (TRENDEL 16, Last sequence update)
DT 01-DEC-2001 (TRENDEL 19, Last annotation update)
DE NTG94 (Fragment)
OS Nicotiana tabacum (Common tobacco)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asterididae; Lamiales; Solanales; Solanaceae; Nicotiana
CX NCBI TaxID=4597
RN [1]
RP SEQUENCE FROM N.A.
RA Biermann B.J., Price J.R., Crowe J.D.N., Kandall S.K.
RC "A collection of cDNAs encoding isoprenylated plant proteins."
RJ Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL: U64325; AAC09518.1;
DR HSP: PC2649; I1E4.
FT raw data
SQ SEQUENCE 344 AA; 38526 MW; 14975564.6643 CP 0.4,

Query Match 78.7%; Score 177; DB 9; Length 344;
Best Local Similarity 75.0%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGQWYDVO 9
DB 69 EDGQWYDVO 76

RESULT 3
Q9S142 PRELIMINARY; PRT: 947 AA
ID Q9S142
AC Q9S142
DT 01-JUN-2002 (TRENDEL 21, Created)
DT 01-JUN-2002 (TRENDEL 21, Last sequence update)
DT 01-JUN-2002 (TRENDEL 21, Last annotation update)
DE PHK2120.
OS Pseudomonas phage PHK2.
OC Viruses; dsDNA viruses, no RNA stage; Gatedeltavirus; Gatedeltavirus
CX NCBI TaxID=149690
RN [1]
RP SEQUENCE FROM N.A.
RA Maslyanzhinov V.V., Robben J., Gytis R., Kopylov V.V., Maslyanzhinov V.V.,
RA Maslyanzhinov V.V., Robben J., Gytis R., Kopylov V.V., Maslyanzhinov V.V.,
RA Maslyanzhinov V.V., Syklinda N.N., Kopylov V.V., Maslyanzhinov V.V.,
RA "The genome of bacteriophage PHK2 of Pseudomonas aeruginosa."
RJ J. Mol. Biol. 317:11-19(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Maslyanzhinov V.V., Robben J., Gytis R., Kopylov V.V., Maslyanzhinov V.V.,
RA Maslyanzhinov V.V., Syklinda N.N., Kopylov V.V., Maslyanzhinov V.V.,
RA Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF199011; AA:83021.1;
SQ SEQUENCE 947 AA; 82929 MW; 6876584.76584 CP 0.4,

Query Match 78.7%; Score 177; DB 9; Length 947;
Best Local Similarity 100.0%; Pred. No. 1947;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWYDVO 9
DB 459 EDGQWYDVO 415

RESULT 4
Q9K595 PRELIMINARY; PRT: 1250 AA
ID Q9K595
AC Q9K595
DT 01-OCT-2000 (TRENDEL 15, Created)
DT 01-OCT-2000 (TRENDEL 18, Last sequence update)
DT 01-MAR-2003 (TRENDEL 23, Last annotation update)
DE Hypothetical 142.7 kDa protein.
GN Y110A/Y.16.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Rhabditinae; Caenorhabditis
CX NCBI TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2015(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Czerzsky P., Wohlmann P., Carter T.;
RA "The sequence of C. elegans cosmid Y.10A7A."
RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission."
RL Submitted (SEP 2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AC006708; AAC0410.2;
DR WormRef: Y.10A7A.16; GE28103.
DR InterPro: PR006849; IK13.
DR Pfam: PF04762; IK13; 1.
RW Hypothetical protein.
SQ SEQUENCE 1250 AA; 142709 MW; AFF1E4F31727DED CRC64;

Query Match 76.7%; Score 17; DB 5; Length 1250;
Best Local Similarity 66.7%; Pred. No. 2.4e-02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGQWYDVO 9
DB 86 EDGQWYDVO 80

RESULT 5
Q9LFE0 PRELIMINARY; PRT: 448 AA
ID Q9LFE0
AC Q9LFE0
DT 01-OCT-2002 (TRENDEL 22, Created)
DT 01-OCT-2002 (TRENDEL 22, Last sequence update)
DT 01-MAR-2003 (TRENDEL 23, Last annotation update)
DE Hypothetical protein.
OS Arabidopsis thaliana (Mouse ear cress);
OC Arabidopsis thaliana
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosid 1; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Raas B.A., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White G., Salzberg S.L.;
RT "Full length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 3:10.6(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Blyover V., Troukhan M., Alexandrov N., Lu Y. P., Flavell R.,
RA Feldmann K.;

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BT "Full length cDNA from Arabidopsis thaliana";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DP EMBL; AY094697; AAY61258.1; -;  
 DR InterPro: IPR003613; Znf\_modRING.  
 DR SMART: SM0504; tbox; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 448 AA; 43011 MW; 4A06975D8594F263 CRC64;

Query Match 76.6%; Score 36; DB 10; Length 444;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGQWMDV 9  
 DB 20 DGGVLDLD 27

## RESULT 6

Q8N021 PRELIMINARY; PRT; 450 AA

ID Q8N021  
 AC Q8N021  
 DT 01-OCT-2002 (TRENBLREL 22, Created)  
 DT 01-OCT-2002 (TRENBLREL 22, Last sequence update)  
 DT 01-MAR-2003 (TRENBLREL 23, Last annotation update)  
 DE Uncharacterized AtPase related to the helicase subunit of the Holliday junction resolvase.  
 DE  
 GN GNL5633

OS Corynebacterium glutamicum (Brevibacterium flavum)  
 CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales  
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium  
 OX NCBI\_TaxID:1718

RN [1]  
 RP SEQUENCE FROM N.A.

RA STRAIN ATCC 13030 / DSM 20100 / NCIB 10225;  
 RA Nakagawa S.

BT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13030";  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 DP EMBL; AB004294; BAB99026.1; -;  
 DR InterPro: IPR003959; AAA\_Arase\_cent1

DR InterPro: IPR000862; RFB\_Domain  
 DR Pfam: PF00004; AAA; 1  
 KW Helicase; Complete proteome

SQ SEQUENCE 459 AA; 49478 MW; 8A58F8FA7594D5 CRC64;

Query Match 76.6%; Score 36; DB 10; Length 444;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGGQWMDV 9  
 DB 245 DGGVLDLD 253

## RESULT 7

Q9MXX7 PRELIMINARY; PRT; 460 AA

ID Q9MXX7  
 AC Q9MXX7  
 DT 01-OCT-2000 (TRENBLREL 15, Created)  
 DT 01-OCT-2000 (TRENBLREL 15, Last sequence update)  
 DT 01-MAR-2002 (TRENBLREL 20, Last annotation update)  
 DE Hypothetical 55.6 kDa protein.  
 DE T16K5.160.  
 OS Arabidopsis thaliana (Mouse-ear cress)  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot, Eusidae  
 OX euroids 11; Brassicales; Brassicaceae; Arabidopsis  
 OX NCBI\_TaxID:1072

RN [1]  
 RP SEQUENCE FROM N.A.

RA Plesner M., Gable C., Mueller-Auer S., Schneider M., Ziff M.,  
 RA Yewers H.W., Gerke X., Mayer K.F.X., Gantier F., Gullberg M.

FL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RV [2]

RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DP EMBL; AL132965; CAB6619.1; -;  
 DR InterPro: IPR003613; Znf\_modRING  
 DR SMART: SM0504; Ubox; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 480 AA; 52645 MW; CC4E011E9306FBA CRC64;

Query Match 76.6%; Score 36; DB 10; Length 480;  
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGGQWMDV 9  
 DB 20 DGGVLDLD 27

## RESULT 8

Q8W426 PRELIMINARY; PRT; 487 AA

ID Q8W426  
 AC Q8W426  
 DT 01-MAR-2002 (TRENBLREL 20, Created)  
 DT 01-MAR-2002 (TRENBLREL 20, Last sequence update)  
 DT 01-OCT-2002 (TRENBLREL 22, Last annotation update)  
 DE 21D7.  
 GN OS21D7.  
 OS Oryza sativa (Rice).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OX Ehrhartoideae; Oryzaceae; Oryza  
 OX NCBI\_TaxID:4510

RN [1]  
 RP SEQUENCE FROM N.A.

RA STRAIN cv. Nipponbare;  
 RA Yanagawa Y., Hasegawa S., Kuragaki E., Fujimuro M., Yokosawa H.,  
 RA Tanaka K., Komamine A., Hashimoto S., Sato T., Nakagawa H.;  
 RT "Clonalization of protease subunits and plant specific  
 RT microtubules, preprotease bands and phragoplast, during cell cycle";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB031299; BAB92474.1;

DR Gramine; Q8W426

DR InterPro: IPR003917; PCT1

DR Pfam: PF01399; PCT1

DR SMART: SM00088; PINT; 1

SQ SEQUENCE 487 AA; 54980 MW; 9B91593A4812AC1 CRC64;

Query Match 76.6%; Score 36; DB 10; Length 487;  
 Best Local Similarity 77.5%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGGQWMDV 9  
 DB 91 DGGSEMDVC 99

## RESULT 9

Q8LQGI PRELIMINARY; PRT; 569 AA

ID Q8LQGI  
 AC Q8LQGI  
 DT 01-OCT-2002 (TRENBLREL 22, Created)  
 DT 01-OCT-2002 (TRENBLREL 22, Last sequence update)  
 DT 01-MAR-2003 (TRENBLREL 23, Last annotation update)  
 DE Vacuolar sorting receptor-like protein.  
 GN P00C40.2.8.  
 OS Oryza sativa (Japonica cultivar-group)  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OX Ehrhartoideae; Oryzaceae; Oryza  
 OX NCBI\_TaxID:39547

RN [1]  
 RP SEQUENCE FROM N.A.

RA STRAIN cv. Nipponbare.



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RESULT 13
C99914
AC C99914 PRELIMINARY; PRT: 158 AA.
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Nitrate reductase subunit 2 (EC 1.1.1.94)
GN NARH
OS Halococcus marismortui (Halobacterium marismortui), 403
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriaceae
OC Halobacteriaceae; Halobacteria
OX NCBI_TaxID=2238, 122093;
RN 1;
RF SEQUENCE FROM N.A.
RC SPECIES: marismortui;
RA Yoshinaka K., Iwasaki T., Fujiwara T.;
RT "Sequence and Electron Paramagnetic Resonance Analyses of the Archaeal Nitrate Reductase NARH from the Denitrifying Halophilic Euryarchaeote Halococcus marismortui."
RL Submitted (JAN-2002) to the EMBL/GenBank/CDR databases.
RN 12;
RF SEQUENCE FROM N.A.
RC SPECIES: marismortui subsp. marismortui;
RA Yoshimatsu K., Yamamoto A., Fujiwara T.;
RT "Sequence analysis of the dissimilatory nitrate reductase from a denitrifying halophilic archaeon, Halococcus marismortui."
RL Submitted (APR-2000) to the EMBL/GenBank/CDR databases.
DR EMBL: A342007; CAC22070.1;
DR EMBL: A327440; CAB89122.1;
DR InterPro: IPR001450; 4FeS_ferredoxin.
DR Pfam: PF00337; fer4.1.
KW Oxidoreductase.
SQ SEQUENCE 358 AA; 41122 MW; 380A308740516105 CP564;

Query Match 74.5%; Score 35; DB 16; Length 554;
Best Local Similarity 55.8%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CY 1 EDGQVMDVD 9
|||
DB 292 EGQTVMD 300

RESULT 14
C99914
AC C99914 PRELIMINARY; PRT: 158 AA.
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN LAL389
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetiales; Leptospiraceae; Leptospira.
OX NCBI_TaxID 173;
RN 1;
RF SEQUENCE FROM N.A.
RC STRAIN: S6601 / Serogroup Icterohaemorrhagiae / Serovar 1a;
RA Ren S.;
RL Submitted (MAR 2002) to the EMBL/GenBank/CDR databases
DR EMBL: AE011318; AAM48588.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 574 AA; 65826 MW; 1F5E251C81933060 CP564;

Query Match 74.5%; Score 35; DB 16; Length 554;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 2 DGEVVDVD 9
|||
DB 280 EQGVLDVD 288

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DB 497 DGEVVDVD 504

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RESULT 15
C99914
AC C99914 PRELIMINARY; PRT: 846 AA.
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Primosomal protein N.
GN AL54248.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=101690;
RN 1;
RF SEQUENCE FROM N.A.
RC MEDLINE=21595265; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iiguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shingo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tacata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL: AP003595; BAB75947.1;
DR InterPro: IPR001410; DEAC.
DR InterPro: IPR001650; Helicase C.
DR InterPro: IPR005259; PriA.
DR Pfam: PF03271; Helicase C; 1.
DR SMART: SM00487; DEXOC; 1.
DR SMART: SM00490; HELICC; 1.
DR TIGRFAMs: TIGR00595; priA; 1.
KW Complete proteome.
SQ SEQUENCE 846 AA; 94775 MW; 7352DF49D40A6726 CRC64;

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Query Match 74.5%; Score 35; DB 16; Length 846;  
 Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 2 EDGQVMDVD 9  
 |||  
 DB 280 EQGVLDVD 288

Search completed: November 5, 2003, 15:53:53  
 Job time: 20.4777 sec

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 15:43:03, Search time: 25.65 seconds

(without alignment)  
55,694 Million cell updates/sec

Title: US 09-914 088-1

Perfect score: 47

Sequence: EDCQVNDVD 9

Scoring table: BLOSUM62

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Searched: 1107863 seqs, 158726533 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chosen to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	47	100.0	9	AA820867	Immunoglobulin E
2	47	100.0	9	AA825916	IgE C epsilon-2 de
3	47	100.0	9	AAU16641	Peptide P15 deriv
4	47	100.0	9	AAU16642	IgE peptide #1, X
5	47	100.0	9	ABJ00217	Human IgE immuno
6	47	100.0	10	AA825429	PI mimotope peptid
7	47	100.0	10	AAU16654	Peptide P15 deriv
8	47	100.0	10	ABJ00218	Human IgE immuno
9	47	100.0	13	AA820872	Anti-IgE-agg peptid

10	47	100.0	13	AA825914	PI mimotope peptid
11	47	100.0	13	AA825916	PI mimotope peptid
12	47	100.0	13	AA825917	Peptide P15 deriv
13	47	100.0	13	AAU16639	Peptide P15 deriv
14	47	100.0	13	AAU16641	Peptide P15q deriv
15	47	100.0	13	AAU16642	IgB peptide #6, X
16	47	100.0	13	AA820828	Human IgE immuno
17	47	100.0	13	ABJ00224	Human IgE immuno
18	47	100.0	13	ABJ00226	Human IgE cyclic 1
19	47	100.0	13	ABJ00312	Human IgE cyclic 1
20	47	100.0	14	ABJ00540	Human IgE cyclic 1
21	47	100.0	16	ABJ00542	Human IgE cyclic 1
22	47	100.0	20	AA823442	Human IgE cyclic 1
23	47	100.0	20	AA825921	PI mimotope peptid
24	47	100.0	20	AA825971	PI mimotope peptid
25	47	100.0	20	AAU16645	Peptide PT1079GS d
26	47	100.0	20	AAU16695	Peptide PT1079HBC
27	47	100.0	20	ABJ00316	Human IgE cyclic 1
28	47	100.0	20	ABJ00358	Human IgE cyclic 1
29	47	100.0	20	ABJ00544	Human IgE cyclic 1
30	47	100.0	21	AA825922	PI mimotope peptid
31	47	100.0	21	AA825972	PI mimotope peptid
32	47	100.0	21	AAU16647	Peptide PT1078 der
33	47	100.0	21	AAU16697	Peptide PT1079HBC
34	47	100.0	21	ABJ00317	Human IgE cyclic 1
35	47	100.0	21	ABJ00359	Human IgE cyclic 1
36	47	100.0	22	AA825920	PI mimotope peptid
37	47	100.0	22	AAU16645	Peptide PT-079 der
38	47	100.0	22	ABJ00315	Human IgE cyclic 1
39	47	100.0	22	ABJ00543	Human IgE cyclic 1
40	47	100.0	98	AA825988	Pc(epsilon) CH2, C
41	47	100.0	106	AA825987	Pc(epsilon) CH2, C
42	47	100.0	128	ABG74778	Human modified IgE
43	47	100.0	23F	ABG74780	Human modified IgE
44	47	100.0	255	AA820105	Fused antibody reg
45	47	100.0	315	AA825982	Pc(epsilon) CH2, C

#### ALIGNMENTS

RESULT 1  
AA820867  
ID AA820867 standard: peptide, 9 AA.  
XX AA820867  
XX  
XX  
XX 93 JAN 2001 (first entry)  
XX  
XX Immunoglobulin E epitope immunogenic peptide SEQ ID NO:5.  
XX  
XX Immunoglobulin E, IgE; immunogenic; immunogen; Protein D; carrier;  
KW prostate cancer; Haemophilus influenzae; vaccine; infectious disease;  
KW malaria; cytostatic; anti-allergic; neurotropic; neuroprotective;  
KW procoagulant; Alzheimer's disease; allergy.  
XX  
XX Homo sapiens.  
XX  
XX WC200050077 A1.  
XX  
XX 31-AUG-2000.  
XX  
XX 22-FEB-2000; 2000WC:EP01457.  
XX  
XX 25-FEB-1999; 99GB C004405.  
XX  
XX 25-FEB-1999; 99GB C004408.  
XX  
XX 25-FEB-1999; 99GB C004412.  
XX  
XX 13 AUG 1999; 99GB C019243.  
XX  
XX (SWIK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
XX Coste M, Lohet Y, Van Mechelen MP, Verliest C







DT 05 JAN 2001 (first entry)  
 XX  
 DE P1 Mimotope peptide P1st SEQ ID NO:211  
 XX  
 KW Epitope; mimotope; human; immunoglobulin E; IgE; Cepsilon2 domain;  
 KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW Allergy; atopy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2000050460 A1.  
 XX  
 XX 31 AUG 2001.  
 XX  
 XX 22-FEB-2001; 2003WO-EPC1455.  
 XX  
 XX 26-FEB-1999; 99GB-0004405.  
 XX 29-MAR-1999; 99GB-0007151.  
 XX 07-MAY-1999; 99GB-0010537.  
 XX 03-MAY-1999; 99GB-0010538.  
 XX 07 AUG 1999; 99GB 0018594.  
 XX 07 AUG 1999; 99GB-0018603.  
 XX 07 SEP-1999; 99GB-0021546.  
 XX 07 SEP-1999; 99GB-0021547.  
 XX 29-OCT-1999; 99GB-0025619.  
 XX 23-NOV-1999; 99GB-0027659.  
 XX  
 XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX (SEPT) PEPTIDE THERAPEUTICS LTD.  
 XX  
 XX Dwyer M., Flade M., Greenwood J., Hewitt E., Lantieri A., Mason S.,  
 XX Randall R., Turner W., Van Vechelen XP., Vinals De Bascols Y.  
 XX  
 XX WPI: 2000-52207453.  
 XX  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 XX diseases, comprising an isolated surface exposed group of a specific  
 XX domain from immunoglobulin E.  
 XX  
 XX Disclosure, Page 9; 1999; English.  
 XX  
 XX The present invention describes a peptide (I) comprising an isolated  
 XX surface exposed group/epitope (E) of C epsilon2 domain (C2) of  
 XX immunoglobulin E (IgE), or its mimotope. Also described are (II) an  
 XX immunogen (III) for treating allergy comprising the C2 vaccine (III)  
 XX for treating allergies comprising (II), (III) and (IV) capable of  
 XX recognising (II), (III) and (IV) and (V) comprising (II),  
 XX (III) a peptide (II) capable of being recognized by (V) and (VI) and (VII)  
 XX (VII) comprising (II), (III) and (IV) and (V) and (VI) are  
 XX as a vaccine and histamine release inhibitor (II), (III) and (IV) are  
 XX useful in medicine and in the manufacture of medicaments for treating  
 XX and preventing allergies. (IV) is useful for identifying mimotopes of (I),  
 XX in medicine and also in manufacturing medicaments for treating  
 XX allergies. (I) is useful in diagnostics and in the affinity purification  
 XX of circulating anti-IgE antibodies from blood. (II), (III) and (IV) are  
 XX useful for treating a patient susceptible to or suffering from allergies.  
 XX (VI) is also useful in diagnosing atopy. WO1999-1148699 represent  
 XX peptide sequences which are used in the exemplification of the present  
 XX invention.  
 XX  
 XX Sequence 10 AA:  
 XX  
 XX Query Match 100.0%; Score 47; DB 21; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 0.01;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 EDGQVMDVD 9  
 XX |||||  
 XX 2 EDGQVMDVD 10  
 XX  
 XX RESULT 8  
 XX ABJ00228  
 XX ID ABJ00228 standard; Peptide; 10 AA.  
 XX  
 XX ASJ00128.  
 XX

RESULT 7  
 AAU16654  
 ID AAU16654 standard; Peptide; 10 AA.  
 XX  
 AC AAU16654;  
 XX  
 DT 07-NOV-2001 (first entry)  
 XX  
 DE Peptide P1st derived as mimotope of Cepsilon2 region of human IgE.  
 XX  
 KW Human; linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200145745-A2.  
 XX  
 XX 28-JUN-2001.  
 XX  
 XX 21-DEC-2000; 2003WO GB04935.  
 XX  
 XX 21-DEC-1999; 99GB 0030233.  
 XX 22-FEB-2000; 2003GB 0034096.  
 XX 22-AUG-2000; 2003GB-0020707.  
 XX 22-AUG-2000; 2003GB-0020708.  
 XX  
 XX (ACAM) ACAMBI'S RES LTD.  
 XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 XX Flinn N., Johnson T;  
 XX  
 XX WPI: 2001-521367453.  
 XX  
 XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
 XX mediated diseases  
 XX  
 XX Example 4; Page 21; 48pp; English.  
 XX  
 XX The present invention relates to linkage methodology for use in the  
 XX conjugation of compounds (e.g. peptides) to carrier vehicles  
 XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 XX biological and immunological constructs. The invention provides a  
 XX method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 XX protein) for use in a pharmaceutical composition or a vaccine. The  
 XX invention describes peptides derived from or mimotopes of the  
 XX Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 XX (IgE) which are used to produce conjugated compounds. The compounds or  
 XX compositions of the invention are useful in the manufacture of a  
 XX medicament for the treatment of IgE mediated diseases. The invention  
 XX allows for controlled conjugation of a peptide epitope (antigen) to a  
 XX protein so as to form an immunogenic conjugate which may be able to  
 XX raise a protective antibody response in an animal or human patient.  
 XX AAU16632-AAU1693 represent peptides derived from or mimotopes of  
 XX the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 XX Sequence 10 AA:  
 XX  
 XX Query Match 100.0%; Score 47; DB 22; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 0.01;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 EDGQVMDVD 9  
 XX |||||  
 XX 2 EDGQVMDVD 10  
 XX



PR 07-AUG-1999; 99GB-0018603.  
 PR 07-SEP-1999; 99GB-0021046.  
 PR 07-SEP-1999; 99GB-0021047.  
 PR 29-OCT-1999; 99GB-0025619.  
 PR 23-NOV-1999; 99GB-0027698.  
 XX  
 PA (SMK) : SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Dyson M, Friesle M, Greenwood J, Hewitt E, Lamont A, Mason S,  
 PI Randall R, Turnell WG, Van Mechelen MP, Vinals De Bassois YC,  
 XX  
 DR WPI: 2000-572073/51.  
 XX  
 PS Claim 14; Page 9; 129pp; English.  
 XX  
 CC The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (II) of C-epsilon-2 domain (D) of  
 CC immunoglobulin E (IgE), or its microtope. Also described are: (1) an  
 CC immunogen (III) for treating allergy comprising (II); (2) a vaccine (III)  
 CC for treating allergies comprising (II); (3) a ligand (IV) capable of  
 CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (IIa) capable of being recognised by (IV); (6) an immunogen  
 CC (IIa) comprising (IIa); and (7) producing (III) by producing (II); (1)  
 CC can have antiallergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (II), (II) and (III) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (IV) is useful for identifying mimotopes of P1,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (II) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (II), (III) and (IV) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AAB25917, AAB25918 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 100.0%; Score 47; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EDSQWMDVD 9  
 DB 3 EDSQWMDVD 11  
 RESULT 12  
 AAB25917  
 ID AAB25917 standard; Peptide; 13 AA  
 XX  
 AC AAB25917;  
 XX  
 DT 05 JAN 2001 (first entry);  
 XX  
 DE P1 microtope peptide P15p SEQ ID NO:11.  
 XX  
 KW Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;  
 KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy  
 XX  
 OS Homo sapiens.  
 XX  
 PR W020050440-A1.  
 PR  
 PR 21 AUG 2000.  
 PR 20 FEB 2001; E02000-EP01455.

XX  
 PR 25-FEB-1999; 99GB-0004403.  
 PR 29-MAR-1999; 99GB-0007151.  
 PR 07-MAY-1999; 99GB-0010537.  
 PR 07-MAY-1999; 99GB-0010538.  
 PR 07-AUG-1999; 99GB-0018594.  
 PR 07-AUG-1999; 99GB-0018603.  
 PR 07-SEP-1999; 99GB-0021046.  
 PR 07-SEP-1999; 99GB-0021047.  
 PR 29-OCT-1999; 99GB-0025619.  
 PR 23-NOV-1999; 99GB-0027698.  
 XX  
 PA (SMK) : SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Dyson M, Friesle M, Greenwood J, Hewitt E, Lamont A, Mason S,  
 PI Randall R, Turnell WG, Van Mechelen MP, Vinals De Bassois YC,  
 XX  
 DR WPI: 2000-572073/51.  
 XX  
 PS Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 PS Disclosure; Page 9; 129pp; English.  
 XX  
 CC The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (II) of C-epsilon-2 domain (D) of  
 CC immunoglobulin E (IgE), or its microtope. Also described are: (1) an  
 CC immunogen (III) for treating allergy comprising (II); (2) a vaccine (III)  
 CC for treating allergies comprising (II); (3) a ligand (IV) capable of  
 CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (IIa) capable of being recognised by (IV); (6) an immunogen  
 CC (IIa) comprising (IIa); and (7) producing (III) by producing (II); (1)  
 CC can have antiallergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (II), (II) and (III) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (IV) is useful for identifying mimotopes of P1,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (II) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (II), (III) and (IV) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AAB25917, AAB25918 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 100.0%; Score 47; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EDSQWMDVD 9  
 DB 3 EDSQWMDVD 11  
 RESULT 12  
 AAB25917  
 ID AAB25917 standard; Peptide; 13 AA  
 XX  
 AC AAB25917;  
 XX  
 DT 05 JAN 2001 (first entry);  
 XX  
 DE P1 microtope peptide P15p SEQ ID NO:11.  
 XX  
 KW Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;  
 KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy  
 XX  
 OS Homo sapiens.

XX  
FN WO2000/04404-A1.

XX  
PD 31-AUG-2000.

XX  
PF 22 FEB 2000; 2000WO EP01455.

XX  
PR 24-FEB-1999; 94GB-0004405.

XX  
PR 29-MAR-1998; 94GB-0007151.

XX  
PR 07-MAY-1998; 94GB-0010537.

XX  
PR 07-MAY-1999; 94GB-0010538.

XX  
PR 07-AUG-1999; 94GB-0018094.

XX  
PR 07-AUG-1999; 94GB-0018603.

XX  
PR 07-SEP-1999; 94GB-0021046.

XX  
PR 07-SEP-1999; 94GB-0021047.

XX  
PR 29-OCT-1999; 94GB-0025619.

XX  
PR 23 NOV 1999; 94GB-0027698.

XX  
PA (SMIK) SYNTHKLIN BEECHAM BIOLOGICALS.

XX  
PA (PEPT) PEPTIDE THERAPEUTICS LTD.

XX  
PI Tyson M, Friede M, Greenwood J, Hewitt E, Lambert A, Mason S,

XX  
PI Randall P, Turnell WG, Van Mechelen MP, Vinale De Russis YD,

XX  
OR WPI: 2001-521967/59.

XX  
XX Peptides useful for treating, preventing and ameliorating allergic

XX  
PT diseases, comprising an isolated surface exposed group of a specific

XX  
PT domain from immunoglobulin E

XX  
PS Claim 14, Page 9; 129pp; English.

XX  
XX The present invention describes a peptide (I) comprising an isolated

XX  
CC surface exposed group/epitope (E1) of Cepsilon2 domain (D) of

XX  
CC immunoglobulin E (IgE), or its mimotope. Also described are (II) an

XX  
CC immunogen (II) for treating allergy comprising (II), (2) a vaccine (III)

XX  
CC for treating allergies comprising (II); (3) a ligand (IV) capable of

XX  
CC recognising E1; (4) a pharmaceutical composition (V) comprising (IV);

XX  
CC (5) a peptide (Ia) capable of being recognised by (IV), as an immunogen

XX  
CC (Iia) comprising (Ia); and (7) producing (III) by producing (II); (II)

XX  
CC can have anti-allergic and immunosuppressive activities, and can be used

XX  
CC as a vaccine and histamine release inhibitor. (II), (Ia) and (Iii) are

XX  
CC useful in medicine and in the manufacture of medicaments for treating

XX  
CC and preventing allergies. (IV) is useful for identifying mimotopes of E1,

XX  
CC in medicine and also in manufacturing medicaments for treating

XX  
CC allergies. (II) is useful in diagnostics and in the affinity purification

XX  
CC of circulating anti-IgE antibodies in a blood sample and (Ia) and (Iii) are

XX  
CC useful for treating a patient susceptible to allergic diseases. (Iii)

XX  
CC (IV) is also useful in diagnosing allergy. (V) and (Iii) are also useful in

XX  
CC peptide sequences which are used in the preparation of the present

XX  
XX Sequence 13 AA;

XX

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XX

Human; linkage technology; conjugated compound; carrier vehicle; epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E; IgE mediated disease; antibody response.

Human sapiens.

Synthetic.

WO2000145745-A2.

29-JUN-2001.

21-DEC-2000; 2000WO GB24915.

21-DEC-1999; 95GB-0030214.

22-FEB-2000; 2000GB-0004096.

22-AUG-2000; 2000GB 0023707.

22-AUG-2000; 2000GB-0023708.

(ACAN) ACMEIS RES LTD.

(SMIK) SYNTHKLIN BEECHAM BIOLOGICALS.

Flann N, Johnson T.

WPI: 2001-521967/59.

A linkage comprising an immunogenic conjugate useful treatment of IgE mediated diseases.

Example 4, Page 21; 48pp; English.

The present invention relates to linkage methodology for use in the conjugation of compounds (e.g. peptides) to carrier vehicles

(e.g. macromolecules, polymers, dendrimers, proteins) to produce biological and immunological constructs. The invention provides a

method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition or a vaccine. The

invention describes peptides derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E

(IgE) which are used to produce conjugated compounds. The compounds or compositions of the invention are useful in the manufacture of a

medicament for the treatment of IgE mediated diseases. The invention allows for controlled conjugation of a peptide epitope (antigen) to a

protein so as to form an immunogenic conjugate which may be able to raise a protective antibody response in an animal or human patient.

AAU16612 AAU16613 represent peptides derived from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.

Sequence 13 AA;

Query Match 100.0%; Score 47; DB 22; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.04;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 EDGQWQVD 9

|||||

3 EDGQWQVD 11

AAU16641 standard; Peptide; 13 AA.

AAU16641;

07-NOV-2001 (first entry)

Peptide P15p derived as mimotope of Cepsilon2 region of human IgE.

Human; linkage technology; conjugated compound; carrier vehicle; epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E; IgE mediated disease; antibody response.

Human sapiens.

OS

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GenCore version 5.1.6  
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OX Protein: protein search, using sw model

Run on: November 5, 2003, 18:54:16 / Search time 18.4937 Seconds  
(without alignment)  
98.494 Million Cells updates/sec

Title: US-09-914-088-1  
Perfect score: 47  
Sequence: : EDGQWMDVD 9

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Seal-thed: 644029 seqs, 17174922 residues

Total number of hits satisfying chosen parameters: 644029

Minimum DB seq length: 2  
Maximum DB seq length: 200000000  
Post processing: Minimum Match 3%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/pdatat2/fubpaai/US06\_NEW PUB.pep.  
4: /cgn2\_6/pdatat2/fubpaai/US06\_PUBCOMB.pep.  
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9: /cgn2\_6/pdatat2/fubpaai/US09\_PUBCOMB.pep.  
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19: /cgn2\_6/pdatat2/fubpaai/US09\_PUBCOMB.pep.

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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3	47	100.0	10	12	US-10-082-014-282
4	47	100.0	10	12	US-10-372-076-136
5	47	100.0	128	15	US-10-152-190-9
6	47	100.0	236	15	US-10-152-190-9
7	47	100.0	320	11	US-09-847-208-6
8	47	100.0	323	10	US-09-949-375A-2
9	47	100.0	323	10	US-09-949-375A-4
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11	47	100.0	330	10	US-09-949-375A-10
12	47	100.0	331	9	US-09-401-636-1
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14	47	100.0	331	15	US-10-207-655-334
15	47	100.0	336	10	US-09-949-375A-8

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22	47	100.0	427	11	US-09-847-208-5
23	47	100.0	428	10	US-09-916-230-1
24	47	100.0	428	10	US-09-949-375A-1
25	47	100.0	428	14	US-10-047-542-60
26	47	100.0	441	10	US-09-949-375A-7
27	47	100.0	549	11	US-09-847-208-7
28	47	100.0	549	12	US-10-050-898-176
29	47	100.0	574	12	US-10-050-902-176
30	47	100.0	574	14	US-10-047-542-45
31	47	100.0	574	15	US-10-214-524-37
32	47	100.0	592	15	US-10-207-655-334
33	41	87.2	110	12	US-10-144-188-55
34	38	80.9	249	15	US-10-156-761-14113
35	37	78.7	821	9	US-09-848-035-2
36	37	78.7	821	10	US-09-986-224-2
37	37	78.7	980	9	US-09-848-035-13
38	37	78.7	980	10	US-09-986-224-13
39	37	78.7	1249	12	US-10-239-663-42
40	37	78.7	1178	14	US-10-041-856-9
41	36	76.6	383	15	US-10-078-770-170
42	36	76.6	459	10	US-09-738-626-5333
43	35	74.5	328	15	US-10-128-714-8134
44	35	74.5	330	15	US-10-128-714-8134
45	33	70.2	139	9	US-09-815-242-10722

ALIGNMENTS

RESULT 1  
US-10-082-014-273  
; Sequence 273, Application US-10-082014  
; Publication No. US20030185858A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL C  
; FILE REFERENCE: 100-130,045,647/85124  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/940,415  
; PRIOR FILING DATE: 2001-09-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 273  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-273

Query Match 100.0% Score 47: DB 12: Length 9:  
Best Local Similarity 100.0% Pred. No. 5.9e+05;  
Matches 9: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY : EDGQWMDVD 9  
DB : EDGQWMDVD 9

RESULT 2  
US-10-372-076-127  
; Sequence 127, Application US/10372076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS

```

; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 127
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372 076 127

```

```

Query Match 100.0% Score 47; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 EDGQWMDV 9
   ||| |||
Db : EDGQWMDV 9

```

```

RESULT 3
US-10-082-014-282
; Sequence 282, Application US/10082014
; Publication No. US2003018588A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CYSTEINE
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 282
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-082-014-282

```

```

Query Match 100.0% Score 47; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 EDGQWMDV 9
   ||| |||
Db 2 EDGQWMDV 10

```

```

RESULT 4
US-10-372 076 126
; Sequence 136, Application US/10/372,076
; Publication No. US2003018645A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Martin
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR CHRONIC HEPATITIS
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 126
; LENGTH: 10

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-076-136

```

```

Query Match 100.0% Score 47; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 EDGQWMDV 9
   ||| |||
Db 2 EDGQWMDV 10

```

```

RESULT 5
US-10-152-190-7
; Sequence 7, Application US/10/152190
; Publication No. US20030096369A1
; GENERAL INFORMATION:
; APPLICANT: Morsey, Mohamad A
; TITLE OF INVENTION: NO US20030096369A1 anaphylactogenic IgE vaccines
; FILE REFERENCE: PC11011A
; CURRENT APPLICATION NUMBER: US/10/152,190
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Modified Human CH2 domain
US-10-152-190-7

```

```

Query Match 100.0% Score 47; DB 15; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.217;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 EDGQWMDV 9
   ||| |||
Db 70 EDGQWMDV 78

```

```

RESULT 6
US-10-152-190-9
; Sequence 9, Application US/10/152190
; Publication No. US20030096369A1
; GENERAL INFORMATION:
; APPLICANT: Morsey, Mohamad A
; TITLE OF INVENTION: NO US20030096369A1 anaphylactogenic IgE vaccines
; FILE REFERENCE: PC11011A
; CURRENT APPLICATION NUMBER: US/10/152,190
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 9
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Modified Human CH2 CH4 carrier protein
US-10-152-190-9

```

```

Query Match 100.0% Score 47; DB 15; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.4; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 EDGQWMDV 9
   ||| |||
Db 70 EDGQWMDV 78

```

```

RESULT 7
US-09-947-238-6
; Sequence 6, Application US/0947238
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew

```



APPLICANT: Zhang, Ke  
APPLICANT: Zhu, Daoheng  
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF  
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES  
FILE REFERENCE: U097-002A  
CURRENT APPLICATION NUMBER: US/09/847,123  
CURRENT FILING DATE: 2001-05-01  
NUMBER OF SEQ ID NOS: 177  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 320  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-847-238-6

Query Match 100.0%; Score 47; DB 11; Length 320;  
Best Local Similarity 100.0%; Pred. No. 0.57;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDVD 9  
||| |||  
DB 43 EDGQWMDVD 51

## RESULT 8

US-09-949-375A-2  
Sequence 2, Application US/09949375A  
Patent No. US20020172673A1  
GENERAL INFORMATION:  
APPLICANT: KLYSNER, Steen et al.  
TITLE OF INVENTION: METHOD FOR DOWN REGULATING IGE  
FILE REFERENCE: 3631-0111P  
CURRENT APPLICATION NUMBER: US/09/949,375A  
CURRENT FILING DATE: 2002-01-18  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2

LENGTH: 327  
TYPE: PRT  
ORGANISM: homo sapiens  
FEATURES:  
NAME/KEY: DOMAIN  
LOCATION: 111-311  
OTHER INFORMATION: Human Ige heavy chain C2 domain  
NAME/KEY: DOMAIN  
LOCATION: 312-311  
OTHER INFORMATION: Human Ige heavy chain C3 domain  
FEATURES:

NAME/KEY: DOMAIN  
LOCATION: 1216-1317  
OTHER INFORMATION: Human Ige heavy chain C4 domain  
FEATURES:

NAME/KEY: MISC FEATURE  
LOCATION: 1104-1111  
OTHER INFORMATION: Linker between domains C2 and C3  
FEATURES:

NAME/KEY: MISC FEATURE  
LOCATION: 1212-1215  
OTHER INFORMATION: Linker between domains C3 and C4  
FEATURES:

NAME/KEY: MISC FEATURE  
LOCATION: 1007-1114  
OTHER INFORMATION: Epitope including C2/C3 linker  
FEATURES:

NAME/KEY: MISC FEATURE  
LOCATION: 1210-1218  
OTHER INFORMATION: Epitope including C3/C4 linker  
FEATURES:

NAME/KEY: MISC FEATURE  
LOCATION: 1130-1145  
OTHER INFORMATION: Epitope in AC loop  
FEATURES:

NAME/KEY: MISC FEATURE  
LOCATION: 1167-1175  
OTHER INFORMATION: Epitope in DE loop  
FEATURES:  
NAME/KEY: MISC FEATURE  
LOCATION: 1196-1226  
OTHER INFORMATION: Epitope in FG loop  
US-09-949-375A-2

Query Match 100.0%; Score 47; DB 10; Length 323;  
Best Local Similarity 100.0%; Pred. No. 0.57;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDVD 9  
||| |||  
DB 46 EDGQWMDVD 54

## RESULT 9

US-09-949-375A-4  
Sequence 4, Application US/09949375A  
Patent No. US20020172673A1  
GENERAL INFORMATION:  
APPLICANT: KLYSNER, Steen et al.  
TITLE OF INVENTION: METHOD FOR DOWN REGULATING IGE  
FILE REFERENCE: 3631-0111P  
CURRENT APPLICATION NUMBER: US/09/949,375A  
CURRENT FILING DATE: 2002-01-18  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 323  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:

OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 3.  
US-09-949-375A-4

Query Match 100.0%; Score 47; DB 10; Length 323;  
Best Local Similarity 100.0%; Pred. No. 0.57;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDVD 9  
||| |||  
DB 46 EDGQWMDVD 54

## RESULT 10

US-09-949-375A-6  
Sequence 6, Application US/09949375A  
Patent No. US20020172673A1  
GENERAL INFORMATION:  
APPLICANT: KLYSNER, Steen et al.  
TITLE OF INVENTION: METHOD FOR DOWN REGULATING IGE  
FILE REFERENCE: 3631-0111P  
CURRENT APPLICATION NUMBER: US/09/949,375A  
CURRENT FILING DATE: 2002-01-18  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 323  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:

OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 5.  
US-09-949-375A-6

Query Match 100.0%; Score 47; DB 10; Length 323;  
Best Local Similarity 100.0%; Pred. No. 0.57;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDVD 9  
||| |||

Db 46 EDGQVMDVD 54

## RESULT 11

US-09-949-375A-10  
Sequence 10, Application US/09949375A  
Patent No. US20020172673A1  
GENERAL INFORMATION:  
APPLICANT: KLYSNER, Steen et al.  
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING ICE  
FILE REFERENCE: 3631-011P  
CURRENT APPLICATION NUMBER: US/09/949,375A  
CURRENT FILING DATE: 2002-01-18  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 10  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO 9.

## Query Match

US-10-207-655-329 Score 47; DB 15; Length 331;

Best Local Similarity 100.0%; Pctd. No. 0.59; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 EDGQVMDVD 9

DB 46 EDGQVMDVD 54

## RESULT 12

US-09-401-616-1  
Sequence 10, Application US/0940163F  
Patent No. US20020048943A1  
GENERAL INFORMATION:  
APPLICANT: Hellman, Lars T.  
TITLE OF INVENTION: ENHANCED VACCINES  
FILE REFERENCE: 10223/056001  
CURRENT APPLICATION NUMBER: US/09/401,616-1  
CURRENT FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: US 60/106,652  
PRIOR FILING DATE: 1998-11-02  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 331  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated proteins

## Query Match

US-09-949-375A-8 Score 47; DB 9; Length 331;

Best Local Similarity 100.0%; Pctd. No. 0.59; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 EDGQVMDVD 9

DB 54 EDGQVMDVD 62

## RESULT 13

US-10-176-664-1  
Sequence 10, Application US/10176664  
Publication No. US20030031663A1  
GENERAL INFORMATION:  
APPLICANT: Hellman, Lars T.  
TITLE OF INVENTION: ENHANCED VACCINES  
FILE REFERENCE: 10031/006001  
CURRENT APPLICATION NUMBER: US/10/176,664-1  
CURRENT FILING DATE: 2002-06-19

PRIOR APPLICATION NUMBER: US/09/401,636  
PRIOR FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: US 60/106,652  
PRIOR FILING DATE: 1998-11-02  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 331  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated proteins  
US 10-176-664-1

## Query Match

US-10-207-655-329 Score 47; DB 15; Length 331;

Best Local Similarity 100.0%; Pctd. No. 0.59; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 EDGQVMDVD 9

DB 54 EDGQVMDVD 62

## RESULT 14

US-10-207-655-329  
Sequence 129, Application US/10207655  
Publication No. US20030118592A1  
GENERAL INFORMATION:  
APPLICANT: Ledbetter, Jeffrey A.  
APPLICANT: Hayden-Ledbetter, Martha S.  
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
FILE REFERENCE: 390049.401C  
CURRENT APPLICATION NUMBER: US/10/207,655  
CURRENT FILING DATE: 2002-07-25  
NUMBER OF SEQ ID NOS: 426  
SOFTWARE: Patent In version 3.0  
SEQ ID NO 329  
LENGTH: 331  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: fusion polypeptide  
US-10-207-655-329

## Query Match

US-09-949-375A-8 Score 47; DB 15; Length 331;

Best Local Similarity 100.0%; Pctd. No. 0.59; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 EDGQVMDVD 9

DB 50 EDGQVMDVD 56

## RESULT 15

US-09-949-375A-8  
Sequence 8, Application US/09949375A  
Patent No. US20020172673A1  
GENERAL INFORMATION:  
APPLICANT: KLYSNER, Steen et al.  
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING ICE  
FILE REFERENCE: 3631-011P  
CURRENT APPLICATION NUMBER: US/09/949,375A  
CURRENT FILING DATE: 2002-01-18  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 8  
LENGTH: 336  
TYPE: PRT  
ORGANISM: BOMB SAPIENS  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: 174-183  
OTHER INFORMATION: ICE heavy chain C2 domain



GenCore version 5.1.6  
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QX Protein - protein search, using sw model

Run on: November 5, 2003, 17:18:39 ; Search time 13.5 seconds  
(without alignments)  
56,989 Million cell updates/sec

Title: US-09-914 088 2

Perfect score: 39

Sequence: 1 STR-EGEL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 36168692 residues

Total number of hits satisfying chosen parameters: 604

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 761\*

1: PIR1\*

2: PIR2\*

3: PIR3\*

4: PIR4\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	41.0	8	D61512	variant surface gl
2	15	40.5	6	JH0784	neuropeptide TE-6
3	15	33.5	5	JT0520	gamma chain V I
4	13	43.3	7	PT0581	T-cell receptor be
5	13	33.3	8	C39690	neuronal cell adesi
6	12	30.8	4	I40697	biofilm A - Citroba
7	12	30.8	5	PT0684	T-cell receptor be
8	12	30.8	6	S29637	jacalin beta-II ch
9	12	30.8	6	A20186	fatty acid synthas
10	12	30.8	6	PT0662	T-cell receptor be
11	12	30.8	6	PT0648	T-cell receptor be
12	12	30.8	7	E61491	seed protein ws-5
13	12	30.8	7	PT0529	T-cell receptor be
14	12	30.8	7	PT0667	T-cell receptor be
15	12	30.8	8	S37141	tpsa protein - Brw
16	12	30.8	8	S63493	dissimulatory sulf
17	12	30.8	8	PT0595	T-cell receptor be
18	12	30.8	8	PT0653	T-cell receptor be
19	11	28.2	4	PT0677	T-cell receptor be
20	11	28.2	4	A26209	protein-glutamine
21	11	28.2	5	B45525	actin 1 - Ma.aria
22	11	28.2	5	PT0543	T-cell receptor be
23	11	28.2	6	A61419	serine dehydrog
24	11	28.2	6	PT0516	BLM transcription
25	11	28.2	6	PT0516	T-cell receptor be
26	11	28.2	6	PT0657	T-cell receptor be
27	11	28.2	6	PT0726	T-cell receptor be
28	11	28.2	7	S46364	opacity protein P.
29	11	28.2	7	S46365	opacity protein P.

30	11	28.2	7	2	A44428	platelet aggregati
31	11	28.2	7	2	H33098	180K exoantigen -
32	11	28.2	7	2	PC1316	large granule L3 c
33	11	28.2	7	2	PT0526	T-cell receptor be
34	11	28.2	7	2	PT0676	T-cell receptor be
35	11	28.2	7	2	S58797	serine/threonine-s
36	11	28.2	7	4	I55382	hypothetical pepti
37	11	28.2	8	2	S20162	leghemoglobin II
38	11	28.2	8	2	S43971	tumor-associated a
39	11	28.2	8	2	S43972	tumor-associated a
40	11	28.2	8	2	S13661	polygalacturonase
41	11	28.2	8	2	S71919	alcohol dehydrogen
42	11	28.2	8	2	I48934	apolipoprotein A-I
43	11	28.2	8	2	PT0613	T-cell receptor be
44	11	28.2	8	2	PT0554	T-cell receptor be
45	11	28.2	8	2	PT0691	T-cell receptor be

ALIGNMENTS

RESULT 1

D61512  
variant surface glycoprotein XITat 1.6 - Trypanosoma brucei (fragment)  
C:Species: Trypanosoma brucei  
C:Date: 28-Oct-1994 #sequence\_revision: 28-Oct-1994 #text\_change 07-May-1999  
C:Accession: D61512  
R:Holder, A.A.; Cross, G.A.M.  
Mol. Biochem. Parasitol. 2, 135-150, 1981

A:Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-term  
A:Reference number: A61512; MUID:8172836; PMID:6163983  
A:Accession: D61512  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <HCL>  
C:Keywords: glycoprotein

Query Match 41.0%; Score 16; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. NO. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EGE 7  
DB 2 EGE 4

RESULT 2

JH0784  
neuropeptide TE-6 pig roundworm (fragment)  
C:Species: Ascaris suum (pig roundworm)  
C:Date: 10-Jun-1993 #sequence\_revision: 10-Jun-1993 #text\_change 28-Apr-1995  
C:Accession: JH0784  
R:Smart, D.; Shaw, C.; Curry, W.J.; Johnston, C.F.; Thim, L.; Halton, D.W.; Buchanan, Y.  
Biochem. Biophys. Res. Commun. 187, 1323-1329, 1992  
A:Title: The primary structure of TE-6: a novel neuropeptide from the nematode Ascaris  
A:Reference number: JH0784; MUID:93038603; PMID:1417808  
A:Accession: JH0784  
A:Molecule type: protein  
A:Residues: 1-6 <SMA>  
A:Experimental source: gonoduct  
C:Keywords: neuropeptide

Query Match 38.5%; Score 15; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. NO. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGE 7  
DB 1 TQGELE 6

RESULT 3

JT0520

19 kappa chain V H1 region (SD1) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 23-Oct-1992 #sequence\_revision 23-Oct-1992 #text\_change 18-Aug-1996  
 C:Accession: U09220  
 R:Anker, R.; Conley, M.E.; Follok, B.A.  
 J. Exp. Med. 169, 2109-2119, 1989  
 A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia  
 A:Reference number: J70511; MUID:89279157; PMID:2786447  
 A:Accession: J70511  
 A:Molecule type: mRNA  
 A:Residues: 1-5 <AKK>  
 A:Note: the sequence shown here is one of eight productive V H1 mu chain rearrangements  
 A:Note: a stop codon terminates the sequence in the V region  
 C:Keywords: heterotrimer; immunoglobulin  
 F:1-5/Domain: V kappa region <RE>

Query Match 33.8% Score 13; DB 2; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TQEG 6  
 DB 1 TQEG 4

RESULT 4  
 P0684  
 T-cell receptor: beta chain V D-J region (159 AA) mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: P0684  
 R:Petrey, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: P0684; MUID:91277601; PMID:1711558  
 A:Accession: P0684  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-7 <PEE>  
 A:Experimental source: day 15 fetal thymus, strain BALB/c  
 C:Keywords: T cell receptor

Query Match 33.8% Score 13; DB 2; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TQEG 6  
 DB 2 SSEG 7

RESULT 5  
 P0684  
 neutral cell adhesion molecule, cardiac splice form (159 AA) rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 24-Jan-1997 #sequence\_revision 24-Jan-1997 #text\_change 16-Jul-1999  
 C:Accession: C09690  
 R:Reyes, A.A.; S-will, S.J.; Akerson, R.  
 Mol. Cell. Biol. 11, 1654-1661, 1991  
 A:Title: At least 22 alternatively spliced forms of the neutral cell adhesion molecule mRNA  
 A:Reference number: A39690; MUID:91415161; PMID:1996115  
 A:Accession: C09690  
 A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <PEE>  
 A:Cross references: GRN63970  
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 33.8% Score 13; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSEG 7

Db 4 QGE 6

RESULT 6  
 I40697  
 bactin A - Citrobacter freundii (fragment)  
 C:Species: Citrobacter freundii  
 C>Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
 C:Accession: I40697  
 R:Shuan, C.; Campbell, A.  
 Gene 67, 203-211, 1985  
 A:Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter  
 A:Reference number: I40697; MUID:89006280; PMID:2971595  
 A:Accession: I40697  
 A>Status: preliminary; translated from GE/EMBL/DCBU  
 A:Molecule type: DNA  
 A:Residues: 1-4 <RES>  
 A:Cross references: GB:M2:922; NID:9144434

Query Match 30.8% Score 12; DB 2; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TQEG 5  
 DB 1 TQEG 4

RESULT 7  
 P0684  
 T-cell receptor: beta chain V D-J region (140-18X) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: P0684  
 R:Petrey, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: P0684; MUID:91277601; PMID:1711558  
 A:Accession: P0684  
 A>Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-5 <PEE>  
 A:Experimental source: day 18 fetal thymus, strain BALB/c  
 C:Keywords: T cell receptor

Query Match 30.8% Score 12; DB 2; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TQEG 6  
 DB 2 SSEG 5

RESULT 8  
 S29637  
 jacalin beta-II chain - Artocarpus champedon (fragment)  
 C:Species: Artocarpus champedon  
 C>Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
 C:Accession: S29637  
 R:Ngoc, L.; Brillard, M.; Hoebeke, J.  
 Biochim. Biophys. Acta 1156, 219-222, 1993  
 A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-k  
 A:Reference number: S29635; MUID:91152601; PMID:8427879  
 A:Accession: S29637  
 A:Molecule type: protein  
 A:Residues: 1-6 <KCO>  
 A:Experimental source: seed  
 C:Complex: heterotetramer; two alpha and two beta chains  
 C:Function  
 A:Description: seed storage protein  
 A:Note: lectin for L-galactosyl-beta-1,3-N-acetylgalactosamine

C;Keywords: heterotetramer; lectin; seed; storage protein

Query Match 30.8%; Score 12; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QSGE 7  
|||  
Db 3 QSGK 6

RESULT 9  
A20186  
Fatty-acid synthase (F02.3.1.185) - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 05-May-2000  
C;Accession: A20186  
R;McCarthy, A.D.; Aiken, A.; Hardie, G.; Santikarn, S.; Williams, D.H.  
FEBS Lett. 160, 296-303, 1983  
A;Title: Amino acid sequence around the active serine in the acyl transferase domain of  
A;Accession: A20186  
A;Reference number: A20186; MUID:83287768; PMID:6554204  
A;Molecule type: Protein  
A;Residues: 1-6 <P>  
C;Keywords: acyl-transferase; coenzyme A

Query Match 30.8%; Score 12; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GEL 8  
|||  
Db 3 GEV 5

RESULT 10  
PT0662  
T-cell receptor beta chain V-D-J region (121-138) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0662  
R;Feeney, A.C.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0662  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <P>  
A;Experimental source: day 4 postnatal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 30.8%; Score 12; DB 2; Length 6;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 TQGE 7  
|||  
Db 2 SRTGE 6

RESULT 11  
PT0648  
T-cell receptor beta chain V-D-J region (121-138) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0648  
R;Feeney, A.C.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0648  
A;Status: translation not shown

A;Molecule type: mRNA  
A;Residues: 1-6 <P>  
A;Experimental source: day 4 postnatal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 30.8%; Score 12; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TQEG 6  
|||  
Db 2 SSEG 5

RESULT 12  
E61491  
Seed protein ws-5 - winged bean (fragment)  
C;Species: Psophocarpus tetragonolobus (winged bean)  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C;Accession: E61491  
R;Hirano, H.  
J. Protein Chem. 8, 115-130, 1989  
A;Title: Microsequence analysis of winged bean seed proteins electrophoretically from two-d  
A;Reference number: A61491; MUID:89351806; PMID:2765119  
A;Accession: E61491  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <P>  
C;Keywords: glycoprotein; seed

Query Match 30.8%; Score 12; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 STQEG 6  
|||  
Db 1 STVPGG 6

RESULT 13  
PT0529  
T-cell receptor beta chain V-D-J region (100-4K) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0529  
R;Feeney, A.C.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0529  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-7 <P>  
A;Experimental source: adult thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 30.8%; Score 12; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TQEG 6  
|||  
Db 2 SSEG 5

RESULT 14  
PT0667  
T-cell receptor beta chain V-D-J region (121-21) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0667  
R;Feeney, A.C.  
J. Exp. Med. 174, 115-124, 1991

A:Title: Functional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: P70509; MUID:91277601; PMID:1711558  
 A:Accession: P70667  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-7 <PE>  
 A:Experimental source: day 4 postnatal thymus, strain HA.H/c  
 C:Keywords: T-cell receptor

Query Match 30.8%; Score 12; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.9e-05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCEG 6  
 DB 2 SSEG 5

## RESULT 15

S37141  
 ipSA protein - Erwinia chrysanthemi  
 C:Species: Erwinia chrysanthemi  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Oct 1999  
 C:Accession: S37141  
 R:Docille, A.; Toussaint, A.; Faelen, M.  
 submitted to the EMBL Data Library, August 1993  
 A:Description: Identification of the integration host factor genes of E. chrysanthemi.  
 A:Reference number: S37139  
 A:Accession: S37141  
 A>Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-8 <DCU>  
 A:Cross-references: EMBL:X74750; NID:g393669; PID:CAA52769.1; PDB:g581138

Query Match 30.8%; Score 12; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 2.9e-05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 EGE 7  
 DB 6 KGE 5

Search completed: November 5, 2003, 17:22:55  
 Job time: 14.5 secs

GenCore version 5.1.6  
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Query protein - protein search, using sw mode:

Run on: November 5, 2003, 17:15:14 Search time 9.5 seconds  
(without alignment)  
37.60: Million cell updates/sec

Title: US-09-914-088-2  
Perfect score: 39  
Sequence: 1 STRGEGEL 8

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 6  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	41	0	7 1 UF03_MOUSE	P38541: rat musculus
2	16	41	0	8 1 CLP_THICU	P80488: thiacetabitu
3	13	33	3	7 1 UNIL_RAT	P64576: ratius novy
4	13	33	3	8 1 LMT1_DESM	P22306: lorusta nig
5	12	30	5	1 BICA_CITR	P10001: citrobacter
6	12	30	5	7 1 PPR2_TYES	P40029: lyobacterio
7	12	30	5	8 1 RSI_EPMCH	P14745: etwinia chr
8	11	28	2	8 1 UPA1_HUMAN	P14745: etwinia chr
9	11	28	2	8 1 WPI_PESAT	P38105: pekinus a
10	10	25	6	5 1 PSK_DASCA	P04661: dactylus caro
11	10	25	6	7 1 EIO5_LITRU	P04661: dactylus caro
12	10	25	6	7 1 UC24_MAIZE	P04661: dactylus caro
13	10	25	6	7 1 UN06_PINPS	P04661: dactylus caro
14	10	25	6	8 1 ORVY_ORCL	P04661: dactylus caro
15	10	25	6	8 1 UN09_RAT	P04661: dactylus caro
16	9	23	4	1 RM01_YEAST	P04661: dactylus caro
17	9	23	4	1 BR06_CLOFA	P04661: dactylus caro
18	9	23	4	1 BR06_CONIX	P04661: dactylus caro
19	9	23	4	7 1 GFRP_MOUSE	P04661: dactylus caro
20	9	23	4	7 1 MNPI_LEPCE	P04661: dactylus caro
21	9	23	4	1 AKHG_GRYBI	P04661: dactylus caro
22	9	23	4	8 1 GJLR_HUMAN	P04661: dactylus caro
23	8	20	5	4 1 OCPI_CCTNY	P04661: dactylus caro
24	8	20	5	1 UXA4_CHEJTR	P04661: dactylus caro
25	8	20	5	7 1 PARI_HESCT	P04661: dactylus caro
26	8	20	5	7 1 IGAC_DACLE	P04661: dactylus caro
27	8	20	5	8 1 ACI_THUAI	P04661: dactylus caro
28	8	20	5	8 1 ALI2_CARVA	P04661: dactylus caro
29	8	20	5	8 1 PARI_PENXG	P04661: dactylus caro
30	8	20	5	8 1 LCK3_LEUNA	P04661: dactylus caro
31	8	20	5	8 1 RS7_MYCIT	P04661: dactylus caro
32	8	20	5	8 1 UF06_MOUSE	P04661: dactylus caro
33	7	17	9	5 1 TRM3_BACUL	P04661: dactylus caro

34	7	17	9	7	1	PARS_HIRME	P42564: hirudo medi
35	7	17	9	7	1	LANC_CARUT	P36960: carnobacter
36	7	17	9	7	1	WMA1_ACHFU	P35919: achatina fu
37	7	17	9	7	1	WMA1_ACHFU	P35921: achatina fu
38	7	17	9	8	1	AKH_TABAT	P14595: tabanus atr
39	7	17	9	8	1	LPK_LEUNA	P13049: leucophaea
40	7	17	9	8	1	RT34_BOVIN	P82929: bcs taurus
41	7	17	9	8	1	UPAA_HUMAN	P30096: homo sapien
42	7	17	9	8	1	VGIG_HSV2B	P81780: herpes simp
43	6	15	4	3	1	GRWM_HUMAN	P01157: homo sapien
44	6	15	4	4	1	ACH1_ACHFU	P35904: achatina fu
45	6	15	4	4	1	DCML_PSECH	P19916: pseudomonas

# ALIGNMENTS

RESULT 1  
UF03\_MOUSE  
ID UF03\_MOUSE STANDARD: PRT: 7 AA.  
AC P38641:  
DT 01-OCT-1994 (Rel. 30, Created:  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE  
RC TrSUS=Fibroblast;  
RX MEDLINE=9509937; PubMed=7521108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk C.K.;  
RT "Separation and sequencing of familial and novel murine proteins  
RT using preparative two-dimensional gel electrophoresis.";  
RL Electrophoresis 15:735-745(1994);  
CC -!- MUSCELLANEUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.1, ITS MW IS: 36 kDa.  
FT NON TER 7  
SQ SEQUENCE 7 AA; 842 MW; 6AA72B10DB1B180 CRC64;

Query Match 41.0% Score 16; DB 1; Length 7;  
Best Local Similarity 60.0%; Pred. NC. 1.3e-05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QV 4 QEGEL 8  
DB 2 EEAEI 6

RESULT 2  
CLP\_THICU  
ID CLP\_THICU STANDARD: PRT: 8 AA.  
AC P80488:  
DT 01-OCT-1996 (Rel. 34, Created:  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Chemothitroph specific protein (fragment).  
OS Thiobacillus cuprinus.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Comamonadaceae; Thiomonas.  
OX NCBI\_TaxID=36862;  
RN [1]  
RP SEQUENCE  
RC STRAIN=DSM 5494;  
RA Martin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;  
RT Submitted (SEP-1995) to the SWISS-PROT data bank.  
CC -!- MUSCELLANEUS: FOUND SPECIFICALLY IN CELLS CULTURED  
CC CHEMOLITHOTROPHICALLY.  
FT NON TER 8  
SQ SEQUENCE 8 AA; 185 MW; 91487B06DC2076D CRC64;



Query Match 41.0%; Score 16; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QEG 6  
 DB 5 QEG 7

RESULT 3  
 ID UNIL RAT STANDARD; PRT; 7 AA.  
 AC P56576;  
 DT 15-DEC-1998 (Rel. 37, Created);  
 DT 15-DEC-1998 (Rel. 37, Last sequence update);  
 DT 15-DEC-1998 (Rel. 37, Last annotation update);  
 DE Unknown protein from 2nd-page of heart tissue (Spot P11) (Fragment).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Rattus.  
 CC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 CC STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
 RA Jurgbitt P.R.;  
 RA Submitted P.R.;  
 CC -1- MISCCELLANEOUS: ON THE 2D-GEL THE DETERMINED P: OF THIS UNKNOWN  
 CC PROTEIN IS: 8.5, ITS MW IS: 42 KDa.  
 CC UNSURE 2 2 OR A.  
 FT NON TER 7 7  
 SQ SEQUENCE 7 AA; 775 MW; 6866BPC4DQCSA6B0 CRC64;

Query Match 33.3%; Score 13; DB 1; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 STCEG 6  
 DB 2 SAREQG 7

RESULT 4  
 ID LMT2\_LCCMI STANDARD; PRT; 8 AA  
 AC P22356;  
 DT 01-AUG-1991 (Rel. 19, Created);  
 DT 01-AUG-1991 (Rel. 19, Last sequence update);  
 DT 01-AUG-1991 (Rel. 19, Last annotation update);  
 DE Locustamyotropin 2 (LOM-MT-2).  
 CC Locusta migratoria (migratory locust).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pretygola;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 CC NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 CC TISSUE=Corpora cardiaca;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.D., de Loof A.;  
 RA "Isolation, identification and synthesis of locustamyotropin II, an  
 RT additional neuropeptide of Locusta migratoria. Member of the  
 RT cephalomyotropic peptide family."  
 RA Insect Biochem. 20:479-484 (1990).  
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY  
 CC InterPro: IPR001484; Pyrokinin.  
 CC PROSITE: PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD RES 5 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA875 CRC64;

Query Match 33.3%; Score 13; DB 1; Length 8;

Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 EGE 7  
 DB 1 EGD 3

RESULT 5  
 ID BIOA\_CITFR STANDARD; PRT; 5 AA.  
 AC P13071;  
 DT 01-JAN-1990 (Rel. 13, Created);  
 DT 01-JAN-1990 (Rel. 13, Last sequence update);  
 DT 16-OCT-2001 (Rel. 40, Last annotation update);  
 DE Adenosylmethionine 8-amino-7-oxonanoate aminotransferase  
 DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA  
 DE aminotransferase) (Fragment).  
 GN BIOA.  
 OS Citrobacter freundii.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Citrobacter.  
 CC NCBI\_TaxID=546;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89006280; PubMed=2971595;  
 RA Shivan D., Campbell A.;  
 RT "Transcriptional regulation and gene arrangement of Escherichia coli.  
 RT Citrobacter freundii and Salmonella typhimurium biotin operons."  
 RL Gene 67:203-211 (1988).  
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-  
 CC oxonanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-  
 CC diaminonanoate.  
 CC -1- COFACTOR: Pyridoxal phosphate.  
 CC -1- PATHWAY: Biotin biosynthesis.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SIMILARITY: Belongs to class III of pyridoxal-phosphate-dependent  
 CC aminotransferases.  
 CC  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 CC EMBL: M21922; -1- NOT\_ANNOTATED\_CDS.  
 CC PIR: I40697; I40697.  
 CC InterPro: IPR005814; Aminotrans\_3.  
 CC PROSITE: PS00600; AA\_TRANSFER\_CLASS\_3; PARTIAL.  
 CC Biotin biosynthesis; Transferase; Aminotransferase;  
 CC Pyridoxal phosphate.  
 CC NON TER 5 5  
 SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 30.8%; Score 12; DB 1; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TIOE 5  
 DB 2 TDD 5

RESULT 6  
 ID PH2\_LYCES STANDARD; PRT; 7 AA.  
 AC P83379;  
 DT 28-FEB-2003 (Rel. 41, Created);  
 DT 28-FEB-2003 (Rel. 41, Last sequence update);  
 DT 28-FEB-2003 (Rel. 41, Last annotation update);  
 DE Purple acid phosphatase isozyme LeSAP2 (EC 3.1.3.2) (Fragment).

OS Lycopersicon esculentum (Tomato).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;  
 CC Asteridae; families; Solanales; Solanaceae; Solanum.  
 CC NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND  
 RP GLYCOSYLATION.  
 RC STRAIN=cv. MoneyMaker; TISSUE=Seed;  
 RX MEDLINE=22361242; PubMed=12473124;  
 RA Bozzo G.S., Raghothama K.G., Pixton W.C.;  
 RT "Purification and characterization of two secreted purple acid  
 RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon  
 RT esculentum) cell cultures."  
 RL Eur. J. Biochem. 269:6278-6286(2002)  
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H<sub>2</sub>O → an  
 CC alcohol + phosphate.  
 CC -!- SUBUNIT: Monomeric.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: Glycosylated.  
 CC -!- MISCELLANEOUS: In L. esculentum there are at least two isozymes of  
 CC purple acid phosphatase.  
 CC Hydrolyase; Glycoprotein.  
 FT NON\_TER 1  
 FT NON\_TER 7  
 SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;  
 Query Match 30.8%; Score 12; DB 1; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 QEGEL 8  
 DB 5 GDEL 7  
 RESULT 7  
 RS1\_ERWCH STANDARD; PRT; 9 AA.  
 AC P37985;  
 DT 01-OCT-1994 (Rel. 10, Created).  
 DT 01-OCT-1994 (Rel. 32, Last sequence update).  
 DT 01-NOV-1995 (Rel. 32, Last annotation update).  
 DE 30S ribosomal protein S1 (fragment).  
 GN RPSA.  
 CS Ewingia chrysanthemi.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Pectobacterium.  
 CC NCBI\_TaxID=556;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=3937;  
 RA Douillie A., Toussaint A., Faelen M.;  
 RL Submitted (Aug-1993) to the EMBL/GenBank/DBS databases.  
 CC -!- FUNCTION: BINDS MRNA; THIS FACILITATES RECOGNITION OF THE  
 CC INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT  
 CC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.  
 CC  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC or send an email to [license@1st-sib.ch](mailto:license@1st-sib.ch)).  
 CC  
 CC EMBL; X74750; CAA52769.1;  
 DR PIR; S3714.1; S37141.  
 KW Ribosomal protein; Repeat; RNA-binding.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 837 MW; 9E18733D58339C9 CRC64;

Query Match 30.8%; Score 12; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 EGE 7  
 DB 6 KGE 8  
 RESULT 8  
 UPAL\_HUMAN STANDARD; PRT; 8 AA.  
 ID CPAL\_HUMAN  
 AC P30087;  
 DT 01-APR-1993 (Rel. 25, Created).  
 DT 01-APR-1993 (Rel. 25, Last sequence update).  
 DT 16-OCT-2001 (Rel. 40, Last annotation update).  
 DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=94092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing."  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.  
 DR SWISS-2DPAGE; P30087; HUMAN.  
 FT NON\_TER 1  
 FT NON\_TER 8  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 944 MW; C01772C455BB36DA CRC64;  
 Query Match 28.2%; Score 11; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 QEGEL 8  
 DB 2 QESNV 6  
 RESULT 9  
 WP1\_PERAT STANDARD; PRT; 9 AA.  
 ID WP1\_PERAT  
 AC P83195;  
 DT 28-FEB-2003 (Rel. 41, Created).  
 DT 28-FEB-2003 (Rel. 41, Last sequence update).  
 DT 28-FEB-2003 (Rel. 41, Last annotation update).  
 DE Wall protein-1 (WP1-1) (Fragment).  
 OS Perkinsus atlanticus.  
 CC Eukaryota; Alveolata; Perkinsa; Perkinsida; Perkinsidae; Perkinsus.  
 CC NCBI\_TaxID=106964;  
 RN [1]  
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RX MEDLINE=22044350; PubMed=12049410;  
 RA Montes J.F., Durfort M., Ilado A., Garcia-Valero J.;  
 RT "Characterization and immunolocalization of a main proteinaceous  
 RT component of the cell wall of the protozoan parasite Perkinsus  
 RT atlanticus."  
 RL Parasitology 124:477-484(2002).  
 CC -!- FUNCTION: Is a major protein component of the cell wall. May play  
 CC a key role in the organization of the cell wall and in promoting  
 CC the survival of this parasite.  
 CC -!- SUBCELLULAR LOCATION: Cell wall. Disulfide-linked to other cell  
 CC wall components.  
 CC -!- DEVELOPMENTAL STAGE: Expressed throughout all walled developmental  
 CC stages.

KW Cell wall.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 765 MW; F1787D087B:AA516 CRC64;  
 Query Match 28.2%; Score 1; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 EG 6  
 DB 4 EG 5  
 RESULT 10  
 PSK DAUCA  
 ID PSK DAUCA STANDARD; PRT; 5 AA.  
 AC P58761;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)]  
 OS Daucus carota (Carrot).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Asteridae; campanulids; Apiales; Apiaceae; Daucus.  
 CX NCBI\_TaxID:4039;  
 RN [1]  
 RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.  
 RC STRAIN:cv. US-Harumakigosun;  
 RX MEDLINE=20212743; PubMed=10750705;  
 RA Harai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,  
 RA Kanada H., Sakagami Y.;  
 RT "A secreted peptide growth factor, phytosulfokine, acting as a  
 RT stimulatory factor of carrot somatic embryo formation";  
 RJ Plant Cell Physiol. 41:27-32(2000).  
 CC FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE  
 CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC  
 CC EMBRYOS.  
 CC SUBCELLULAR LOCATION: Secreted.  
 CC PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A  
 CC PUTATIVE NEURANE RECEPTOR (BY SIMILARITY).  
 CC SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.  
 KW Growth factor; Sulfolipin.  
 FT PEPTIDE 1 4 PHYTOSULFOKINE BETA.  
 FT MCD\_RES 1 1 SULFATION.  
 FT MCD\_RES 3 3 SULFATION.  
 SQ SEQUENCE 5 AA; 687 MW; 76C1B504B300000 CRC14;  
 Query Match 25.6%; Score 10; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 TO 4  
 DB 4 TO 5  
 RESULT 11  
 EY05 LITRU  
 ID EY05 LITRU STANDARD; PRT; 7 AA.  
 AC P82101.  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Electrin 5.  
 OS Litoria rubella (Desert tree frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 CC Pelodyadinae; Litoria.  
 CX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC SUBCELLULAR LOCATION: Secreted.  
 CC TISSUE SPECIFICITY: Skin.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 834 MW; 6DC05B076B0B5030 CRC64;  
 Query Match 25.6%; Score 10; DB 1; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 EGEL 8  
 DB 3 EPEI 6  
 RESULT 12  
 UC24 MAIZE  
 ID UC24 MAIZE STANDARD; PRT; 7 AA.  
 AC P86630;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein: from 2D-page of etiolated coleoptile (Spot 447);  
 DE (Fragment).  
 OS Zea mays (Maize).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC PACAD clade; Panicoideae; Andropogoneae; Zea.  
 CX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Tourlet P., Riccardi F., Moxin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 30.0 kDa.  
 DR Maize-2PAGE: P86630; COLEOPTILE.  
 DR MaizeDB: 123956;  
 FT NON\_TER 1 1  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;  
 Query Match 25.6%; Score 10; DB 1; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 STTQ 4  
 DB 1 STAK 4  
 RESULT 13  
 UN06 PINPS  
 ID UN06 PINPS STANDARD; PRT; 7 AA.  
 AC P81675;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of needles (N141) (Fragment).  
 OS Pinus pinaster (Maritime pine).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 CX NCBI\_TaxID=71647;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Needle;  
 RX MEDLINE=99274C88; PubMed=10344297;  
 RA Costa P., Plomieu C., Bauw G., Dubos C., Bahrman K., Kroebe A.,  
 RA Frigerio J.-M., Plomieu C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 RT proteins";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.  
 FT NON\_TER 1 1  
 FT NON\_TER 2 7  
 SQ SEQUENCE 7 AA; 523 MW; 69D76724486B5743 CRC64;  
 Query Match 25.6%; Score 10; DB 1; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 GEL 8  
 DB 3 GNU 5

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1] SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pleissner K.-P., Scheier C., Regitz-Zagrosek V., Salikov C.,  
 RA Jungblut P.R.;  
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.  
 FT NON\_TER 1 8  
 FT NON\_TER 2 8  
 SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;  
 Query Match 25.6%; Score 10; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 QE 5  
 DB 1 QE 2

Search completed: November 5, 2003, 17:21:08  
 Job time : 13.5 secs

RESULT 14  
 ORMY CRCL1 STANDARD; PRT; 8 AA.  
 AC PB2455;  
 DT 16-OCT-2001 (Rel. 40, Created;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update);  
 DT 16-OCT-2001 (Rel. 42, Last annotation update)  
 DE Oricostyptoplin (CMT).  
 CS Oricostes limosus (Spinycheek crayfish).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Asacidea;  
 CC Astacodea; Carabidae; Oricostes.  
 OX NCBI\_TaxID=28379;  
 RN [1]  
 RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.  
 RC TISSUE=Hindgut;  
 RX MEDLINE=20411310; PubMed=10952880;  
 RA Dirksen H., Burdick S., Sauter A., Keller R.;  
 RT "Two oricostins and the novel octapeptide oricostyptoplin in the hindgut  
 RT of the crayfish Oricostes limosus: identified myostimulatory  
 RT neuropeptides originating together in neurones of the terminal  
 RT abdominal ganglion";  
 RL J. Exp. Biol. 203:2807-2818(2000).  
 CC -1- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND  
 CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED  
 CC BY ABDOMINAL GANGLIONIC NEURONS.  
 CC -1- MASS SPECTROMETRY: MW=904.8; METHOD: FAB  
 KW Amidation; Neuropeptide.  
 FT MOD\_RES 8 8  
 FT MOD\_RES 8 8  
 SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;  
 Query Match 25.6%; Score 10; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CT 3  
 DB 5 TT 6

RESULT 15  
 UH09 RAT STANDARD; PRT; 8 AA.  
 AC P56575;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OM protein: - protein search, using sw model

Run on: November 5, 2003, 17:18:09 : Search time 27.5 seconds  
(without alignments):  
75.070 Million cell updates/sec

Title: US-09 914-388-2

Perfect score: 39

Sequence: 1 STQEGEL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 452

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
SPREMBL23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriaph:
17: sp_archaeap:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	41.0	8	5 Q94695	Q94695 physarum po
2	14	35.9	8	4 Q16428	Q16428 homo sapien
3	14	35.9	8	5 Q97WH6	Q97WH6 perinereis
4	14	35.9	8	6 Q9MYL5	Q9MYL5 pongo pygma
5	13	33.3	8	13 Q90ZV5	Q90ZV5 fulica leuc
6	12	30.8	7	11 Q63480	Q63480 rattus norv
7	12	30.8	8	2 Q9R9E0	Q9R9E0 bacillus su
8	12	30.8	8	7 Q29810	Q29810 homo sapien
9	11	28.2	7	12 Q65578	Q65578 bovine herp
10	11	28.2	8	2 Q9AGP4	Q9AGP4 arthropacte
11	11	28.2	8	2 Q68485	Q68485 klebsiella
12	11	28.2	8	4 Q9P285	Q9P285 homo sapien
13	11	28.2	8	6 Q9XSV:	Q9XSV: canis famil
14	11	28.2	8	11 Q35835	Q35835 rattus sp.
15	11	28.2	8	11 P70243	P70243 mus musculu
16	11	28.2	8	11 Q60655	Q60655 mus musculu

## ALIGNMENTS

## RESULT 1

```
Q94695 Q94695 PRELIMINARY; PRT; 8 AA.
AC Q94695:
DT 01-FEB-1997 (TREMBLrel. C2, Created)
DT 01-FEB-1997 (TREMBLrel. C2, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. C8, Last annotation update)
DE Actin (Fragment).
GN ARDC.
OS Physarum polycephalum (Slime mold).
OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
OC Physarum.
OX NCBI_TaxID=5791;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=96182101; PubMed=8622700;
RA Benard M., Lagnel C., Pallotta D., Pierron G.;
RT "Mapping of a replication origin within the promoter region of two
RT unlinked, abundantly transcribed actin genes of Physarum
RL polycephalum".
RL Mol. Cell. Biol. 16:968-976(1996).
DR EMBL; M73459; AAC03706.1; -
FT NON_TER
SQ SEQUENCE 8 AA: 878 MW: F4C6C2CAAB187B16 CRC64;
```

Query Match 41.0%; Score 16; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred.No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EGE 7  
DB 2 EGE 4

## RESULT 2

```
Q16428 Q16428 PRELIMINARY; PRT; 8 AA.
ID Q16428
AC Q16428;
DT 01-NOV-1996 (TREMBLrel. C1, Created)
```

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update);  
DE Dystrophin protein (Fragment).  
GN DYSTROPHIN.  
OS Homo sapiens (HUMAN).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96163531; PubMed=8566360;  
RA Holder E., Maeda M., Bies R.D.;  
RT "Expression and regulation of the dystrophin Purkinje promoter in  
human skeletal muscle, heart, and brain";  
RL Hum. Genet. 97:232-239 (1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kitano T., Kobayakawa H., Saitou N.;  
RT "Silver Project";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB037493; BAA90413.1; -;  
DR EMBL: AB037493; BAA90413.1; -;  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 825 MW; F21865A5A2CB05B6 CRC64;  
  
Query Match 35.9%; Score 14; DB 4; Length 8;  
Best Local Similarity 42.9%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY : STTQSGE 7  
DB |  
2 SEVSAGE 8  
  
RESULT 3  
Q9TWH6 PRELIMINARY; PRT; 8 AA.  
AC Q9TWH6  
DT 01-MAY-2000 (TrEMBLrel. 13, Created);  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update);  
DE BIOACTIVE PEPTIDE P-PUTATIVE ENDPHASEAL NEUROREGULATOR.  
OS Perinereis varicaurica.  
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Annelida;  
OC Physlococida; Nereididae; Perinereis.  
OX NCBI\_TaxID=6355;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95323338; PubMed=7599979;  
RA Takahashi T., Fukukawa Y., Muneoka Y., Matsushima T., Ikeda T.,  
Fujita T., Mirakata H., Nonoto K.;  
RT "Isolation and characterization of four novel bioactive peptides from  
a polychaete annelid, Perinereis varicaurica";  
RL Comp. Biochem. Physiol. C, Pharmacol. Toxicol. Endocrinol. 110:297  
304 (1996).  
SQ SEQUENCE 8 AA; 989 MW; 954772CA87B5E59 CRC64;  
  
Query Match 35.9%; Score 14; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 EGE 8  
DB |||  
3 EGDV 6

DE Dystrophin.  
OS Pongo pygmaeus (Orangutan),  
OS Pan troglodytes (Chimpanzee), and  
OS Gorilla gorilla (gorilla).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
OX NCBI\_TaxID=9600, 9598, 9593;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES: P. pygmaeus, P. troglodytes, and G. gorilla;  
RA Kitano T., Kobayakawa H., Saitou N.;  
RT "Silver Project";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB037496; BAA90419.1; -;  
DR EMBL: AB037494; BAA90415.1; -;  
DR EMBL: AB037495; BAA90417.1; -;  
SQ SEQUENCE 8 AA; 825 MW; F21865A5A2CB05B6 CRC64;  
  
Query Match 35.9%; Score 14; DB 6; Length 8;  
Best Local Similarity 42.9%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 STTQSGE 7  
DB |  
2 SEVSAGE 8  
  
RESULT 5  
Q90ZV5 PRELIMINARY; PRT; 8 AA.  
AC Q90ZV5  
DT 01-DEC-2001 (TrEMBLrel. 19, Created);  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update);  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update);  
DE Adenylate kinase (Fragment).  
OS Pulica leucopetra.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Gruiformes; Rallidae; Fulica.  
OX NCBI\_TaxID=156758;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shapiro J.H., Dumbacher J.P.;  
RT "Adenylate kinase intron 5: a new nuclear locus for avian  
systematics";  
RL Auk 118:248-255 (2001).  
DR EMBL: AF307998; AAK47537.1; -;  
KW Kinase.  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 994 MW; 96333B19CB1B1866 CRC64;  
  
Query Match 33.3%; Score 13; DB 13; Length 8;  
Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 EGE 7  
DB |||  
1 QGE 3  
  
RESULT 6  
Q63480 PRELIMINARY; PRT; 7 AA.  
AC Q63480  
DT 01-NOV-1996 (TrEMBLrel. 01, Created);  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update);  
DE TR4-NS orphan receptor (Fragment).  
GN TR4.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;

RN SEQUENCE FROM N.A.  
 RP MEDLINE=96198747; PubMed=8612486;  
 RA Yoshikawa T., Makino S., Gao X.M., Xing S.C., Chuang D.M.,  
 RT "Splice variants of rat TR4 orphan receptor: differential expression  
 RT of novel sequences in the 5'-untranslated region and C-terminal  
 domain."  
 RL Endocrinology 137:1562-1571(1996).  
 DR EMBL: J59125; A802827.1; .  
 KW Receptor.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 758 MW; 672AAR78640C0535C CRC64;

Query Match 30.8%; Score 12; DB 1; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 GEL 8  
 Db 5 GDL 7

## RESULT 7

Q9R9E0 PRELIMINARY; PRT; 8 AA.  
 AC Q9R9E0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update;  
 DE Stage V sporulation protein E (Fragment).  
 GN SPOVE.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 CX NCBI\_TaxID=1423;  
 RN [1]\_TaxID=1423;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=9300329; PubMed=1391053;  
 RA Henriquez A.C., de Lencastre H., Pigot P.J.,  
 RT "A Bacillus subtilis morphogene cluster that includes spoVE is  
 RT homologous to the ara region of Escherichia coli."  
 RL Biochimie 74:735-748(1992).  
 DR EMBL: X64258; CAA4556.1; .  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 893 MW; EET5A.A332.H1AA (F064);

Query Match 30.8%; Score 12; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTQE 5  
 Db 2 TTKE 5

## RESULT 8

Q29810 PRELIMINARY; PRT; 8 AA.  
 AC Q29810;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update;  
 DE HLA class II DR-beta chain (Fragment).  
 GN HLA-DRB5\*5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96175156; PubMed=9110934;  
 RA Svensson A.C., Setterblad N., Pilgrim U., Rask L., Andersson G.;

RT "Evolutionary relationship between different human major  
 RT histocompatibility complex HLA-DR haplotypes."  
 RL Immunogenetics 43:304-314(1996).  
 DR EMBL: X88792; CAA61271.1; .  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 909 MW; 62C6C1A9CAA731A8 CRC64;

Query Match 30.8%; Score 12; DB 7; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TQE 5  
 Db 6 TQO 8

## RESULT 9

Q65578 PRELIMINARY; PRT; 7 AA.  
 AC Q65578;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hypothetical 0.8 kDa protein (Fragment).  
 OS Bovine herpesvirus 1.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirus.  
 CX NCBI\_TaxID=10320;  
 RN [1]\_TaxID=10320;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Cooper;  
 RX MEDLINE=95313343; PubMed=7793062;  
 RA Vleck C., Beres V., Lu Z., Kutish G.F., Paces V., Rock D.,  
 RA Letchworth G.J., Schwyer M.;  
 RT "Nucleotide sequence analysis of a 30-kb region of the bovine  
 RT herpesvirus 1 genome which exhibits a colinear gene arrangement with  
 RT the UL21 to UL4 genes of herpes simplex virus."  
 RL Virology 210:100-108(1995).  
 DR EMBL: Z48053; CAA88130.1; .  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 756 MW; 6DD33455B1F1B1C0 CRC64;

Query Match 28.2%; Score 11; DB 12; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTQEG 7  
 Db 1 TTSHK 6

## RESULT 10

Q9AGP4 PRELIMINARY; PRT; 8 AA.  
 AC Q9AGP4;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Serine hydroxymethyltransferase (Fragment).  
 GN GLYA.  
 OS Arthrobacter sp. IIN.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micrococccineae; Micrococaceae; Arthrobacter.  
 CX NCBI\_TaxID=153502;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IIN.  
 RA Meskys R., Harris R.J., Casalte V., Basran J., Scrutton N.S.;  
 RT "Genetic organization of the genes involved in dimethylglycine and  
 RT sarcosine degradation in Arthrobacter spp.: implications for glycine  
 RT betaine catabolism.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF229478; AAK16486.1; -  
 KW Nucleoside transferase; transferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 898 MW; 651870533372457 CRC64;

Query Match 28.2%; Score 11; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 6 GE 7  
 Db 7 GE 8

## RESULT 11

ID O68485 PRELIMINARY; PRT; 8 AA.  
 AC O68485;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Amino-ycoside 3'-O-nucleoside transferase (Fragment).  
 GN AAD01.  
 OS Klebsiella pneumoniae.  
 OG Bacteroidetes.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCB: TaxID=573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:K1;  
 RX MEDLINE=98287600; PubMed=9624504;  
 RA Centron D., Roy P.H.;  
 RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene  
 ac6'::q from the integrin of a natural multiresistance plasmid".  
 RL Antimicrob. Agents Chemother. 42:506-508(1998).  
 DR EMBL: AF047556; AAC25501.1; -  
 KW Plasmid; transferase.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 878 MW; EFC1B5A2CBDD256 CRC64;

Query Match 28.2%; Score 11; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 2 TIG 4  
 Db 5 STC 8

## RESULT 12

ID Q9P285 PRELIMINARY; PRT; 8 AA.  
 AC Q9P285;  
 DT 01-OCT-2003 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 15, Last annotation update)  
 DE Clotting factor VIII (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCB: TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shibata M., Shima M., Morichika S., Yoshio A.;  
 RT "Human clotting factor VIII gene, junction regions of the deletion of  
 exon 4 through 7".  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases  
 DR EMBL: AB240872; BAA9412.1; -  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 866 MW; IC16987AAB05BDD3 CRC64;

Query Match 28.2%; Score 11; DB 4; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy 3 TOSG 6  
 Db 3 SEDG 6

## RESULT 13

ID O9XSY1 PRELIMINARY; PRT; 8 AA.  
 AC O9XSY1;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
 DE Retinoblastoma protein (Fragment).  
 GN RBL.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCB: TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97049323; PubMed=8894053;  
 RA Venter P.J., Brault J.A., Yuzbasyan-Gurkan V., Brewer G.J.;  
 RT "Gene-specific universal mammalian sequence-tagged sites: application  
 to the canine genome".  
 RL Biochem. Genet. 34:321-341(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Venter P.J., Cao Y., Alexander L., Yuzbasyan-Gurkan V.;  
 RT "Dinucleotide repeat polymorphism in the canine retinoblastoma (RBL)  
 gene".  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF155737; AAD38807.1; -  
 FT NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 895 MW; 14259B18676721E3 CRC64;

Query Match 28.2%; Score 11; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 6 GE 7  
 Db 5 GE 6

## RESULT 14

ID O35835 PRELIMINARY; PRT; 8 AA.  
 AC O35835;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ORF1 protein.  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCB: TaxID=10118;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=98008057; PubMed=9581555;  
 RA Hospital V., Prat A., Joule C., Cherif D., Day R., Cohen P.;  
 RT "Human and rat testis express two mRNA species encoding variants of  
 NQD convertase, a metalloendopeptidase of the insulinasin family".  
 RL Biochem. J. 327:773-779(1997).  
 DR EMBL: X93208; CAA3695.1; -  
 SQ SEQUENCE 8 AA; 986 MW; EAT8A1B1ADC5A5B6 CRC64;



Query Match 28.2%; Score 11; DB 11; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STT 3  
 DB 4 ATT 6

## RESULT 15

P70243 PRELIMINARY; PRT: 5 AA.  
 AC P70243;  
 DT 01-FEB-1997 (TEMBRel. 02. Created;  
 DT 01-FEB-1997 (TEMBRel. 02. Last sequence update;  
 DT 01-DEC-2001 (TEMBRel. 19. Last annotation update;  
 DE Skeletal muscle specific calcium channel (fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN 11)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:129;  
 RA O'Brien R.A.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X98325; CAA66969.1; -.  
 FT NCN\_TFR 1  
 FT NCN\_TFR 8  
 FT NCN\_TFR 8  
 SQ SEQUENCE 9 AA: 565 MW: D9C37DCB1861AD0E LKRC64;

Query Match: 28.2%; Score 11; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SE 7  
 DB 4 SE 5

Search completed: November 5, 2003, 17:22:17  
 Job time : 10.5 secs

GenCore version 5.1.6  
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OX protein - protein search, using sw model

Run on: November 5, 2003, 17:14:39 ; Search time 33.5 Seconds  
(without alignments)  
37.905 Million cell updates/sec

Title: US-09-914-088-2

Perfect score: 39

Sequence: 1: STTQEGEL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 102276

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.1

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1941.DAT:  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1942.DAT:  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1943.DAT:  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1944.DAT:  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1945.DAT:  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1946.DAT:  
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1960.DAT:  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1961.DAT:  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1962.DAT:  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1963.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	8	AAB23868	Immunoglobulin E
2	39	100.0	8	AAB25908	IgE C-epsilon-2 do
3	39	100.0	8	AAJ16613	Peptide P2 derived
4	39	100.0	8	AAJ16613	IgE peptide #2, M
5	39	100.0	8	ABJ03218	Human IgE immunoge
6	31	79.5	6	AAB25931	PL mimotope peptid
7	31	79.5	6	AAU16666	Peptide P2sh deriv
8	31	79.5	6	ABJ00235	Human IgE immunoge
9	21	53.8	5	AAW66615	Proteoglycan

10	21	53.8	6	21	AAW87756	Potato THR protein
11	21	53.8	7	16	AAW21258	Hydroxymethylgluta
12	21	53.8	8	22	ABP13186	HIV A02 super moti
13	21	53.8	8	22	ABP15880	HIV A24 super moti
14	20	51.3	6	22	AAU05503	Synthetic hexapept
15	20	51.3	7	21	AAW23122	Hsp47-binding phag
16	20	51.3	7	21	AAW02936	Nucleotide-binding
17	20	51.3	7	21	AAW02937	Nucleotide-binding
18	20	51.3	7	23	ABP49021	Zinc finger protei
19	20	51.3	7	23	ABP49022	Zinc finger protei
20	20	51.3	7	23	ABP49049	Zinc finger protei
21	19	48.7	6	13	AAW25035	mAb 42 antigenic d
22	19	48.7	7	11	AAW07089	Glycopeptide again
23	19	48.7	7	21	AAW02935	Nucleotide-binding
24	19	48.7	7	23	ABP48708	Zinc finger protei
25	19	48.7	7	23	ABP48963	Zinc finger protei
26	19	48.7	7	23	ABP49023	Zinc finger protei
27	19	48.7	7	23	ABP50013	Zinc finger protei
28	19	48.7	9	14	AAW43434	Ro/SSA epitope 78.
29	19	48.7	8	19	AAW58632	Platelet factor 4
30	19	48.7	8	21	AAW10329	S. cerevisiae RNA
31	19	48.7	8	21	AAW10335	C. albicans RNA qu
32	19	48.7	8	21	AAW10341	Peptide motif III
33	19	48.7	8	21	AAW32133	Peptide motif III
34	19	48.7	8	21	AAW32139	Peptide motif III
35	19	48.7	8	21	AAW32145	Human DNA derived
36	19	48.7	8	22	ABJ53735	HIV A02 super moti
37	19	48.7	8	22	ABP13227	HIV A24 super moti
38	19	48.7	8	22	ABP15899	HIV B58 super moti
39	19	48.7	8	22	ABP18294	Bacterial conserve
40	19	48.7	8	22	AAU69102	Rat glutamate tran
41	19	48.7	8	22	AAU69188	Peptide motif of R
42	19	48.7	8	23	ABJ05606	Peptide motif of R
43	19	48.7	8	23	ABJ05612	Peptide motif of R
44	19	48.7	8	23	ABJ05618	Peptide motif of R
45	19	48.7	8	23	ABG68930	Signature motif #2

ALIGNMENTS

RESULT 1  
AAB23868  
ID AAB23868 standard; peptide, 8 AA.  
XX  
AC AAB23868:  
XX  
DT 23-JAN-2001 (first entry)  
XX  
DE Immunoglobulin E epitope immunogenic peptide SEQ ID NO:6.  
XX  
KW Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier;  
KW prostate cancer; Haemophilus influenzae; vaccine; infectious disease;  
KW malaria; cytostatic; antiallergic; nontoxic; neuroprotective;  
KW protozoacide; Alzheimer's disease; allergy.  
XX  
OS Homo sapiens.  
XX  
PN WO200050077-A1.  
XX  
PD 31-AUG-2000.  
XX  
PF 22-FEB-2002; 2000MO-EP01457.  
XX  
PR 25-FEB-1999; 99GB-0004405.  
PR 25-FEB-1999; 99GB-0004408.  
PR 25-FEB-1999; 99GB-0004412.  
PR 13-AUG-1999; 99GB-001926C.  
XX  
PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Coste M, Lobet Y, Van Mechelen MP, Verriest C;  
XX

DR WPI; 2000-572040/53.  
 XX Immunogens and vaccine comprising the immunogen useful for preventing  
 PT and treating infectious diseases e.g. malaria and chronic disease e.g.  
 PT cancer, comprises peptide and carrier from protein D of influenzae  
 XX  
 PS Claim 9; Page 37; 53pp; English.  
 XX  
 CC The present invention describes an immunogen (I) comprising a peptide  
 CC (Ia) and a carrier (Ib), derived from protein D of Haemophilus influenzae  
 CC or its fragment. Also described are: (1) a vaccine comprising (I), and  
 CC an excipient; (2) preparation of (I), comprising conjugating a peptide  
 CC to protein D or its fragment; and (3) preparation of a vaccine of (1),  
 CC comprising formulating (I) with an excipient. (I) has cytostatic,  
 CC anti-allergic, nontropic, neuroprotective and protozoacidal activities.  
 CC (1) and the vaccine are useful for the manufacture of a medicament for  
 CC preventing and treating infectious diseases such as malaria or chronic  
 CC disease such as cancer, Alzheimer's disease or allergy in a patient.  
 CC Unlike prior art immunogens, (I) induces high levels of antipeptide  
 CC immune responses while inducing a moderate humoral response against the  
 CC carrier. The present sequence represents a specifically claimed  
 CC immunoglobulin E (IgE) epitope immunogenic peptide sequence, which can  
 CC be used in an immunogen of the present invention.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 39; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 STTQEGEL 8  
 DQ 1 STTQEGEL 8  
 RESULT 2  
 AAH25908  
 ID AAB25908 standard; Peptide; 8 AA.  
 AC AAB25908;  
 XX  
 D- 05 JAN 2001 (first entry)  
 XX  
 DE IgE C epsilon2 domain surface exposed epitope (I) of protein D NCBI2.  
 XX  
 KW Epitope; mimotope; human; immunoglobulin E; IgE; epsilon2 domain;  
 KW allergic disease; immunophoraxis; immunosuppressive; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200003460-A1.  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 22 FEB 2000; 2000WO-EP01455.  
 XX  
 PR 25 FEB-1999; 93GB-0004405.  
 PR 29-MAR-1999; 93GB-0007151.  
 PR 07-MAY 1999; 93GB-0010537.  
 PR 07-MAY 1999; 93GB-0010538.  
 PR 07-AUG-1999; 93GB-0018594.  
 PR 07-AUG-1999; 93GB-0018603.  
 PR 07-SEP-1999; 93GB-0021046.  
 PR 07-SEP-1999; 93GB-0021047.  
 PR 24-OCT-1999; 93GB-0025619.  
 PR 23-NOV-1999; 93GB-0027698.  
 XX  
 PA (SMK) : SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) : PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;

PI Randall R. Turnell WG, Van Mechelen MP, Vinals De Bassols YC;  
 XX WPI; 2000-572073/53.  
 XX  
 PT Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 PS Claim 3; Page 5; 129pp; English.  
 XX  
 CC The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (E1) of C-epsilon-2 domain (D) of  
 CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an  
 CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)  
 CC for treating allergies comprising (II); (3) a ligand (IV) capable of  
 CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
 CC (IIa) comprising (Ia); and (7) producing (III) by producing (II). (I)  
 CC can have anti-allergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (I), (II) and (III) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (IV) is useful for identifying mimotopes of E1,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (I) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (II), (III) and PC are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 39; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 STTQEGEL 8  
 DQ 1 STTQEGEL 8  
 RESULT 3  
 AAU16633  
 ID AAU16633 standard; Peptide; 8 AA.  
 AC AAU16633;  
 XX  
 DT 07-NOV-2001 (first entry)  
 XX  
 DE Peptide P2 derived from Cepsilon2 region of human IgE.  
 XX  
 KW Human; linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200145745-A2.  
 XX  
 PD 28-JUN-2001.  
 XX  
 PF 21-DEC-2000; 2000WO-GB04935.  
 XX  
 PR 21-DEC-1999; 99GB-0030233.  
 PR 22-FEB-2000; 2000GB-0004096.  
 PR 22-AUG-2000; 2000GB-0020707.  
 PR 22-AUG-2000; 2000GB-0020708.  
 XX  
 PA (ACAM) : ACAMBIOS RES LTD.  
 PA (SMK) : SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Flinn N, Johnson T;  
 XX

DR WPI: 2001-521967/57.  
 XX A linkage comprising an immunogenic conjugate useful treatment of IgE mediated diseases.  
 PT  
 XX Example 4; Page 21; 48pp; English.  
 PS  
 XX The present invention relates to linkage methodology for use in the conjugation of compounds (e.g. peptides) to carrier vehicles (e.g. macromolecules, polymers, dendrimers, proteins) to produce biological and immunological constructs. The invention provides a method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition or a vaccine. The invention describes peptides derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E (IgE) which are used to produce conjugated compounds. The compounds or compositions of the invention are useful in the manufacture of a medicament for the treatment of IgE mediated diseases. The invention allows for controlled conjugation of a peptide epitope (antigen) to a protein so as to form an immunogenic conjugate which may be able to raise a protective antibody response in an animal or human patient. CC AAU16632-AAU1693 represent peptides derived from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 CC  
 XX Sequence 8 AA;  
 SQ

Query Match 100.0%; Score 39; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : STTQEGEL 8  
 DQ : STTQEGEL 8

RESULT 4  
 AAB51024  
 ID AAB51024 standard; Peptide; 8 AA.  
 AC AAB51024;  
 XX 21-MAR-2001 (first entry)  
 DE IGE peptide #2.  
 XX Vaccine; immunoglobulin E; IgE; anti-allergy.  
 XX Mammalia.  
 CS WC200074716-A2.  
 PN 14-DEC-2000.  
 PO 06-JUN-2000; 2000WO-EP05164.  
 PF 08-JUN-1999; 99GB-0013327.  
 PR (SM'K) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA Prietels J;  
 XX WPI: 2001-C91150/10.  
 DR New vaccine comprising allergy peptides linked by an inert carrier, useful for boosting an anti-allergy immune response in an individual susceptible to an allergic response.  
 PT  
 XX Claim 5; Page 20; 26pp; English.  
 PS  
 XX The present invention relates to a composition comprising allergy peptides linked by an inert carrier. The allergy peptides are derived from immunoglobulin E (IgE) or IgE receptor. The present peptide is one such peptide from IgE. The composition is useful as a vaccine or for

CC manufacturing a medicament for the prophylaxis or treatment of allergy.  
 CC In particular, for boosting an anti-allergy immune response in an individual susceptible to an allergic response.  
 CC  
 XX Sequence 8 AA;  
 SQ

Query Match 100.0%; Score 39; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTQEGEL 8  
 DQ 1 STTQEGEL 8

RESULT 5  
 AAB300218  
 ID AAB300218 standard; Peptide; 8 AA.  
 XX AAB300218;  
 AC 02-SEP-2002 (first entry)  
 DT Human IgE immunogenic peptide SEQ ID NO: 2.  
 XX  
 DE Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage; KW vaccine; antiallergic.  
 XX Homo sapiens.  
 OS WO200216409-A2.  
 XX 28-FEB-2002.  
 PD 17-AUG-2001; 2001WO-EP09576.  
 PP 22-AUG-2000; 2005GB-0020717.  
 PR (SM'K) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX Friede M, Mason S, Turrell WG, Vinals Bassols YC;  
 XX WPI: 2002-489648/52.  
 DR Conjugate for use in vaccine for treatment of allergy, comprises disulfide bridge cyclized peptide and immunogenic carrier.  
 PT  
 XX Claim 4; Page 9; 45pp; English.  
 PS  
 XX The present invention relates to conjugates suitable for use in vaccines, where the conjugate comprises a disulphide bridge cyclized peptide and an immunogenic carrier. The vaccines can be used in the treatment of allergies. The present sequence is a peptide immunogen derived from human immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
 CC  
 XX Sequence 8 AA;  
 SQ

Query Match 100.0%; Score 19; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTQEGEL 8  
 DQ 1 STTQEGEL 8

RESULT 6  
 AAB25931  
 ID AAB25931 standard; Peptide; 6 AA.  
 XX AAB25931;  
 CC

DT 05-JAN-2001 (first entry)  
 DE P2 minotope peptide P2sh SEQ ID NO:25.  
 XX Epitope; minotope; human; immunoglobulin E; IgE; C epsilon2 domain;  
 KW allergic disease; immunoprophylaxis; immunotherapy; anti-allergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy.  
 XX Homo sapiens.  
 OS  
 XX WO2000050460 A1.  
 XX 31 AUG-2000.  
 XX 22-FEB-2000; 2000WO-EP01455.  
 XX 25-FEB-1999; 99GB-0004405.  
 PR 29-MAR-1999; 99GB-0007151.  
 PR C7-MAY-1999; 99GB-0010537.  
 PR C7-MAY-1999; 99GB-0010538.  
 PR C7-AUG-1999; 99GB-0018594.  
 PR C7-AUG-1999; 99GB-0018663.  
 PR C7-SEP-1999; 99GB-0021046.  
 PR C7-SEP-1999; 99GB-0021047.  
 PR 23-OCT-1999; 99GB-0025619.  
 PR 23-NOV-1999; 99GB-0027698.  
 XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (SPPT); PEPTIDE THERAPEUTICS LTD.  
 XX Dyson M, Friede M, Greenwood J, Hewitt E, Lambert A, Mason S;  
 PI Randall R, Turnell WG, Van Mechelen WP, Vinals De Rasse GY.  
 DR WP; 2000-572073/53.  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX Disclosure; Page 9; 129pp; English.  
 XX The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (EI) of C epsilon2 domain (D) of  
 CC immunoglobulin E (IGE), or its minotope. Also defined are (II) an  
 CC immunogen (II) for treating allergy comprising (I) and (II) a vaccine (III)  
 CC for treating allergies comprising (I) and (II) a human (IV) capable of  
 CC recognising (I) (4) a pharmaceutical composition comprising (IV);  
 CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
 CC (Iia) comprising (Ia); and (7) producing (Iii) by producing (Ii). (I)  
 CC can have anti-allergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (II), (III) and (IV) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (IV) is useful for identifying mimotopes of PI,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (I) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (II), (III) and (IV) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AAB25927 to AAB26099 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX Sequence 6 AA;  
 SQ Query Match 79.5%; Score 31; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 TTQEGE 7  
 DB 1 TTQEGE 6

RESULT 7  
 AAU16656  
 ID AAU16656 standard; Peptide; 6 AA.  
 XX  
 AC AAU16656;  
 XX  
 DT C7-NOV-2001 (first entry)  
 XX  
 DE Peptide P2sh derived as minotope of C epsilon2 region of human IgE.  
 XX Human; linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; C epsilon2; C epsilon3; C epsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200145745-A2.  
 XX 28-JUN-2001.  
 XX 21-DEC-2000; 2000WO-GB04935.  
 XX 21-DEC-1999; 99GB-0030233.  
 PR 22-FEB-2000; 2000GB-0004096.  
 PR 22-AUG-2000; 2000GB-C020707.  
 PR 22-AUG-2000; 2000GB-C020708.  
 XX (ACAM-) ACAYBIS RES LTD.  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX Flinn N, Johnson T;  
 PI WPI; 2001-521967/57.  
 DR  
 XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
 PT mediated diseases  
 PT Example 4; Page 21; 48pp; English.  
 XX The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC C epsilon2, C epsilon3 or C epsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU16632-AAU16913 represent peptide sequences derived from or mimotopes of  
 CC the C epsilon2/C epsilon3/C epsilon4 region of human IgE.  
 XX Sequence 6 AA;  
 SQ Query Match 79.5%; Score 31; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 TTQEGE 7  
 DB 1 TTQEGE 6

RESULT 8  
 ABJ00230  
 ID ABJ00230 standard; Peptide; 6 AA.  
 XX  
 AC ABJ00230;

XX DT 02-SEP-2002 (first entry)  
 XX DE Human IgE immunogenic peptide SEQ ID NO: 14.  
 XX KW Immunogen: human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 XX KW vaccine; antiallergic.  
 XX OS Homo sapiens.  
 XX PN WO200216409-A2.  
 XX PD 28 FEB-2002.  
 XX FF 17-AUG-2001: 2001WO-EP09576.  
 XX PR 22-AUG-2000: 2000GB-0020717.  
 XX PA (SMIK : SMITHKLINE BEECHAM BIOLOGICALS.  
 XX PA (PEPT:) PEPTIDE THERAPEUTICS LTD.  
 XX PI Friede M, Mason S, Turnell WG, Vinals Russell YC.  
 XX DR WPI: 2002-489648/52.  
 XX PR Conjugate for use in vaccine for treatment of allergy, comprises  
 PT disulfide bridge cyclized peptide and immunogenic carrier.  
 XX PS Claim 4; Page 9; 45pp; English.  
 XX CC The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a peptide immunogen derived from human  
 CC immunoglobulin E (IgE) suitable to be cyclized and used in the invention.  
 XX Sequence 6 AA;  
 Query Match 79.5%; Score 11; DR 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 TTDGE 7  
 Db 1 TTDGE 6  
 RESULT 9  
 AAW66615  
 ID AAW66615 standard; peptide; 5 AA.  
 AC AAW66615;  
 XX 27-NOV-1998 (first entry)  
 DE Phosphopeptide.  
 XX Casein; calcium phosphate complex; amorphous calcium phosphate; ACP;  
 KW phosphopeptide; delivery vehicle; calcium fluoride; calcium deficiency;  
 KW osteoporosis; osteomalacia; tooth; bone disease.  
 XX Synthetic.  
 OS Bos taurus.  
 XX Key location/Qualifiers  
 XX Modified-site 2 /note= "Thr(P)"  
 XX Modified-site 3 /note= "Thr(P)"  
 XX W09240406 A1.  
 XX 17-SEP-1998.

XX PF 13-MAR-1998; 98WO-AU00160.  
 XX PR 13-MAR-1997; 97AJ-C005662.  
 XX (UYNE) UNIV MELBOURNE.  
 XX PA (VICT-) VICTORIAN DAIRY IND AUTHORITY.  
 XX PI Reynolds EC;  
 XX DR WPI: 1998-520803/44.  
 XX PT Stable calcium phosphate complex including phospho-peptide  
 PT stabilised amorphous calcium phosphate - useful for treatment of  
 PT dental caries, calcium malabsorption and bone diseases such as  
 PT osteoporosis and osteomalacia.  
 XX Example 2; Page 17; 43pp; English.  
 XX CC The invention relates to a stable calcium phosphate complex including  
 CC phosphopeptide stabilised amorphous calcium phosphate (ACP) or its  
 CC derivative, where the phosphopeptide includes the amino acid sequence:  
 CC Ser(P)-Ser(P)-Glu-Glu. The amorphous phases stabilised by the  
 CC phosphopeptides are a delivery vehicle for co-localisation of Ca, form  
 CC P and phosphate at the tooth surface in a slow-release amorphous  
 CC producing superior anticaries efficacy over prior art. The amorphous  
 CC phases stabilised by the phosphopeptides are also useful as dietary  
 CC supplements to increase calcium bioavailability and to help prevent  
 CC diseases associated with calcium deficiencies. They are particularly  
 CC useful for treatment or prevention of dental caries, calcium  
 CC malabsorption and bone diseases such as osteoporosis and osteomalacia.  
 CC The compositions are useful in humans and in veterinary medicine in  
 CC domestic animals such as cattle, sheep, horses and companion animals  
 CC e.g. cats and dogs as well as zoo animals. The relationship between the  
 CC phosphopeptide structure and interaction with amorphous calcium  
 CC phosphate was investigated using a series of synthetic peptide homologues  
 CC and analogues (AAW66615-22). These studies showed that the cluster  
 CC sequence Ser(P)-Ser(P)-Glu-Glu- was mainly responsible for the  
 CC interaction with ACP and that all three contiguous Ser(P) residues are  
 CC required for maximal interaction with ACP.  
 XX Sequence 5 AA;  
 Query Match 53.8%; Score 21; DR 19; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 STDGE 5  
 Db 1 STDGE 5  
 RESULT 10  
 AAY87756  
 ID AAY87756 standard; Protein; 6 AA.  
 AC AAY87756;  
 XX 17-AUG-2000 (first entry)  
 DE Potato THT protein fragment #5.  
 XX THT protein; transgenic plant; resistance; phytopathogen; oomycete;  
 KW hydroxycinnamic acid-coenzyme A; potato; fungicide; infection;  
 KW tyramine N-hydroxycinnamic acid transferase; tyraminamide biosynthesis.  
 XX Solanum tuberosum.  
 OS DE19846001 A1.  
 XX 27-APR-2000.  
 XX 06-OCT-1998; 94SE-1046001.

XX 06-OCT-1998; 98CE-1046001.  
 XX (BIOPLANT BIOTECHNOLOGISCHES FORSCHUNGSLAB.  
 PA (IPRP); IPB INST. PFLANZENBIOCHEMIE.  
 XX Scheel D, Rosahl S, Strack D, Schmidt A.  
 XX WPI; 2000-319:17/28.  
 XX Transgenic plant, especially potato, resistant to Phytophthora  
 PT infestans, contains gene for hydroxycinnamic acid:tyramine  
 PT N-hydroxycinnamic acid transferase.  
 XX Claim 5a; Column 11-12; 12pp; German.  
 XX This invention describes a novel transgenic plant with increased  
 CC resistance to infection by phytopathogens, especially Phytophthora  
 CC infestans, contains, in its genome, a gene construct comprising a  
 CC heterologous promoter, and a sequence (1) encoding a hydroxycinnamic  
 CC acid coenzyme A:tyramine N-(hydroxycinnamic acid) transferase (11),  
 CC under the control of the promoter. The products of the invention have  
 CC fungicide activity. (1) is involved in biosynthesis of tyramineamide  
 CC which is incorporated into plant cell walls to provide a chemical  
 CC barrier against pathogens, extracellular tyramineamide inhibits the  
 CC growth of pathogens. The introduction of (11), into tobacco, cotton,  
 CC rape, melon, sugar beet, maize, and especially potato or tomato, is  
 CC used to improve resistance to phytopathogens, particularly P. infestans  
 CC or other Oomycetes. (1) can also be used to express (11) in prokaryotic  
 CC or eukaryotic cells and its fragments can be used to isolate homologous  
 CC sequences from bacteria, fungi, plants and animals. In the antisense  
 CC orientation, (1) and its fragments can be used to inhibit expression of  
 CC (11) in cells. AAY8752-Y8771 represent fragments of the potato  
 CC (Solanum tuberosum) THT protein described in the method of the  
 CC invention.  
 XX SQ Sequence 6 AA;  
 Query Match 53.8%; Score 21; DB 21; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 TTQES 6  
 |||  
 DQ 2 TTNES 6  
 RESULT 1:  
 AAW21258  
 ID AAW21258 standard; peptide: 7 AA.  
 XX AC AAW21258;  
 CT 29 JUL 1997 (first entry)  
 XX Hydroxymethylglutaryl coenzyme A reductase signal oligopeptide #17.  
 KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; HIV;  
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;  
 KW change; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;  
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; thesus;  
 KW gonadolibirin precursor; plasminogen activator inhibitor 2; prorenin;  
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;  
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV; human; OMVVS;  
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;  
 KW Treponema pallidum membrane protein; TMRA; isoleucyl-amyloid polypeptide;  
 KW fibroblast MP1; schistosoma elastase precursor; schistosomin;  
 KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.  
 XX Homo sapiens.  
 OS WC9511568-A1.  
 XX

PD 20-JUL-1995.  
 XX 12-JAN-1995; 95WO-US00575.  
 XX 14-JAN-1994; 94US-0182249.  
 XX (RATH//) RATH M.  
 XX Rath M;  
 XX WPI; 1995-263953/34.  
 DR Identifying signal oligopeptide(s) in protein sequence(s) - shown as  
 PT regions of max. hydrophilicity, used in modulating communication  
 PT between proteins;  
 XX Claim 5; Page 32; 88pp; English.  
 XX The sequences given in AAW21201-56C represent hydrophilic signal oligo-  
 CC peptides. These signal oligopeptides are localised on the surface  
 CC of the protein and are represented by the hydrophilicity maxima of  
 CC the protein. These peptides are enriched in charged amino acids  
 CC arranged with neutral spacer amino acids. The specific signal  
 CC character of these oligopeptides is determined by a characteristic  
 CC combination of conformation and charge within the signal sequence.  
 CC These oligopeptides may be used as vaccines in the treatment of  
 CC human disease, as competitive inhibitors to prevent or reduce the  
 CC metabolic action or interaction of a selected protein by blocking  
 CC its specific signal sequences, or as therapeutic agents to function  
 CC as feedback regulators to reduce synthesis rate of a selected protein.  
 CC These peptides may be modified by omitting one or more amino acids at  
 CC the N- and/or C-terminal, by substituting one or more amino acids  
 CC without consideration of charge and polarity, by substituting one or  
 CC more amino acids with amino acid residues with similar charge and/or  
 CC polarity, by omitting one or more amino acids or a combination of these.  
 XX SQ Sequence 7 AA;  
 Query Match 53.8%; Score 21; DB 16; Length 7;  
 Best Local Similarity 80.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 STQEE 5  
 |||  
 DQ 3 STTEE 7  
 RESULT 12  
 ABP13186  
 ID ABP13186 standard; Peptide: 8 AA.  
 XX AC ABP13186;  
 XX 15-JUL-2002 (first entry)  
 XX HIV A02 super motif pol peptide #101.  
 DE HIV; HIV-1; human immunodeficiency virus; erv; pol; gag; nef; vpr;  
 KW vpr; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX Human immunodeficiency virus type 1.  
 OS WO200124810-A1.  
 PN 12-APR-2001.  
 XX 05-OCT-2000; 2000WO-US27766.  
 XX 05-OCT-1999; 99US-0412863.  
 XX (EPIN-) EPIMUNE INC.  
 XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX Claim 32; Page 138; 448pp; English.  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral  
 CC tumour associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 8 AA;  
 SQ Query Match 53.8%; Score 21; DB 22; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 TQEGEL 8  
 DB 3 TEAEEL 8  
 RESULT 13  
 ABP15880  
 ID ABP15880 standard; Peptide: 8 AA.  
 XX  
 AC ABP15880;  
 DT 15-JUL-2002 (first entry)  
 DE HIV A24 super motif pol peptide #60.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WC200124810-A1.  
 XX  
 XX 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX Claim 32; Page 138; 448pp; English.  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral  
 CC tumour associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 8 AA;  
 SQ Query Match 53.8%; Score 21; DB 22; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DR WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX Claim 32; Page 194; 448pp; English.  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 8 AA;  
 SQ Query Match 53.8%; Score 21; DB 22; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 TQEGEL 8  
 DB 3 TEAEEL 8  
 RESULT 14  
 AAU05503  
 ID AAU05503 standard; Peptide: 6 AA.  
 XX  
 AC AAU05503;  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Synthetic hexapeptide ligand 15.  
 XX  
 KW Hexapeptide ligand; drug design; high throughput screening; HTS; MOSAR;  
 KW Multivariate Quantitative Structure Activity relationships.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200136980-A2.  
 XX  
 PD 25-MAY-2001.  
 XX  
 PF 20-NOV-2000; 2000WO-GB04420.  
 XX  
 PR 18-NOV-1999; 99GB-0027346.  
 XX  
 PA (MELA-) MELACURE THERAPEUTICS AB.  
 PA (PETT/) PETT C P.  
 XX  
 PI Lundstedt T, Andersson P, Wikberg J, Muceniece R, Prusis P;  
 XX WPI: 2001-432565/46.  
 XX  
 PT A novel method for identifying the interaction site, binding site or  
 active site in a macromolecule, using of informative combinatorial





GenCore version 5.1.6  
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OM protein protein search, using sw model

Run on: November 5, 2003, 17:22:25 / Search time 22 Seconds  
(without alignments)  
62,454 Million Cell updates/sec

Title: US-09-914-088-2  
Perfect score: 39  
Sequence: 1 STTOEGEL 8

Scoring table: BLOSUM62

Gapcp 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 42362

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications, AA.\*

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- 2: /cgn2\_6/prodata/2/pubaa/PCR\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/2/pubaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/2/pubaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/2/pubaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/2/pubaa/PCRUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/2/pubaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/2/pubaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/2/pubaa/US09\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*
- 13: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/2/pubaa/US09\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*
- 18: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	8	12	US-10-082-014-274
2	39	100.0	8	12	US-10-372-076-128
3	20	51.3	7	9	US-09-989-994-1017
4	20	51.3	7	9	US-09-989-994-1222
5	20	51.3	7	9	US-09-989-994-1231
6	20	51.3	7	11	US-09-990-186-1017
7	20	51.3	7	11	US-09-990-186-1222
8	20	51.3	7	11	US-09-990-186-1231
9	20	51.3	7	11	US-09-989-994-1017
10	20	51.3	7	11	US-09-989-994-1222
11	20	51.3	7	11	US-09-989-994-1231
12	19	48.7	7	9	US-09-989-994-708
13	19	48.7	7	9	US-09-989-994-793
14	19	48.7	7	9	US-09-989-994-813
15	19	48.7	7	9	US-09-989-994-2617

16	19	48.7	7	11	US-09-990-186-708	Sequence 708, App
17	19	48.7	7	11	US-09-990-186-793	Sequence 793, App
18	19	48.7	7	11	US-09-990-186-813	Sequence 813, App
19	19	48.7	7	11	US-09-990-186-2617	Sequence 2617, App
20	19	48.7	7	11	US-09-989-994-708	Sequence 708, App
21	19	48.7	7	11	US-09-989-994-793	Sequence 793, App
22	19	48.7	7	11	US-09-989-994-813	Sequence 813, App
23	19	48.7	7	11	US-09-989-994-2617	Sequence 2617, App
24	19	48.7	7	12	US-09-990-832C-33	Sequence 33, Appl
25	19	48.7	8	12	US-10-167-831-4	Sequence 4, Appl
26	19	48.7	8	12	US-10-167-831-10	Sequence 10, Appl
27	19	48.7	8	12	US-10-167-831-16	Sequence 16, Appl
28	19	48.7	8	12	US-10-167-831-88	Sequence 88, Appl
29	19	48.7	8	12	US-10-167-831-17	Sequence 17, Appl
30	18	46.2	5	15	US-10-205-270-14	Sequence 14, Appl
31	18	46.2	6	9	US-09-736-611-17	Sequence 17, Appl
32	18	46.2	6	9	US-09-740-359-8	Sequence 8, Appl
33	18	46.2	6	10	US-09-894-711-8	Sequence 8, Appl
34	18	46.2	6	12	US-10-205-110-6	Sequence 6, Appl
35	18	46.2	6	12	US-10-205-110-46	Sequence 46, Appl
36	18	46.2	6	12	US-10-299-183A-2	Sequence 2, Appl
37	18	46.2	6	12	US-10-128-587A-64	Sequence 64, Appl
38	18	46.2	6	12	US-10-316-421-17	Sequence 17, Appl
39	18	46.2	6	15	US-10-166-241-2	Sequence 2, Appl
40	18	46.2	6	15	US-10-128-590-64	Sequence 64, Appl
41	18	46.2	7	9	US-09-765-086-145	Sequence 145, App
42	18	46.2	7	9	US-09-812-471-16	Sequence 16, Appl
43	18	46.2	7	10	US-09-812-633-16	Sequence 16, Appl
44	18	46.2	7	10	US-09-988-117-16	Sequence 16, Appl
45	18	46.2	7	12	US-10-375-992-145	Sequence 145, App

#### ALIGNMENTS

##### RESULT 1

US-10-082-014-274  
; Sequence 274, Application US/10082014  
; Publication No. US20030185858A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL C  
; FILE REFERENCE: ICC-130.0 4564/85124  
; CURRENT APPLICATION NUMBER: US/10/082.014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/930,915  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 274  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-274

Query Match 100.0%; Score 39; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTOEGEL 8  
|:|||||  
DB 1 STTOEGEL 8

##### RESULT 2

US-10-372-076-128  
; Sequence 128, Application US/10372076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; CHRONIC HEPATITIS

FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/372,076  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/080,295  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 128  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US 10 372-076-128

Query Match 100.0%; Score 39; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTCEGEL 8  
| | | | |  
Db 1 STTCEGEL 8

RESULT 3  
US-09-989-789-1017  
; Sequence 1017, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1017  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-989-789-1017

Query Match 51.3%; Score 20; DB 9; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QEGEL 8  
| | | |  
Db 1 QSGEL 5

RESULT 4  
US-09-989 789-1222  
; Sequence 1222, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1222  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP

US-09-989-789-1222

Query Match 51.3%; Score 20; DB 9; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QEGEL 8  
| | | |  
Db 1 QSGEL 5

RESULT 5  
US-09-989 789-1231  
; Sequence 1231, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1231  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-989-789-1231

Query Match 51.3%; Score 20; DB 9; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QEGEL 8  
| | | |  
Db 1 QSGEL 5

RESULT 6  
US-09-990-186-1017  
; Sequence 1017, Application US/09990186  
; Publication No. US20030368675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2003-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1017  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-990-186-1017

Query Match 51.3%; Score 20; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QEGEL 8  
| | | |  
Db 1 QSGEL 5

RESULT 7  
US-09-990-186-1222

; Sequence 1222, Application US/09990186  
; Publication No. US20030668675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1222  
; LENGTH: 7

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-990-186-1222

Query Match 51.3%; Score 20; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 4 QEGEL 8  
| | |  
Db 1 QSGEL 5

## RESULT 8

US-09-990-186-1231  
; Sequence 1231, Application US/09990186  
; Publication No. US20030668675A1  
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3

; CURRENT APPLICATION NUMBER: US/09/990,186

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1231

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-990-186-1231

Query Match 51.3%; Score 20; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 4 QEGEL 8  
| | |  
Db 1 QSGEL 5

## RESULT 9

US-09-989-994-1017  
; Sequence 1017, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,994

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1017

; LENGTH: 7

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-989-994-1017

Query Match 51.3%; Score 20; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 4 QEGEL 8  
| | |  
Db 1 QSGEL 5

## RESULT 10

US-09-989-994-1222  
; Sequence 1222, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,994

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1222

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-989-994-1222

Query Match 51.3%; Score 20; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 4 QEGEL 8  
| | |  
Db 1 QSGEL 5

## RESULT 11

US-09-989-994-1231  
; Sequence 1231, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,994

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1231

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-989-994-1231

Query Match 51.3%; Score 20; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 4 QEGEL 8  
| | |  
Db 1 QSGEL 5

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RESULT 12
US-09-989-789-708
; Sequence 728, Application US/09989789
; Patent No. US2002063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 708
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-708

Query Match      48.7%; Score 19; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 QGCEL 8
DB      1 QTCEL 5

RESULT 13
US-09-989-789-793
; Sequence 783, Application US/09989789
; Patent No. US2002063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 793
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-793

Query Match      48.7%; Score 19; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 QGCEL 8
DB      1 QTCEL 5

RESULT 14
US-09-989-789-813
; Sequence 813, Application US/09989789
; Patent No. US2002063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
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; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 813
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-813

Query Match      48.7%; Score 19; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 QGCEL 8
DB      1 QTCEL 5

RESULT 15
US-09-989-789-2617
; Sequence 2617, Application US/09989789
; Patent No. US2002063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2617
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-2617

Query Match      48.7%; Score 19; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 QGCEL 8
DB      1 QTCEL 5

Search completed: November 5, 2003, 17:30:35
Job time : 22 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CorpuGen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2003, 17:19:19 : Search time 14 Seconds  
(without alignments)  
24.178 Million col updates/sec

Title: US-09-914-088-2

Perfect score: 39

Sequence: 1 STTQEGEL 8

Scoring table: BLCSM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 61971

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:

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- 2: /cgn2\_6/prodata/1/iaa/5B COMB pep.\*
- 3: /cgn2\_6/prodata/1/iaa/6A COMB pep.\*
- 4: /cgn2\_6/prodata/1/iaa/6B COMB pep.\*
- 5: /cgn2\_6/prodata/1/iaa/6CTUS COMB pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backf:esl pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53.8	7	2	US-08-869-506-9	Sequence 9, Appl
2	53.8	7	3	US-09-128-362-5	Sequence 9, Appl
3	51.3	7	3	US-09-173-941-76	Sequence 77, Appl
4	51.3	7	3	US-09-173-941-76	Sequence 78, Appl
5	19.487	6	1	US-08-253-854-91	Sequence 91, Appl
6	19.487	7	3	US-09-173-941-76	Sequence 76, Appl
7	19.487	8	1	US-08-259-550A-90	Sequence 90, Appl
8	19.487	8	3	US-09-188-579-2	Sequence 2, Appl
9	19.487	8	3	US-08-188-573-8	Sequence 9, Appl
10	19.487	8	3	US-09-188-579-14	Sequence 14, Appl
11	19.487	8	3	US-09-315-444-2	Sequence 2, Appl
12	19.487	8	3	US-09-315-444-8	Sequence 8, Appl
13	19.487	8	3	US-09-315-444-14	Sequence 14, Appl
14	19.487	8	4	US-09-320-548-10	Sequence 10, Appl
15	19.487	8	4	US-09-321-362-2	Sequence 2, Appl
16	19.487	8	4	US-09-321-362-5	Sequence 5, Appl
17	19.487	8	4	US-09-321-362-14	Sequence 14, Appl
18	19.487	8	4	US-09-752-165-4	Sequence 4, Appl
19	19.487	8	4	US-09-752-165-10	Sequence 10, Appl
20	19.487	8	4	US-09-752-165-16	Sequence 16, Appl
21	19.487	8	4	US-09-752-165-88	Sequence 88, Appl
22	18.462	5	1	US-08-704-170-64	Sequence 109, Appl
23	18.462	5	1	PCT-US94-02631-169	Sequence 109, Appl
24	18.462	5	5	PCT-US94-02631-164	Sequence 64, Appl
25	18.462	5	5	PCT-US94-02631-169	Sequence 109, Appl
26	18.462	6	3	US-09-012-669F-44	Sequence 44, Appl
27	18.462	6	4	US-08-057-430A-31	Sequence 31, Appl

Sequence 2, Appl  
Sequence 17, Appl  
Sequence 145, Appl  
Sequence 29, Appl  
Sequence 145, Appl  
Sequence 145, Appl  
Sequence 9, Appl  
Sequence 15, Appl  
Sequence 60, Appl  
Sequence 27, Appl  
Sequence 7, Appl  
Sequence 9, Appl  
Sequence 45, Appl  
Sequence 45, Appl  
Sequence 45, Appl  
Sequence 174, Appl  
Sequence 9, Appl

## ALIGNMENTS

RESULT 1  
US-08-869-506-9  
; Sequence 9, Application US/08869506  
; Patent No. 5827710  
; GENERAL INFORMATION:  
; APPLICANT: Uchida, Kohji  
; APPLICANT: Matsukawa, Hirokazu  
; APPLICANT: Matuo, Yushi  
; APPLICANT: Fujita, Tsuchi  
; TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN  
; TITLE OF INVENTION: LACTATE DEHYDROGENASE  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 No. 5827710th Glebe Rd. 8th floor  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201-4741  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/869,506  
; FILING DATE: 05-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 73797/1996  
; FILING DATE: 29-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crawford, Arthur R.  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 559-43  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4000  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-869-506-9

Query Match 53.8%, Score 21: DB 2: Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

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QY      4 QCEG 7
      1
      3 QCEG 6
DB

RESULT 2
US 09 128-967-9
; Sequence 9, Application US/09128967
; Patent No. 605714;
; GENERAL INFORMATION:
; APPLICANT: Uchida, Kohji
; APPLICANT: Matsukawa, Hirokazu
; APPLICANT: Matuc, Yushi
; APPLICANT: Fujita, Tuvos;
; TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
; TITLE OF INVENTION: LACTATE DEHYDROGENASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 605714th Grebe Rd. 8th floor;
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,967
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/869,506
; FILING DATE: 05-JUN-1997
; APPLICATION NUMBER: JP 73797/1996
; FILING DATE: 29-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 159-43
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US 09 128-967-9

Query Match 53.8%; Score 21; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 QCEG 7
      1
      3 QCEG 6
DB

RESULT 3
US 09-173-941-77
; Sequence 77, Application US/09173941
; Patent No. 6140081
; GENERAL INFORMATION:
; APPLICANT: BARBAS, Carlos F.
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
; FILE REFERENCE: NC000815
; CURRENT APPLICATION NUMBER: US/09/173,941

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; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.1;
; SEQ ID NO 77
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: codon binding sequence
US-09-173-941-77

Query Match 51.3%; Score 20; DB 3; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 QCEG 8
      1
      1 QSGEL 5
DB

RESULT 4
US-09-173-941-78
; Sequence 78, Application US/09173941
; Patent No. 6140081
; GENERAL INFORMATION:
; APPLICANT: BARBAS, Carlos F.
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
; FILE REFERENCE: NC000815
; CURRENT APPLICATION NUMBER: US/09/173,941
; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: codon binding sequence
US-09-173-941-78

Query Match 51.3%; Score 20; DB 3; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 QCEG 8
      1
      1 QSGEL 5
DB

RESULT 5
US-08-253-854-91
; Sequence 91, Application US/08253854
; Patent No. 5504190
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard A.
; APPLICANT: Cuervo, Julio H.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Appel Jr., Jon R.
; APPLICANT: Blondelle, Silvie
; TITLE OF INVENTION: Synthesis Of Equimolar Multiple
; TITLE OF INVENTION: Oligomer Mixtures, Especially Of Oligopeptide Mixtures
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressier, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milwaukee, Ltd.
; STREET: 180 No. 5504190th Stetson Avenue, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60601
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,854
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Garsen, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: PRL-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-253-854-91

Query Match: 48.7%; Score 19; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 STTCGG 6
DB 1 STTGTG 6

RESULT 6
US-09-173-941-76
; Sequence 76, Application US/09173941
; Patent No. 614308;
; GENERAL INFORMATION:
; APPLICANT: BARBAS, Carlos F.
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GGN
; FILE REFERENCE: NC000815
; CURRENT APPLICATION NUMBER: US/09/173,941
; CURRENT FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: codon binding sequence
US 09-173-941-76

Query Match: 48.7%; Score 19; DB 3; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QEGEL 8
DB 1 QPGEL 5

RESULT 7
US-08-259-550A-90
; Sequence 90, Application US/0825955CA
; Patent No. 5776892
; GENERAL INFORMATION:
; APPLICANT: Counts, David F.
; APPLICANT: Duff, Ronald G.
; TITLE OF INVENTION: Anti-Inflammatory Peptides
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,550A
; FILING DATE: 16-JUN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7142-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-259-550A-90

Query Match: 48.7%; Score 19; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTQEGE 7
DB 1 TTREVE 6

RESULT 8
US-09-188-579-2
; Sequence 2, Application US/09188579B
; Patent No. 6107040
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185
; CURRENT APPLICATION NUMBER: US/09/188,579B
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; OTHER INFORMATION: Motif III of RNA guanylyltransferase.
US-09-188-579-2

Query Match: 48.7%; Score 19; DB 3; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.5e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGEL 8
DB 1 TLLDQEL 7

RESULT 9
US-09-188-579-8
; Sequence 8, Application US/09188579B
; Patent No. 6107040
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
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Query Match 48.7% Score 19; DB 3; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
FILE REFERENCE: D6185  
CURRENT APPLICATION NUMBER: US/09/315,444A  
CURRENT FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 114  
SEQ ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Schizosaccharomyces pombe  
FEATURE:  
OTHER INFORMATION: Motif III of RNA guanylyltransferase  
US-09-315-444-8

Query Match 48.7% Score 19; DB 3; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGEL 8  
| | | |  
DB 1 TLDOGEL 7

RESULT 10  
US-09-315-444-8  
Sequence 14, Application US/091885798  
Patent No. 6107040  
GENERAL INFORMATION:  
APPLICANT: Shuran, Stewart  
TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
FILE REFERENCE: D6185  
CURRENT APPLICATION NUMBER: US/09/315,444A  
CURRENT FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 114  
SEQ ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Candida albicans  
FEATURE:  
OTHER INFORMATION: Motif III of RNA guanylyltransferase  
US-09-315-444-8

Query Match 48.7% Score 19; DB 3; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGEL 8  
| | | |  
DB 1 TLDOGEL 7

RESULT 11  
US-09-315-444-2  
Sequence 2, Application US/09315444A  
Patent No. 6232070  
GENERAL INFORMATION:  
APPLICANT: Shuran, Stewart  
TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
FILE REFERENCE: D6185CIP  
CURRENT APPLICATION NUMBER: US/09/315,444A  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: US 09/168,579  
PRIOR FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
FEATURE:  
OTHER INFORMATION: Motif III of RNA guanylyltransferase  
US-09-315-444-2

Query Match 48.7% Score 19; DB 3; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 TTQEGEL 8  
| | | |  
DB 1 TLDOGEL 7  
RESULT 12  
US-09-315-444-6  
Sequence 8, Application US/09315444A  
Patent No. 6232070  
GENERAL INFORMATION:  
APPLICANT: Shuran, Stewart  
TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
FILE REFERENCE: D6185CIP  
CURRENT APPLICATION NUMBER: US/09/315,444A  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: US 09/168,579  
PRIOR FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Schizosaccharomyces pombe  
FEATURE:  
OTHER INFORMATION: Motif III of RNA guanylyltransferase  
US-09-315-444-8

Query Match 48.7% Score 19; DB 3; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGEL 8  
| | | |  
DB 1 TLDOGEL 7

RESULT 13  
US-09-315-444-14  
Sequence 14, Application US/09315444A  
Patent No. 6232070  
GENERAL INFORMATION:  
APPLICANT: Shuran, Stewart  
TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation  
FILE REFERENCE: D6185CIP  
CURRENT APPLICATION NUMBER: US/09/315,444A  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: US 09/168,579  
PRIOR FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 14  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Candida albicans  
FEATURE:  
OTHER INFORMATION: Motif III of RNA guanylyltransferase  
US-09-315-444-14

Query Match 48.7% Score 19; DB 3; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGEL 8  
| | | |  
DB 1 TLDOGEL 7

RESULT 14  
US-09-230-549-10  
Sequence 10, Application US/09230548  
Patent No. 6326466  
GENERAL INFORMATION:  
APPLICANT: Barraco, Donald P

? APPLICANT: Petryshyn, Raymond  
? APPLICANT: The Government of the United States of America  
? APPLICANT: as represented by the Secretary,  
? APPLICANT: Department of Health and Human Services  
? TITLE OF INVENTION: Double-Stranded RNA Dependent Protein Kinase Derived  
? TITLE OF INVENTION: Peptides to Promote Proliferation of Cells and Tissues  
? TITLE OF INVENTION: in a Controlled Manner  
? FILE REFERENCE: 015280-286200US  
? CURRENT APPLICATION NUMBER: US/09/230,548  
? CURRENT FILING DATE: 1999-07-23  
? EARLIER APPLICATION NUMBER: US 60/023,307  
? EARLIER FILING DATE: 1996-07-30  
? EARLIER APPLICATION NUMBER: WO PCT/US97/14350  
? EARLIER FILING DATE: 1997-07-29  
? NUMBER OF SEQ ID NOS: 31  
? SOFTWARE: Patent In. Ver. 2.1  
? SEQ ID NO 10  
? LENGTH: 8  
? TYPE: PRT  
? ORGANISM: Artificial Sequence  
? FEATURE:  
? OTHER INFORMATION: Description of Artificial Sequence: double-stranded  
? OTHER INFORMATION: RNA dependent protein kinase (PKR) peptide  
? OTHER INFORMATION: antagonist  
? US-09-230,548-10

Query Match 48.7% Score 19; DB 4; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STQGE 7  
|||  
Db 2 STQGE 8

RESULT 15  
US-09-721,362-2  
? Sequence 2, Application US/09721362  
? Patent No. 6423163  
? GENERAL INFORMATION:  
? APPLICANT: Shuman, Stewart  
? TITLE OF INVENTION: Pharmacological Targeting of tRNA Cap Formation  
? FILE REFERENCE: 06185CIP/C  
? CURRENT APPLICATION NUMBER: US/09/721,362  
? CURRENT FILING DATE: 2000-11-22  
? PRIOR APPLICATION NUMBER: US 09/315,444  
? PRIOR FILING DATE: 1999-05-20  
? NUMBER OF SEQ ID NOS: 116  
? SEQ ID NO 2  
? LENGTH: 9  
? TYPE: PRT  
? ORGANISM: Saccharomyces cerevisiae  
? FEATURE:  
? OTHER INFORMATION: Motif III of RNA guanylyltransferase  
? US-09-721,362-2

Query Match 48.7% Score 19; DB 4; Length 8;  
Best Local Similarity 57.1% Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTQEGEL 8  
|||  
Db 1 TLLDDEL 7

Search completed: November 5, 2003, 17:23:15  
Job time : 14 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:29:45 / Search time 11 seconds  
(without alignments)  
87,426 Million cell updates/sec

Title: US-09-914-088-3

Perfect score: 57

Sequence: 1 SQKHWLSDRT 10

Scoring table: BLOSUM62  
Gapcp 10.0, Gapext 0.5

Searched: 283:08 seqs, 96:68682 residues

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAR:ES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	40.4	10	2 A49187	gonadotropin-relea
2	20	35.1	10	1 RHPCS	gonadolibetin - p
3	20	35.1	10	1 RHSHG	gonadolibetin - sh
4	20	35.1	10	1 RHAQ	gonadolibetin I -
5	20	35.1	10	1 RHAQ	gonadolibetin II -
6	20	35.1	10	1 A61126	gonadolibetin - sp
7	20	35.1	10	2 B46530	gonadolibetin I -
8	20	35.1	10	2 A46530	gonadolibetin -
9	20	35.1	10	2 A21114	gonadolibetin - ch
10	19	33.3	10	2 PQ0177	neurotrophin C - lac
11	19	33.3	10	2 A60647	neurotrophin C - bov
12	18	31.6	10	2 PT0289	Ig heavy chain CRD
13	17	29.8	6	2 S29881	Na+/K+-exchanging
14	16	28.1	7	2 PT0576	T-cell receptor be
15	16	28.1	8	2 T14306	hypothetical prote
16	16	28.1	9	2 A43848	cell surface adhes
17	16	28.1	9	2 PT0231	Ig heavy chain CDR
18	16	28.1	10	2 T17054	cytochrome-c oxida
19	15	26.3	5	2 PT0672	T-cell receptor be
20	15	26.3	7	2 S3567	tubulin beta-3 cha
21	15	26.3	7	4 A58725	virotaxin - destro
22	15	26.3	9	2 A6C108	exotoxin A - Strept
23	15	26.3	9	2 PT0324	Ig heavy chain CRD
24	15	26.3	9	2 A37027	macrophage chemota
25	15	26.3	9	2 PT0562	T-cell receptor be
26	15	26.3	10	2 L40532	trpE protein - Bac
27	15	26.3	10	2 T17375	cytochrome-c oxida
28	15	26.3	10	2 T17563	cytochrome-c oxida
29	15	26.3	10	2 T12325	cytochrome-c oxida

# ALIGNMENTS

## RESULT 1

A49187  
gonadotropin-releasing hormone III - sea lamprey  
C:Species: Petromyzon marinus (sea lamprey)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 03-Mar-1995  
C:Accession: A49187  
R:Sower, S.A.; Chiang, Y.C.; Lovas, S.; Conlon, J.M.  
Endocrinology 132, 1125-1131, 1993  
A:Title: Primary structure and biological activity of a third gonadotropin-releasing hormone (NCRIP:126381)  
A:Reference number: A49187; MUID:93178316; PMID:8440174  
A:Accession: A49187  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <SOW>  
A:Experimental source: brain  
A:Note: sequence extracted from NCBI backbone (NCRIP:126381)

Query Match 40.4%; Score 23; DB 2; Length 10;  
Best: Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KWLSD 8  
DB 1 FHWSD 6

## RESULT 2

RHPGG  
gonadolibetin - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 18-Mar-1997  
C:Accession: A01411  
R:Baba, Y.; Yatsuo, H.; Schally, A.V.  
Biochem. Biophys. Res. Commun. 44, 459-463, 1971  
A:Title: Structure of the porcine LH- and FSH-releasing hormone. II. Confirmation of th  
A:Reference number: A90172; MUID:72114303; PMID:494667  
A:Accession: A01411  
A:Molecule type: protein  
A:Residues: 1-10 <BAB>  
R:Matsuoka, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V.  
Biochem. Biophys. Res. Commun. 45, 822-827, 1971  
A:Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid-phase meth  
A:Reference number: A90176; MUID:72065376; PMID:4946726  
A:Contents: annotation; synthesis  
A:Note: the synthetic and natural hormones have the same physicochemical and biological  
R:Baba, Y.; Arimura, A.; Schally, A.V.  
Biochem. Biophys. Res. Commun. 45, 483-487, 1971  
A:Title: On the tryptophan residue in porcine LH and FSH-releasing hormone.  
A:Reference number: A90175; MUID:72117544; PMID:4946275  
A:Contents: annotation  
A:Note: Trp-3 appears to be essential for biological activity  
C:Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and f

cytochrome-c oxida  
cytochrome-c oxida  
cytochrome-c oxida  
cytochrome-c oxida  
thyroliberin poten  
T-cell receptor be  
T-cell receptor be  
T-cell receptor be  
xeropsin-related p  
xeropsin-related p  
pyrimidine synthe  
ribosomal protein  
hemoglobin alpha c  
viral protein - huma  
viral protein - Agr  
hypothetical prote

C:Superfamily: gonadoliberin  
C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.1%; Score 20; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
DB 1 QHW 3

RESULT 3  
RHAQ2

gonadoliberin - sheep  
C:Species: Ovis orientalis aries (domestic sheep)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 18-Mar-1997  
C:Accession: A93780; A01411  
R:Burgus, R.; Butcher, M.; Amoss, M.; Ling, N.; Mohan, V.; Rivier, J.; Fellows, R.; Bl  
Proc. Natl. Acad. Sci. U.S.A. 69, 278-282, 1972  
A:Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing facto  
A:Reference number: A93780; MUID:72094314; PMID:4550308  
A:Accession: A93780  
A:Molecule type: protein  
A:Residues: 1-10 <LOV>  
A:Superfamily: gonadoliberin  
A:Note: the natural and synthetic hormones have the same biological activity  
C:Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and fo  
C:Superfamily: gonadoliberin  
C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.1%; Score 20; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
DB 1 QHW 3

RESULT 4  
RHAQ1

gonadoliberin I - American alligator  
N:Alternate names: gonadotropin-releasing hormone I  
C:Species: Alligator mississippiensis (American alligator)  
C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 18-Mar-1997  
C:Accession: A60066  
R:Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanso  
Regul. Pept. 33, 105-116, 1991  
A:Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of  
A:Reference number: A60066; MUID:91352338; PMID:1882082  
A:Accession: A60066  
A:Molecule type: protein  
A:Residues: 1-10 <LOV>  
C:Superfamily: gonadoliberin  
C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.1%; Score 20; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
DB 1 QHW 3

RESULT 5  
RHAQ2

gonadoliberin II - American alligator  
N:Alternate names: gonadotropin-releasing hormone II  
C:Species: Alligator mississippiensis (American alligator)  
C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 18-Mar-1997  
C:Accession: B60066  
R:Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanso  
Regul. Pept. 33, 105-116, 1991  
A:Title: Primary structure of two forms of gonadotropin-releasing hormone from brains o  
A:Reference number: A60066; MUID:91352338; PMID:1882082  
A:Accession: B60066  
A:Molecule type: protein  
A:Residues: 1-10 <LOV>  
C:Superfamily: gonadoliberin  
C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.1%; Score 20; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
DB 1 QHW 3

RESULT 6  
A61126

gonadoliberin - spotted ratfish  
N:Alternate names: gonadotropin-releasing hormone  
C:Species: Hydrologus collieri (spotted ratfish)  
C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 18-Mar-1997  
C:Accession: A61126  
R:Lovejoy, D.A.; Sherwood, N.W.; Fischer, W.H.; Jackson, B.C.; Rivier, J.E.; Lee, T.  
Gen. Comp. Endocrinol. 82, 152-161, 1991  
A:Title: Primary structure of gonadotropin-releasing hormone from the brain of a holoco  
A:Reference number: A61126; MUID:91340667; PMID:1678723  
A:Accession: A61126  
A:Molecule type: protein  
A:Residues: 1-10 <LOV>  
A:Experimental source: brain  
C:Superfamily: gonadoliberin  
C:Keywords: amidated carboxyl end; brain; hormone; pyroglutamic acid  
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.1%; Score 20; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
DB 1 QHW 3

RESULT 7  
B46030

gonadoliberin I - spiny dogfish  
N:Alternate names: gonadotropin-releasing hormone  
C:Species: Squalus acanthias (spiny dogfish)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jan-2003  
C:Accession: B46030  
R:Lovejoy, D.A.; Fischer, W.H.; Ngamvongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter,  
Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992  
A:Title: Distinct sequence of gonadotropin-releasing hormone (GnRH) in dogfish brain pr  
A:Reference number: A46030; MUID:92335300; PMID:1631133  
A:Accession: B46030  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <LOV>  
C:Superfamily: gonadoliberin  
C:Keywords: hormone; pyroglutamic acid  
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match: 35.1%; Score 20; DB 2; Length 10;  
 Best Local Similarity: 66.7%; Pred. No. 1.1e+03;  
 Matches: 2; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 3 KHW 5  
 :  
 Db 1 QHW 3

RESULT 2  
 A46030  
 gonadolibetin I - spiny dogfish  
 N:Alternate names: gonadotropin-releasing hormone  
 C:Species: Squalus acanthias (spiny dogfish);  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Dec 1998  
 C:Accession: A46030  
 R:Lovejoy, D.A.; Fischer, W.H.; Ngamvongtong, S.; Craig, A.G.; Naborniak, C.S.; Peter, R.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992  
 A:Title: Distinct sequence of gonadotropin-releasing hormone (GRH) in dogfish brain pro  
 A:Reference number: A46030; MUID:92335300; PMID:1631133  
 C:Accession: A46030  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <LOW>  
 C:Keywords: hormone; pyroglutamic acid  
 F:1/Modified site: pyroglutamic acid (Gln; #status experimental;

Query Match: 35.1%; Score 20; DB 2; Length 10;  
 Best Local Similarity: 66.7%; Pred. No. 1.1e+03;  
 Matches: 2; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 3 KHW 5  
 :  
 Db 1 QHW 3

RESULT 3  
 A21114  
 gonadolibetin - chum salmon  
 C:Species: Oncorhynchus keta (chum salmon);  
 C:Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 18 Jun 1993  
 C:Accession: A21114  
 R:Sherwood, N.; Eiden, J.; Brownstein, M.; Spiess, J.; Rivier, J.; Vale, W.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983  
 A:Title: Characterization of a teleost gonadotropin-releasing hormone.  
 A:Reference number: A21114; MUID:83195140; PMID:634194  
 C:Accession: A21114  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <SHE>

Query Match: 35.1%; Score 20; DB 2; Length 10;  
 Best Local Similarity: 66.7%; Pred. No. 1.1e+04;  
 Matches: 2; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 3 KHW 5  
 :  
 Db 1 QHW 3

RESULT 10  
 P00177  
 neuromedin C - laughing frog  
 C:Species: Rana ridibunda (laughing frog)  
 C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 11-Jan-2000  
 C:Accession: P00177  
 R:Corlison, C.M.; C.Harte, F.; Vaudry, H.  
 Biochem. Biophys. Res. Commun. 178, 526-530, 1991  
 A:Title: Primary structures of the bombesin-like neuropeptides in frog brain show that b  
 A:Reference number: P00177; MUID:91315477; PMID 1855415  
 C:Accession: P00177  
 A:Molecule type: protein

A:Residues: 1-10 <CON>  
 A:Experimental source: brain  
 C:Superfamily: gastrin-releasing peptide  
 F:1/0/Modified site: amidated carboxyl end (Met) #status predicted

Query Match: 33.3%; Score 19; DB 2; Length 10;  
 Best Local Similarity: 100.0%; Pred. No. 1.7e+03;  
 Matches: 2; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 HW 5  
 :  
 Db 3 HW 4

RESULT 11  
 A60647  
 neuroedin C - bovine  
 C:Species: Bos primigenius taurus (cattle);  
 C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 07-May-1999  
 C:Accession: A60647  
 R:Lemaire, S.; Trifaro, J.M.; Chodunard, L.; Cecyre, D.; Dessureault, J.; Mercier, P.;  
 Peptides 10, 355-360, 1989  
 A:Title: Structural identification, subcellular localization and secretion of bovine ac  
 A:Reference number: A60647; MUID:89331342; PMID:2755876  
 C:Accession: A60647  
 A:Molecule type: protein  
 A:Residues: 1-10 <LEM>  
 A:Note: this neuropeptide was purified from secretory granules of cells in the adrenal  
 C:Superfamily: gastrin releasing peptide  
 C:Keywords: adrenal gland; neuropeptide

Query Match: 33.3%; Score 19; DB 2; Length 10;  
 Best Local Similarity: 100.0%; Pred. No. 1.7e+03;  
 Matches: 2; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 HW 5  
 :  
 Db 3 HW 4

RESULT 12  
 PT0289  
 Ig heavy chain CRD3 region (clone 4-109) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0289  
 R:Yamada, Y.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
 A:Reference number: PT0222; MUID:91102337; PMID:1899102  
 C:Accession: PT0289  
 A:Molecule type: DNA  
 A:Residues: 1-10 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; immunoglobulin

Query Match: 31.6%; Score 18; DB 2; Length 10;  
 Best Local Similarity: 50.0%; Pred. No. 2.6e+03;  
 Matches: 2; Conservative: 2; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 HWLS 7  
 :  
 Db 3 NWS 6

RESULT 13  
 S29881  
 Na+/K+-exchanging ATPase (EC 3.6.3.9; alpha chain - dog (fragment)  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 13-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 19-Apr-2002  
 C:Accession: S29881  
 R:Walterhaug, M.O.; Peet, R.; Saccorani, G.; Leonard, R.T.; Briskin, D.P.

J. Biol. Chem. 265, 3852-3859, 1985  
 A:Title: Structural relatedness of three ion-transport adenine triphosphatases around  
 A:Reference number: S29881; MUID:85131201; PMID:3156136  
 A:Accession: S29881  
 A:Molecule type: Protein  
 A:Residues: 1-6 <WAL>  
 A:Experimental source: kidney  
 C:Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;  
 F:4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 29.8%; Score 17; DB 2; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 SDPT 10  
 |||  
 DB 3 SDKT 6

RESULT 14  
 PT0576  
 T-cell receptor beta chain V-D-J region (141-13): mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 10 May 1997  
 C:Accession: PT0576  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:9227601; PMID:1711559  
 A:Accession: PT0576  
 A:Status: translation not shown  
 A:Molecule type: tRNA  
 A:Residues: 1-7 <FE>  
 A:Experimental source: day 19 fetal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 28.1%; Score 16; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ERT 10  
 |||  
 DB 5 ERT 7

RESULT 15  
 T14936  
 Hypothetical protein - parsley  
 C:Species: Petroselinum crispum (parsley)  
 C:Date: 20-Sep-1999 #sequence\_revision 20 Sep 1999 #text\_change 20 Sep 1999  
 C:Accession: T14906  
 R:Feldbrugge, M.; Sprenger, M.; Dinkelbach, M.; Yazaki, K.; Hartel, K.; Weisshaar, B.  
 Plant Cell 6, 1607-1621, 1994  
 A:Title: Functional analysis of a light-responsive plant r2IP transcriptional regulator.  
 A:Reference number: Z18259; MUID:95128172; PMID:7827494  
 A:Accession: T14906  
 A:Status: preliminary; translated from GB/EXBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <FEL>  
 A:Cross-references: EXBL:S75395; NID:q913201; PDB:194544

Query Match 28.1%; Score 16; DB 2; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHWJS 7  
 |||  
 DB 2 KHTLT 6

Search completed: November 5, 2003, 17:35:21  
 Job time : 12 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:23:40 ; Search time 2:33:33 Seconds  
(without alignments)  
64,127 Million cell updates/sec

Title: US-09-914-088-3  
Perfect score: 57  
Sequence: 1 SQKHWSLDRF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 372

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	23	40.4	10	1	GON3_PETMA	P30948
2	20	35.1	10	1	GON1_ALAMI	P37041
3	20	35.1	10	1	GON1_CHEPR	P36677
4	20	35.1	10	1	GON1_CUEPA	P31749
5	20	35.1	10	1	GON2_CHEPR	P36678
6	20	35.1	10	1	GON2_CHEPR	P37043
7	20	35.1	10	1	GON3_CHEPR	P37367
8	20	35.1	10	1	GON1_CHEPR	P37367
9	20	35.1	10	1	GON1_CHEPR	P37367
10	18	31.6	9	1	DI_NEPNO	P38196
11	17	29.8	10	1	MP2_MICOR	P35339
12	16	28.1	10	1	FAR5_MACRS	P31278
13	15	26.3	8	1	FAR3_ROMAN	P41486
14	14	24.6	9	1	COM_CONVE	P31247
15	13	22.8	5	1	UF01_MOUSE	P36639
16	13	22.8	6	1	E101_LITRU	P32096
17	13	22.8	7	1	FAR2_ASCSU	P31590
18	13	22.8	8	1	CKKN_MACEU	P30369
19	13	22.8	10	1	BPP2_ROTIN	P30422
20	13	22.8	10	1	BPP2_BCTJA	P30422
21	13	22.8	10	1	CAER_LITXA	P36264
22	13	22.8	10	1	URA6_HUMAN	P32083
23	12	21.1	7	1	TPFY_PACTA	P31455
24	12	21.1	8	1	FAR2_MACRS	P31278
25	12	21.1	8	1	HTF1_PERAM	P34548
26	12	21.1	8	1	HTF2_PERAM	P34549
27	12	21.1	8	1	HTF1_FENMO	P32419
28	12	21.1	9	1	LITO_LITAU	P32419
29	12	21.1	9	1	NEUX_HUMAN	P34277
30	12	21.1	10	1	AEGL_AGRAR	P31465
31	12	21.1	10	1	AKHX_LOONI	P31626
32	12	21.1	10	1	ABE_CAGPI	P34474
33	12	21.1	10	1	HTF1_ROMMI	P31110

34	12	21.1	10	1	HTF2_CARMO	P11385
35	12	21.1	10	1	TRU1_UREUN	P40751
36	12	21.1	10	1	TPIS_NICPL	P19118
37	11	19.3	4	1	CCP3_OCTMI	P58649
38	11	19.3	5	1	BPP7_BOTIN	P30425
39	11	19.3	6	1	LOK1_LOONI	P41491
40	11	19.3	7	1	BPP2_CONIM	P58803
41	11	19.3	7	1	FAR1_MACRS	P32774
42	11	19.3	7	1	FAR2_PROCL	P38498
43	11	19.3	7	1	TY5_LITRU	P82065
44	11	19.3	7	1	UF04_MOUSE	P38642
45	11	19.3	7	1	WWA1_ACHFU	P35919

ALIGNMENTS

RESULT 1	
GON3_PETMA	STANDARD; PRT; 10 AA.
ID	GON3_PETMA
DT	01-JUL-1993 (Rel. 26, Created)
DT	01-JUL-1993 (Rel. 26, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III)
DE	(Luliberin III)
OS	Petromyzon marinus (Sea lamprey)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC	Petromyzontiformes; Petromyzontidae; Petromyzon.
OX	NCBI_TaxID=7757;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=Brain;
RX	MEDLINE=93178316; PubMed=8440174;
RA	Sower S.A., Chiang Y.-C., Iovas S., Conlon J.M.;
RT	"Primary structure and biological activity of a third gonadotropin-releasing hormone from lamprey brain";
RL	Endocrinology 132:1125-1131(1993).
CC	!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.
CC	!- SUBCELLULAR LOCATION: Secreted.
CC	!- SIMILARITY: Belongs to the GNRH family.
DR	InterPro: IPR002012; GNRH.
DR	Pfam: PF03446; GNRH; 1.
DR	PROSITE: PS00473; GNRH; 1.
KW	Hormone; Amidation; Hypothalamus; Pyroglutamate carboxylic acid.
FT	MOD_RES 1 10 PYROGLUTAMATE CARBOXYLIC ACID.
FT	MOD_RES 10 10 AMIDATION.
SQ	SEQUENCE 10 AA; 1277 MW; 28435623AAIFSA3 CRC64;
Query Match	40.4%; Score 23; DB 1; Length 10;
Best Local Similarity	50.0%; Pred. No. 1.5e+02;
Matches	3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy	3 KHWLSD 2
Db	1 QHWSHD 6
RESULT 2	
GON1_ALAMI	STANDARD; PRT; 10 AA.
ID	GON1_ALAMI
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-FEB-1991 (Rel. 17, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH I)
DE	(Luliberin I)
OS	Alligator mississippiensis (American alligator).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Crocodylia; Alligatorinae; Alligator.
OX	NCBI_TaxID=8496;

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RN 11
RP SEQUENCE.
RC 11:SSUR=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC 11- FUNCTION: Stimulates the secretion of gonadotropins.
CC 11- SUBCELLULAR LOCATION: Secreted.
CC 11- SIMILARITY: Belongs to the GnRH family.
DR PIR: A6C066; RHAQ1.
DR InterPro: IPR002012; GnRH.
DR Pfam: PF00446; GnRH; 1.
DR PROSITE: PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 35.1%; Score 20; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5
DB 1 QHW 3

RESULT 3
CON: CHEPR
ID _GON1_CHEPR STANDARD; PRT; 10 AA.
AC P80677;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH I)
DE (Luliberin I).
OS Chelyosoma productum.
OC Eukaryota; Metazoa; Chordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Corellidae; Chelyosoma.
OX NCBI_TaxID=71177;
PY SEQUENCE.
RX MEDLINE=96413669; PubMed=8816823;
RA Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;
RT "Two new forms of gonadotropin-releasing hormone in a protochordate
RT and the evolutionary implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).
CC 11- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle stimulating
CC hormones.
CC 11- SUBCELLULAR LOCATION: Secreted.
CC 11- TISSUE SPECIFICITY: GnRH neurons lie within the CNS, close to
CC the gonads and gonads in both juveniles and adults, implying
CC THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.
CC 11- MASS SPECTROMETRY: MW=1246.56; METHOD=MALDI.
CC 11- SIMILARITY: Belongs to the GnRH family.
DR InterPro: IPR002012; GnRH.
DR Pfam: PF00446; GnRH; 1.
DR PROSITE: PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 10 AA; 1264 MW; 284B3639D5B5A3A3 CRC64;

Query Match 35.1%; Score 20; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5

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DB 1 QHW 3

RESULT 4
CON: CLUPA
ID _GON1_CLUPA STANDARD; PRT; 10 AA.
AC P81749;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH)
DE (Luliberin I).
GN GNRH1.
OS Clupea pallasii (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
OC Clupea.
OX NCBI_TaxID=30724;
RN 11
RP SEQUENCE AND FUNCTION.
RC TISSUE=Brain, and Pituitary;
RX MEDLINE=20114351; PubMed=13650929;
RA Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring.";
RL Endocrinology 141:505-512(2000).
CC 11- FUNCTION: Stimulates the secretion of gonadotropins.
CC 11- SUBCELLULAR LOCATION: Secreted.
CC 11- SIMILARITY: Belongs to the GnRH family.
DR InterPro: IPR002012; GnRH.
DR Pfam: PF00446; GnRH; 1.
DR PROSITE: PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1105 MW; 284B20B72871F5A3 CRC64;

Query Match 35.1%; Score 20; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5
DB 1 QHW 3

RESULT 5
CON:2 CHEPR
ID _GON2_CHEPR STANDARD; PRT; 10 AA.
AC P80678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin II (Gonadotropin-releasing hormone II) (GNRH-II)
DE (Luliberin II).
OS Chelyosoma productum.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Corellidae; Chelyosoma.
OX NCBI_TaxID=71177;
PY SEQUENCE.
RX MEDLINE=96413669; PubMed=8816823;
RA Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;
RT "Two new forms of gonadotropin-releasing hormone in a protochordate
RT and the evolutionary implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).
CC 11- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC 11- SUBUNIT: Homodimer; disulfide-linked.

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CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: GnRH neurons lie within blood sinuses close to  
 CC the gonads and gonads in both juveniles and adults, implying  
 CC that the neuropeptide is released into the bloodstream.  
 CC -1- MASS SPECTROMETRY: MW=1117.52; METHCD-VALDI.  
 CC -1- SIMILARITY: Belongs to the GnRH family.  
 DR InterPro: IPR02012; GnRH.  
 DR PROSITE: PS0473; GnRH; 1.  
 KW Hormone; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 6 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT DISULFID 6 6 INTERCHAIN.  
 FT MOD\_RES 10 10 AMIDATION [BY SIMILARITY].  
 SQ SEQUENCE 10 AA; 1135 MW; 2848191EB735A3 CRC64.

Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 5e+02;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
 DB 1 QHW 3

RESULT 6  
 GON3\_CHICK STANDARD; PRT; 10 AA.  
 AC P37043; P20408; P81750;  
 DT 01-FEB-1991 (Rel. 17, Created).  
 DT 01-FEB-1991 (Rel. 17, Last sequence update).  
 DT 28-FEB-2003 (Rel. 41, Last annotation update).  
 DE Gonadoliberin II (Gonadotropin-releasing hormone II) (GnRH-II)  
 DE (LH-RH II) (Luliberin II).  
 CS Gallus gallus (Chicken).  
 CS Alligator mississippiensis (American alligator).  
 OS Squatus acanthias (Spiny dogfish).  
 OS Hydrolagus collieri (Spotted ratfish) (Pacific ratfish), and  
 OS Clupea pallasii (Pacific herring).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 CX NCBI\_TaxID=9031, 8496, 7997, 7673, 30724;  
 RN [1]

SEQUENCE.  
 RC SPECIES=Chicken; TISSUE=Hypothalamus;  
 RX MEDLINE=84222059; PubMed=6427779;  
 RA Miyamoto K., Hasegawa Y., Nomura M., Igarashi M., Kurojima K.,  
 RA Matsuda H.;  
 RT "Identification of the second gonadotropin-releasing hormone in  
 RT chicken hypothalamus: evidence that gonadotropin secretion is  
 RT probably controlled by two distinct gonadotropin-releasing hormones  
 RT in avian species.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:1874-1878(1984).  
 RN [2]

SEQUENCE.  
 RC SPECIES=A.mississippiensis; TISSUE=Brain;  
 RX MEDLINE=91352338; PubMed=1882082;  
 RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,  
 RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;  
 RT "Primary structure of two forms of gonadotropin-releasing hormone  
 RT from brains of the American alligator (Alligator mississippiensis).";  
 RL Regul. Pept. 33:105-116(1991).  
 RN [3]

SEQUENCE.  
 RC SPECIES=S. acanthias; TISSUE=Brain;  
 RX MEDLINE=92335300; PubMed=1631133;  
 RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,  
 RA Nahrniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;  
 RT "Distinct sequence of gonadotropin-releasing hormone (GnRH) in  
 RT dogfish brain provides insight into GnRH evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).  
 RN [4]

SEQUENCE.  
 RC SPECIES=H. collieri; TISSUE=Brain;

RX MEDLINE=91340067; PubMed=1678723;  
 RA Lovejoy D.A., Sherwood N.M., Fischer W.H., Jackson B.C., Rivier J.E.,  
 RA Lee T.;  
 RT "Primary structure of gonadotropin-releasing hormone from the brain  
 RT of a holoccephalan (ratfish: Hydrolagus collieri).";  
 RL Gen. Comp. Endocrinol. 82:152-161(1991).  
 RN [5]

SEQUENCE, AND FUNCTION.  
 RP SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;  
 RX MEDLINE=20114351; PubMed=10650929;  
 RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,  
 RA Chang J.P., Rivier J.E., Sherwood N.M.;  
 RT "Primary structure and function of three gonadotropin-releasing  
 RT hormones, including a novel form, from an ancient teleost, herring.";  
 RL Endocrinology 141:505-512(2000).  
 CC -1- FUNCTION: Stimulates the secretion of gonadotropins.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the GnRH family.  
 DR PIR; A61126; A61126.  
 DR PIR; B46030; B46030.  
 DR PIR; B60366; RHAQ2.  
 DR InterPro: IPR02012; GnRH.  
 DR PROSITE: PS0473; GnRH; 1.  
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1254 MW; 284B2E437871F5A3 CRC64;

Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 5e+02;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
 DB 1 QHW 3

RESULT 7  
 GON3\_ONCKE STANDARD; PRT; 10 AA.  
 AC P20367; P81751;  
 DT 01-FEB-1991 (Rel. 17, Created).  
 DT 01-FEB-1991 (Rel. 17, Last sequence update).  
 DT 28-FEB-2003 (Rel. 41, Last annotation update).  
 DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GnRH-III) (LH-  
 DE RH III) (Luliberin III).  
 DE GnRH3.  
 CS Oncorhynchus keta (Chum salmon), and  
 OS Clupea pallasii (Pacific herring).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 CX NCBI\_TaxID=8018, 30724;  
 RN [1]

SEQUENCE.  
 RC SPECIES=O.keta;  
 RX MEDLINE=83195140; PubMed=6341999;  
 RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;  
 RT "Characterization of a teleost gonadotropin-releasing hormone.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).  
 RN [2]

SEQUENCE, AND FUNCTION.  
 RP SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;  
 RX MEDLINE=20114351; PubMed=10650929;  
 RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,  
 RA Chang J.P., Rivier J.E., Sherwood N.M.;  
 RT "Primary structure and function of three gonadotropin-releasing  
 RT hormones, including a novel form, from an ancient teleost, herring.";  
 RL Endocrinology 141:505-512(2000).  
 CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates  
 CC the secretion of both luteinizing and follicle-stimulating  
 CC hormones.

CC 1- SUBCELLULAR LOCATION: Secreted.  
 CC 1- SIMILARITY: Belongs to the GNRH family.  
 DR PIR: A21114; A21114.  
 DR InterPro: IPR002012; GNRH.  
 DR Pfam: PF00446; GNRH; 1.  
 DR PROSITE: PS00473; GNRH; 1.  
 KW Hormone; Amidation; Hypothalamus; Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1230 MW; 28483233786545A3 CR64;

Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 5e+02;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 KHW 5  
 DB : QHW 3

## RESULT 8

GNL SQAC STANDARD; PRT; 10 AA.  
 AC GNL SQAC  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadoliberin (Gonadotropin-releasing hormone) (GNRH) (LH-RH)  
 DE (Laliberin).  
 CS Squalea acanthias (Spiny dogfish).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 CC Elasmobranchii; Squalea; Squaleidae; Squalidae; Squales.  
 CX NCBI\_TaxID=7797;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Brain;  
 RX MEDLINE=92335300; PubMed=1611133;  
 RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,  
 RA Nakavej J.D., Peter R.E., Rivier J.E., Sherwood N.M.;  
 RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in  
 RT dogfish brain provides insight into GNRH evolution";  
 RT Proc. Natl. Acad. Sci. U.S.A. 89(16):6171-6174 1992;  
 CC 1- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPIN PINS  
 CC 1- SUBCELLULAR LOCATION: Secreted.  
 CC 1- SIMILARITY: Belongs to the GNRH family.  
 DR PIR: A46037; A46130;  
 DR InterPro: IPR002012; GNRH.  
 DR Pfam: PF00446; GNRH; 1.  
 DR PROSITE: PS00473; GNRH; 1.  
 KW Hormone; Amidation; Hypothalamus; Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1204 MW; 28483233786545A3 CR64;

Query Match 35.1%; Score 20; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 5e+02;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 KHW 5  
 DB : QHW 3

## RESULT 9

GRP RANRI STANDARD; PRT; 10 AA.  
 ID GRP RANRI  
 AC P23260;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neomedin C.  
 CC Neomedin C.  
 CC Rana ridibunda (Laughing frog) (Marsh frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Extraneostomi;

CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 CX NCBI\_TaxID=8406;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=91315477; PubMed=159413;  
 RA Conlon J.M., O'Harte F., Vaudry H.;  
 RT "Primary structures of the bombesin-like neuropeptides in frog brain  
 RT show that bombesin is not the amphibian gastrin-releasing peptide";  
 RL Biochem. Biophys. Res. Commun. 178:526-530(1991).  
 CC 1- SUBCELLULAR LOCATION: Secreted.  
 CC 1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 DR PIR: PQ0177; PQ0177.  
 DR InterPro: IPR000874; Bombesin.  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 KW Bombesin family; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1094 MW; F81FBAE862C371 CR64;

Query Match 33.3%; Score 19; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KHW 5  
 DB 3 KHW 4

## RESULT 10

D1 NEPNO STANDARD; PRT; 9 AA.  
 ID D1 NEPNO  
 AC P24816;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 DE Gastrin/cholecystokinin-like peptide D1.  
 OS Nephrops norvegicus (Norway lobster).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 CC Nephropoidea; Nephropidae; Nephrops.  
 CX NCBI\_TaxID=6829;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Stomach;  
 RX MEDLINE=92082847; PubMed=1747388;  
 RA Favrel P., Kegel G., Sedlmeyer D., Keller R., van Wormhoudt A.;  
 RT "Structure and biological activity of crustacean gastrointestinal  
 RT peptides identified with antibodies to gastrin/cholecystokinin";  
 RL Biochimie 73:1233-1239(1991).  
 CC 1- FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.  
 CC 1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
 DR PIR: S47432; S47432.  
 KW Hormone.  
 SQ SEQUENCE 9 AA; 1038 MW; 60EC79CAB6D8787B CR64;

Query Match 31.6%; Score 18; DB 1; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QGFWL 6  
 DB 5 QDFWL 9

## RESULT 11

MP2 MICOC STANDARD; PRT; 10 AA.  
 ID MP2 MICOC  
 AC P81533;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE M22 protein (fragment).  
 OS Microplitis ocellatae (Braconid wasp).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;  
 OC Braconidae; Microgastrinae; Microplitis.  
 OX NCBI\_TaxID=99573;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RA Takahashi M., Quicke D.L.J.,  
 RL Submitted (CCT-1998) to the SWISS-PROT data bank.  
 CC -!- TISSUE SPECIFICITY: SALIVARY GLANDS.  
 CC -!- DEVELOPMENTAL STAGE: LARVAL.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1255 MW; FE4FD33366C41AFA CRC64;  
 Query Match 29.8%; Score 17; DB 1; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 KHW 6  
 DB 5 RQW 8  
 RESULT 12  
 FARS\_MACRS STANDARD; PRT; 10 AA.  
 AC P83278;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 CE FVRamide-like neuropeptide FLPS (DTPALRSP-amide)  
 OS Macrobrachium rosenbergii (Giant freshwater prawn)  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 CC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 KC TISSUE=Eyestalk;  
 RA Sithigorngul P., Sarathongkum W., Jandeechobey S., Ichanyart S.,  
 RT Sithigorngul W.;  
 RT "Novel FVRamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii";  
 RL Comp. Biochem. Physiol. 120B:587-595 (1992).  
 CC -!- MASS SPECTROMETRY: MW=1243.4; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FVRamide-related peptide)  
 CC FAMILY.  
 DR GO:0007218; P:neuropeptide signaling pathway; FARP.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1244 MW; 9A1A5334072DC711 CRC64;  
 Query Match 28.1%; Score 16; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 DRT 10  
 DB 1 DRT 3  
 RESULT 13  
 FARS\_HOMAM STANDARD; PRT; 8 AA.  
 AC P41486;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 CE FVRamide-like neuropeptide 3 (F1: 3) (F2: 1).  
 OS Homarus americanus (American lobster).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Nephropoidea; Nephropidae; Homarus.  
 OX NCBI\_TaxID=6706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RA MEDLINE=86116164; PubMed=3429714;  
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;  
 RT Purification and characterization of FVRamide-like immunoreactive  
 RT substances from the lobster nervous system: isolation and sequence  
 RT analysis of two closely related peptides.";  
 RL J. Comp. Neurol. 268:16-26 (1987).  
 CC -!- MISCELLANEOUS: PERICARDIAL ORGANS RELEASE THIS PEPTIDE WITH 100 NM  
 CC -!- POTASSIUM IN THE PRESENCE OF CALCIUM.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FVRamide-related peptide)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8  
 SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;  
 Query Match 26.3%; Score 15; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 SCR 9  
 DB 1 SDR 3  
 RESULT 14  
 COW\_CONVE STANDARD; PRT; 9 AA.  
 AC P83347;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Contryphan-Vn.  
 OS Conus ventricosus (Mediterranean cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apeogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=17992;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=21547785; PubMed=11688995;  
 RA Massilia G.R., Schinina V.E., Ascenzi P., Politicelli F.;  
 RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean  
 RT snail Conus ventricosus";  
 RL Biochem. Biophys. Res. Commun. 285:908-913 (2001).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=1088.6; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.  
 KW Toxin; Amidation; D-amino acid.  
 FT DISULFID 3 9  
 FT MOD\_RES 5 5  
 FT MOD\_RES 9 9  
 SQ SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;  
 Query Match 24.6%; Score 14; DB 1; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 KHW 5  
 DB 6 KPW 8  
 RESULT 15  
 UF01\_MOUSE STANDARD; PRT; 5 AA.  
 ID UF01\_MOUSE  
 AC P38639;

DT 31-OCT-1994 (Rel: 30, Created:  
 DT 31-OCT-1994 (Rel: 30, Last sequence update)  
 DT 31-FEB-1995 (Rel: 31, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment)  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=95009907; PubMed=7521108;  
 RA Merrick B.A., Patterson R.M., Richter L.D., Ho C., Solovick J.K.  
 RT "Separation and sequencing of familial and novel murine proteins  
 RT using preparative two-dimensional gel electrophoresis."  
 RL Electrophoresis 15:735-745(1994)  
 CC 1: MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED P1 OF THIS UNKNOWN  
 CC PROTEIN IS: 6.6, ITS MW IS: 19 kDa.  
 FT NON TER 5  
 SQ SEQUENCE 5 AA; 717 MW; 736408704110000 CRC64;

Query Match 22.81; Score 13; DB 1; Length 5;  
 Best Local Similarity 50.0%; Pred No. 1,36-05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 WL 6  
 DE : WI 2

Search completed: November 5, 2003, 17:33:04  
 Job time : 8.3333 secs

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: November 5, 2003, 17:29:05 ; Search time 26 seconds  
(without alignments)  
99.251 Million cell updates/sec

Title: US-09-914-088-3

Perfect score: 57 SQHMLSRT 10  
Sequence: 1 SQHMLSRT 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052654 residues

Total number of hits satisfying chosen parameters: 1349

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREXBL23:

- 1: sp\_archea:
- 2: sp\_bacteria:
- 3: sp\_fungi:
- 4: sp\_human:
- 5: sp\_invertebrate:
- 6: sp\_mammal:
- 7: sp\_mhc:
- 8: sp\_organelle:
- 9: sp\_phage:
- 10: sp\_plant:
- 11: sp\_rodent:
- 12: sp\_virus:
- 13: sp\_vertebrate:
- 14: sp\_unclassified:
- 15: sp\_virus:
- 16: sp\_bacterioph:
- 17: sp\_archea:

Pred. No. is the number of results predicted by CHADO to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	21	36.8	9	Q8W8X4	Q8W8X4 diadema mex
2	20	35.1	8	Q8W8X7	Q8W8X7 lomix hirta
3	20	35.1	9	Q8W8X6	Q8W8X6 procambartus
4	20	35.1	10	Q9F9H5	Q9F9H5 helicobacte
5	19	33.3	8	Q82831	Q82831 oryctolagus
6	19	33.3	9	Q94V10	Q94V10 varanus gig
7	19	33.3	10	Q94V35	Q94V35 varanus gri
8	19	33.3	10	Q8SHN1	Q8SHN1 bradypodion
9	19	33.3	10	Q958J8	Q958J8 rana muscos
10	19	33.3	10	Q78580	Q78580 rana musculu
11	18	31.6	9	Q937J8	Q937J8 escherichia
12	18	31.6	9	Q937H9	Q937H9 enterobacte
13	18	31.6	10	Q937J5	Q937J5 acinetobact
14	18	31.6	10	Q79915	Q79915 leiopis b
15	18	31.6	10	Q8SHC2	Q8SHC2 charaeleop l
16	18	31.6	10	Q9G694	Q9G694 leiopis g

17	29.9	8	11	Q99MN0	Q99MN0 mus musculu
18	29.9	9	4	Q9H326	Q9H326 homo sapien
19	29.8	9	12	P90359	P90359 barley mild
20	29.8	10	2	Q47561	Q47561 escherichia
21	29.8	10	8	Q9XMB4	Q9XMB4 aegilops ta
22	29.8	10	8	Q94VD5	Q94VD5 varanus oli
23	29.8	10	8	Q9G362	Q9G362 acanthosaur
24	28.1	9	4	Q15890	Q15890 homo sapien
25	28.1	8	6	Q95M23	Q95M23 sus scrofa
26	28.1	9	2	Q9R5M1	Q9R5M1 staphylococ
27	28.1	10	3	Q8TG88	Q8TG88 pleurotus o
28	28.1	10	6	Q3TU33	Q3TU33 canis famil
29	28.1	10	8	Q9T8P3	Q9T8P3 liolaemus a
30	28.1	10	8	Q9T8L9	Q9T8L9 liolaemus f
31	28.1	10	8	Q9T8W5	Q9T8W5 liolaemus r
32	28.1	10	8	Q8W916	Q8W916 liolaemus m
33	28.1	10	8	Q9T8N7	Q9T8N7 liolaemus o
34	28.1	10	8	Q79888	Q79888 basiliscus
35	28.1	10	8	Q9T8P0	Q9T8P0 liolaemus f
36	28.1	10	13	Q42355	Q42355 brachydanio
37	28.1	10	13	Q90Y93	Q90Y93 gallus gall
38	26.3	7	11	Q8K3H6	Q8K3H6 rattus norv
39	26.3	8	9	Q94V88	Q94V88 varanus tri
40	26.3	8	9	Q94VJ4	Q94VJ4 varanus ben
41	26.3	8	8	Q94V91	Q94V91 varanus tim
42	26.3	8	8	Q94V54	Q94V54 varanus mel
43	26.3	8	8	Q94VF9	Q94VF9 varanus ind
44	26.3	8	11	Q62721	Q62721 rattus norv
45	26.3	8	12	Q64971	Q64971 alfalfa mos

## ALIGNMENTS

## RESULT 1

Q8W8X4	PRELIMINARY;	PRT;	9 AA.
AC	Q8W8X4		
DT	01-MAR-2002 (TREMBLrel. 20, Created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	Cytochrome oxidase subunit II (Fragment).		
GN	COI1		
OS	Diadema mexicanum.		
OG	Mitochondrion.		
OC	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;		
OC	Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;		
OC	Diadema.		
OX	NCBI_TaxID=105353;		
RN	!!_TaxID=105353;		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CC70, and CC117;		
RX	MEDLINE=2123357; PubMed=11430656;		
RA	Lessios H.A., Kessing B.D., Pearse J.S.;		
RT	"Population structure and speciation in tropical seas: global		
RT	phylogeography of the sea urchin Diadema.";		
RL	Evolution 55:955-975(2001).		
RN	!!_TaxID=105353;		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CC70, and CC117;		
RX	MEDLINE=21561594; PubMed=11703875;		
RA	Lessios H.A., Garrido M.J., Kessing B.D.;		
RT	"Demographic history of Diadema antillarum, a keystone herbivore on		
RL	Caribbean reefs.";		
RL	Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).		
DR	EMBL; AY012921; AAL33843.1; ..		
DR	EMBL; AY012921; AAL33844.1; ..		
KW	Mitochondrion.		
FT	NCN TER 1		
SQ	SEQUENCE 9 AA; 1174 MW; 2873173846DDC2D3 CRC64;		
Query Match	36.8%;	Score 21;	DB 8; Length 9;
Best Local Similarity	50.0%;	Pred. No. 8.3e+05;	

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HWLS 7  
DB 2 HWVA 4

## RESULT 2

Q8WGD7 PRELIMINARY; PRT; 8 AA.  
AC Q8WGD7; 01-MAR-2002 (TrEMBLrel. 20, Created;  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update;  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update;  
DE Cytochrome oxidase subunit 1 (Fragment).  
OS Lewis birta.  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Lomidae;  
OC Lomidae; Lomis.  
OX NCBI\_TaxID=177234;  
RN 1;  
RP SEQUENCE FROM N.A.  
RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,  
RA Cunningham C.W.;  
RT "Mitochondrial gene rearrangements support a hypothesis of parallel  
RL evolution to the crab-like form."  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF436035; AAL31611.1;  
KW Mitochondrion.  
FT NON-TER 1  
FT NON-TER 8  
SQ SEQUENCE 8 AA; 1038 MW; C5B5B9C733640321 CRC64;

Query Match 35.1%; Score 20; DB 8; Length 9;  
Best Local Similarity 75.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHWL 6  
DB 2 KRWL 5

## RESULT 3

Q8WGE6 PRELIMINARY; PRT; 6 AA.  
AC Q8WGE6; 01-MAR-2002 (TrEMBLrel. 20, Created;  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update;  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update;  
DE Cytochrome oxidase subunit 1 (Fragment).  
OS Procambarus clarkii (Red swamp crayfish).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;  
OC Astacoidea; Cambaridae; Procambarus.  
OX NCBI\_TaxID=6728;  
RN 1;  
RP SEQUENCE FROM N.A.  
RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,  
RA Cunningham C.W.;  
RT "Mitochondrial gene rearrangements support a hypothesis of parallel  
RL evolution to the crab-like form."  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF436024; AAL31599.1;  
KW Mitochondrion.  
FT NON-TER 1  
FT NON-TER 9  
SQ SEQUENCE 9 AA; 1185 MW; 936B59C733640321 CRC64;

Query Match 35.1%; Score 20; DB 8; Length 9;  
Best Local Similarity 75.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHWL 6  
DB 3 KRWL 6

## RESULT 4

Q9F9H5 PRELIMINARY; PRT; 10 AA.  
AC Q9F9H5; 01-MAR-2001 (TrEMBLrel. 16, Created;  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update;  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update;  
DE Glutamate racemase (fragment).  
OS GLR.  
OC Helicobacter pylori (Campylobacter pylori).  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=210;  
RN 1;  
RP SEQUENCE FROM N.A.  
RC STRAIN=India75A;  
RX MEDLINE=20270152; PubMed=10809702;  
RA Kersulyte D., Mukhopadhyay A.K., Velapattino B., Su W.W., Pan Z.J.,  
RA Garcia C., Hernandez V., Valdez Y., Mistry R.S., Gilman R.H., Yuan Y.,  
RA Gao H., Alarcon T., Lopez-Brea M., Balakrishna R., Chowdhury A.,  
RA Datta S., Shirai M., Nakazawa T., Ally R., Segal I., Wong B.C.,  
RA Lam S.K., Olfat F.O., Boren T., Engstrand L., Torres O., Schneider R.,  
RA Thomas J.E., Czinn S., Berg D.E.;  
RT "Differences in genotypes of Helicobacter pylori from different human  
RT populations."  
RL J. Bacteriol. 182:3210-3218(2000).  
DR EMBL: AF190663; AAG18486.1;  
FT NON-TER 1  
SQ SEQUENCE 10 AA; 1273 MW; CAD126337B133DC6 CRC64;

Query Match 35.1%; Score 20; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHWL 6  
DB 5 KRWL 8

## RESULT 5

G02831 PRELIMINARY; PRT; 8 AA.  
AC G02831; 01-JUL-1997 (TrEMBLrel. 04, Created;  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Pro alpha 1 type III collagen protein (fragment).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN 1;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96377339; PubMed=8783186;  
RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,  
RA Vuorio E.;  
RT "Evidence for insufficient chondrocytic differentiation during repair  
RT of full-thickness defects of articular cartilage."  
RL Matrix Biol. 15:39-47(1996).  
DR EMBL: S83371; AAC14433.1;  
KW Collagen.  
FT NON-TER 1  
SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 33.3%; Score 19; DB 6; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 HW 5
Db 1 HW 2

RESULT 6
Q94VIC PRELIMINARY; PRT; 9 AA.
AC Q94VIC;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment)
GN COI;
OS Varanus giganteus.
CG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
CX NCBI_TaxID=62041;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001);
DR EMBL; AF407498; AAL10048.1; -.
KW Mitochondrion.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1138 MW; 9C4CB7336411A9C1 CRC64;

Query Match 33.3%; Score 19; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WLS 7
Db 6 WLS 8

RESULT 7
Q94VG5 PRELIMINARY; PRT; 10 AA.
AC Q94VG5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment)
GN COI;
OS Varanus griseus griseus.
CG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
CX NCBI_TaxID=169828;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001);
DR EMBL; AF407503; AAL10063.1; -.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1219 MW; C97CCB7336411R2 CRC64;

Query Match 33.3%; Score 19; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WLS 7
Db 6 WLS 8

RESULT 8

```

```

Q8SHN1 PRELIMINARY; PRT; 10 AA.
AC Q8SHN1;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment)
GN COI;
OS Brachypodium taitanum.
CG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
OC Brachypodium.
CX NCBI_TaxID=179888;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF448733; AAL90472.1; -.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1327 MW; 5E2180C733641597 CRC64;

Query Match 33.3%; Score 19; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WLS 7
Db 2 WLS 4

RESULT 9
Q958J9 PRELIMINARY; PRT; 10 AA.
AC Q958J9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment)
GN COI;
OS Rana muscosa.
CG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
CX NCBI_TaxID=162500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184280; PubMed=1285498;
RA Macey S.R., Strassburg J.L., Brissan J.A., Vredenburg V.T.,
RA Jennings M., Larson A.;
RT "Molecular Phylogenetics of Western North American Frogs of the Rana
Mol. Phylogenetic Evol. 13:131-143(2001);
DR EMBL; AF34026; AAK56898.1; -.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1335 MW; COD380C9D371F1A9 CRC64;

Query Match 33.3%; Score 19; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HW 5
Db 5 HW 6

RESULT 10
Q7056C PRELIMINARY; PRT; 10 AA.
ID Q7056C

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AC 076580;
DT 01-AUG-1998 (TrEMBLrel. 07, Created);
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 20, Last annotation update);
DE Carbonic anhydrase III (Fragment);
GN CAR3 OR CAR3 OR CA3;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Surognathi; Muridae; Murinae; Mus;
OX NCBI_TaxID=10290;
RN 1;
RP SEQUENCE FROM N.A.
RA Sowden J.J., Smith H., Morrison K., Edwards Y.;
RT "Sequence comparisons and functional studies of the proximal promoter
of the carbonic anhydrase 3 (CA3) gene.";
RL Gene 314,157-165(1999);
DR EMBL; AJ006474; CAA07057.1; -;
DR MBL; MG1:88270; Car3;
DR MGD; MG1:135:477; Car3;
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1105 MW; 56F7FE71AD037B13 CRC64;

Query Match 33.3%; Score 19; DB 11; Length 10;
Best Local Similarity 37.5%; Pred. No. 8.3e+05;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KHWLSDRT 10
DB 3 KHWLSDRT 10

RESULT 11
Q937J8 PRELIMINARY; PRT; 3 AA.
AC Q937J8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created);
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update);
DE Putative transposition protein TniQ (Fragment);
GN TniQ;
OS Escherichia coli;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia;
OX NCBI_TaxID=562;
RN 1;
RP SEQUENCE FROM N.A.
RA STRAIN-CH210; TRANSPOSON-Tn5057;
RX MEDLINE=21604134; PubMed=11763242;
RA Mindlin S.Z., Khelodii G.Y., Gorkenko Z.M., Minakhina S.V.,
RA Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
RA Yurieva O.V., Nikiforov V.G.;
RT "Mercury resistance transposons of Gram-negative environmental
bacteria and their classification.";
RL Res. Microbiol. 152:811-822(2001);
DR EMBL; AJ302785; CAC82977.1; -;
FT NON TER 1 1
SQ SEQUENCE 9 AA; 1023 MW; 1B963AB5B7287AA4 CRC64;

Query Match 31.6%; Score 18; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QKHWLSDR 9
DB 1 QNDGLSDK 8

RESULT 12
Q937H9 PRELIMINARY; PRT; 9 AA.
AC Q937H9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created);
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update);
GN Cytochrome c oxidase subunit I (fragment);
OS Leptoleptis belliana;
```

```
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update);
DE Putative TniQ protein (Fragment);
GN TniQ;
OS Enterobacter sp. CH2-4;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter;
OX NCBI_TaxID=143777;
RN 1;
RP SEQUENCE FROM N.A.
RA STRAIN-CH2-4; TRANSPOSON-Tn5057v1;
RX MEDLINE=21604134; PubMed=11763242;
RA Minakhin L.S., Khelodii G.Y., Gorkenko Z.M., Minakhina S.V.,
RA Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
RA Yurieva O.V., Nikiforov V.G.;
RT "Mercury resistance transposons of Gram-negative environmental
bacteria and their classification.";
RL Res. Microbiol. 152:811-822(2001);
DR EMBL; AJ291727; CAC83017.1; -;
FT NON TER 1 1
SQ SEQUENCE 9 AA; 1023 MW; 1B963AB5B7287AA4 CRC64;

Query Match 31.6%; Score 18; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QKHWLSDR 9
DB 1 QNDGLSDK 8

RESULT 13
Q93735 PRELIMINARY; PRT; 10 AA.
AC Q93735;
DT 01-DEC-2001 (TrEMBLrel. 19, Created);
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update);
DE Quaternary ammonium compound-resistance protein (Fragment);
GN QACDELTA;
OS Acinetobacter genomosp. 3;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter;
OX NCBI_TaxID=48296;
RN 1;
RP SEQUENCE FROM N.A.
RA STRAIN-YMCU160; TRANSPOSON-class I integron;
RA Yum J.H., Yong E., Lee K., Chong Y., Livermore D.M.;
RT "A 2.2 kb beta-lactamase gene containing integron in an
Acinetobacter (possible genomosp. 3) clinical isolate.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF169871; AAK54205.1; -;
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1178 MW; 2E287BC729C73378 CRC64;

Query Match 31.6%; Score 18; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHWL 6
DB 2 KQWL 5

RESULT 14
Q79915 PRELIMINARY; PRT; 10 AA.
AC Q79915;
DT 01-NOV-1998 (TrEMBLrel. 08, Created);
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update);
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update);
DE Cytochrome c oxidase subunit I (fragment);
GN COI;
OS Leptoleptis belliana;
```



OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Leiolepidinae;  
OC Leiolepis.  
OX NCBI\_TaxID=52196;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97115309; PubMed=9169559;  
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.,  
RT "Evolutionary shifts in three major structural features of the  
RL mitochondria: genome among iguanian lizards."  
J. Mol. Evol. 44:650-674(1997).  
DR EMBL: U82689; AAC62287.1;  
KW Mitochondrion.  
FT NON\_TER 10  
SQ SEQUENCE 10 AA: 1297 MW: 1A3580C733641400 CRGG4;

Query Match 31.6% Score 18; DP 8; Length 10;  
Best Local Similarity 50.0%; Pred. No. 7.6e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SQHWT 6  
Ob 2 SRRWL 7

## RESULT 15

Q8SHG2 PRELIMINARY; PRT; 10 AA.  
AC Q8SHG2;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
ST 01-JUN-2002 (TrEMBLrel. 21, Last sequence update);  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update);  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Chamaeleo jacksonii.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.  
OX NCBI\_TaxID=116114;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Townsend T.M., Larson A.L.;  
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the  
PT Chamaeleonidae (Reptilia, Squamata)."  
RL Submitted (NCV-2001) to the EMBL/GenBank/CCDB databases  
DR EMBL: AF448753; AAL90541.1;  
KW Mitochondrion.  
FT NON\_TER 10  
SQ SEQUENCE 10 AA: 1368 MW: 072180C716471361 SSG4;

Query Match 31.6% Score 18; DP 8; Length 10;  
Best Local Similarity 60.0%; Pred. No. 7.6e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 QXHWL 6  
Ob 3 QLAWL 7

Search completed: November 5, 2003, 17:34:14  
Job time : 28 secs

GenCore version 5.1.6  
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OM protein protein search, using sw model

Run on: November 5, 2003, 17:23:00 / Search time 33.3333 Seconds  
(without alignments)  
47.618 Million cell updates/sec

Title: US-09-914-088-3

Perfect score: 57

Sequence: 1 SQKHWLSDRF:10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 251420

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A\_Geneseq\_19Jun03.\*

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- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARY:ES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	10	21	AAB20869 Immunoglobulin E e
2	57	100.0	10	21	AAB25909 Ige C-epsilon-2 do
3	57	100.0	10	22	AAU16634 Peptide P3 derived
4	57	100.0	10	22	AAB51025 Ige peptide #1. M
5	57	100.0	10	23	ABJ00219 Human Ige immunoge
6	48	84.2	8	20	AA42628 Human Ige peptide
7	48	84.2	8	21	AA455217 Human Ige mutant #
8	48	84.2	8	21	AA455250 Human Ige mutant #
9	37	64.9	9	24	AAE35074 Human immunoglobul

10	37	64.9	9	24	ABP96578 Human immunoglobul
11	35	61.4	8	14	AAE33325 Ige Kabat residue
12	35	61.4	9	24	AAE35054 Immunoglobulin E (
13	35	61.4	9	24	AAE35063 Human immunoglobul
14	35	61.4	9	24	ABP96567 Human immunoglobul
15	30	52.6	9	24	ABR18853 Human cancer-relat
16	30	52.6	9	24	ABR19200 Human cancer-relat
17	30	52.6	9	24	ABR19431 Human cancer-relat
18	30	52.6	10	24	ABR18895 Human cancer-relat
19	30	52.6	10	24	ABR18960 Human cancer-relat
20	30	52.6	10	24	ABR19294 Human cancer-relat
21	30	52.6	10	24	ABR19341 Human cancer-relat
22	30	52.6	10	24	ABR19520 Human cancer-relat
23	30	52.6	10	24	ABR19521 Human cancer-relat
24	30	52.6	10	24	ABR19533 Human cancer-relat
25	30	52.6	10	24	ABR19705 Human cancer-relat
26	30	52.6	10	24	ABR19752 Human cancer-relat
27	30	52.6	10	24	ABR19764 Human cancer-relat
28	28	49.1	7	23	AAU81676 Enterokinase recog
29	27	47.4	9	20	AA48076 Immunogenic peptid
30	27	47.4	9	23	AAE31171 Human epi100 peptid
31	27	47.4	9	23	AAE16429 Mouse antibody 2A4
32	27	47.4	9	24	ABP60558 Murine antibody 14
33	27	47.4	9	24	ABP74204 Human GP100 epitop
34	27	47.4	9	24	ABP74209 Melanoma-specific
35	27	47.4	10	16	AA82181 Immunogenic peptid
36	27	47.4	10	20	AA47116 Growth factor pept
37	27	47.4	10	22	AAB92045 HIV A02 super moti
38	27	47.4	10	24	ABP74205 HIV A24 super moti
39	27	47.4	10	24	ABP74210 HIV A24 super moti
40	26	45.6	5	15	AAE66135 Peptide derived fr
41	26	45.6	7	21	AA484981 Amino acid sequenc
42	26	45.6	9	22	ABP12734 HIV A02 super moti
43	26	45.6	9	22	ABP15684 HIV A24 super moti
44	26	45.6	9	22	ABP15725 HIV A24 super moti
45	26	45.6	9	22	ABP17169 HIV R27 super moti

## ALIGNMENTS

RESULT 1  
AAB20869  
ID AAB20869 standard; peptide; 10 AA.  
XX AAB20869;  
XX  
XX 01-JAN-2001 (first entry;  
XX Immunoglobulin E epitope immunogenic peptide SEQ ID NO:7.  
DE Immunoglobulin E; Ige; immunogenic; immunogen; Protein D; carrier;  
KW prostate cancer; Haemophilus influenzae; vaccine; infectious disease;  
KW malaria; cytostatic; antiallergic; nontropic; neuroprotective;  
KW protozoacide; Alzheimer's disease; allergy.  
XX Homo sapiens.  
OS  
XX WO2000050077-A1.  
PN  
XX 31-AUG-2000.  
XX  
XX 22-FEB-2000; 2000WC-EP01457.  
XX  
XX 25-FEB-1999; 99GB-0004405.  
PR 25-FEB-1999; 99GB-0004408.  
PR 25-FEB-1999; 99GB-0004412.  
PR 13-AUG-1999; 99GB-0019260.  
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
PA Coste M, Lobet Y, Van-Mechelen MP, Verriest C;  
XX

DR WPI; 2000-572040/53.

XX Immunogens and vaccine comprising the immunogen useful for preventing  
XX and treating infectious diseases e.g. malaria and chronic disease e.g.  
XX cancer, comprises peptide and carrier from protein D of influenzae  
XX  
XX Claim 9; Page 37; 53pp; English.

XX The present invention describes an immunogen (I) comprising a peptide  
XX (Ia) and a carrier (Ib) derived from protein D of Haemophilus influenzae  
XX or its fragment. Also described are: (1) a vaccine comprising (I), and  
XX an excipient; (2) preparation of (I), comprising conjugating a peptide  
XX to protein D or its fragment; and (3) preparation of a vaccine of (I),  
XX comprising formulating (I) with an excipient. (I) has cytostatic,  
XX anti-allergic, nontropic, neuroprotective and procoagulative activities.  
XX (I) and the vaccine are useful for the manufacture of a medicament for  
XX preventing and treating infectious diseases such as malaria or chronic  
XX disease such as cancer, Alzheimer's disease or allergy in a patient.  
XX Unlike prior art immunogens, (I) induces high levels of antipeptide  
XX immune responses while inducing a moderate humoral response against the  
XX carrier. The present sequence represents a specifically claimed  
XX immunoglobulin E (IgE) epitope immunogenic peptide sequence, which can  
XX be used in an immunogen of the present invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 57; DB 21; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0025;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQKHWSJSDRT 10  
||| |||||  
DB 1 SQKHWSJSDRT 10

RESULT 2

AAB25909  
ID AAB25909 standard; Peptide; 10 AA.

XX AC AAB25909;

XX DT 05-JAN-2001 (first entry)

XX DE IgE C-epsilon-2 domain surface exposed epitope peptide P3 SEQ ID NO:3.

XX Epitope; mimotope; human: immunoglobulin E; IgE C-epsilon-2 domain;  
XX allergic disease; immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
XX allergy; atopy.

XX CS Homo sapiens.

XX PN WC25050463-A1.

XX XX 31-AUG-2000.

XX PF 22-FEB-2000; 2000WO-EP01455.

XX PR 25-FEB-1999; 93GB-0004405.

XX PR 29-MAR-1999; 99GB-0007151.

XX PR 07-MAY-1999; 99GB-0010537.

XX PR 07-MAY-1999; 99GB-0010538.

XX PR 07-AUG-1999; 99GB-0018594.

XX PR 07-AUG-1999; 99GB-0018603.

XX PR 07-SEP-1999; 99GB-0021046.

XX PR 07-SEP-1999; 99GB-0021047.

XX PR 29-OCT-1999; 99GB-0025619.

XX PR 23-NOV-1999; 99GB-0027698.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX (PEP-) PEPTIDE THERAPEUTICS LTD.

XX Dyson M, Friede M, Greenwood J, Hewitt E, Lament A, Mason S;

PI Randall R, Turnell WG, Van Mectelen MP, Vinals De Bassols YC,  
XX WPI; 2000-572073/53.

XX Peptides useful for treating, preventing and ameliorating allergic  
XX diseases, comprising an isolated surface exposed group of a specific  
XX domain from immunoglobulin E.

XX Claim 4; Page 5; 129pp; English.

XX The present invention describes a peptide (I) comprising an isolated  
XX surface exposed group/epitope (E1) of C-epsilon-2 domain (D) of  
XX immunoglobulin E (IgE), or its mimotope. Also described are: (1) an  
XX immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)  
XX for treating allergies comprising (II); (3) a ligand (IV) capable of  
XX recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
XX (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
XX (Iia) comprising (Ia); and (7) producing (III) by producing (II). (I)  
XX as a vaccine and histamine release inhibitor. (I), (II) and (III) are  
XX useful in medicine and in the manufacture of medicaments for treating  
XX and preventing allergies. (IV) is useful for identifying mimotopes of P1,  
XX in medicine and also in manufacturing medicaments for treating  
XX allergies. (I) is useful in diagnostics and in the affinity purification  
XX of circulating anti-IgE antibodies from blood. (I), (II) and (III) are  
XX useful for treating a patient susceptible to or suffering from allergies.  
XX (IV) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
XX peptide sequences which are used in the exemplification of the present  
XX invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 57; DB 21; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0025;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQKHWSJSDRT 10  
||| |||||  
DB 1 SQKHWSJSDRT 10

RESULT 3

AACU16634  
ID AACU16634 standard; Peptide; 10 AA.

XX AC AACU16634;

XX DT 07-NOV-2001 (first entry)

XX DE Peptide P3 derived from Cepsilon2 region of human IgE.

XX Human; linkage technology; conjugated compound; carrier vehicle;  
XX epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
XX IgE mediated disease; antibody response.

XX OS Homo sapiens.

XX PN WO200145745-A2.

XX XX 28-JUN-2001.

XX PF 21-DEC-2000; 2000WO-GB04935.

XX PR 21-DEC-1999; 99GB-0030233.

XX PR 22-FEB-2000; 2000GB-0004096.

XX PR 22-AUG-2000; 2000GB-0020707.

XX PR 22-AUG-2000; 2000GB-0020708.

XX (ACAM-) ACAMBI RES LTD.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Flinn N, Johnson T;

DR WPI; 2001-521967/57.  
 CC A linkage comprising an immunogenic conjugate useful treatment of IgE mediated diseases.  
 CC  
 CC  
 CC Example 4; Page 21; 48pp; English.  
 CC The present invention relates to linkage methodology for use in the conjugation of compounds (e.g. peptides; to carrier vehicles (e.g. macromolecules, polymers, dendrimers, proteins) to produce biological and immunological constructs. The invention provides a method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition or a vaccine. The invention describes peptides derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E (IgE) which are used to produce conjugated compounds. The compounds or compositions of the invention are useful in the manufacture of a medicament for the treatment of IgE mediated diseases. The invention allows for controlled conjugation of a peptide epitope (antigen) to a protein so as to form an immunogenic conjugate which may be able to raise a protective antibody response in an animal or human patient. CC AAU16632-AAU16913 represent peptides derived from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 CC  
 CC Sequence 10 AA;  
 SQ  
 Query Match 100.0%; Score 57; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0025;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQKHWSLSDRT 10  
 DB 1 SQKHWSLSDRT 10  
 RESULT 4  
 AAB51025  
 ID AAB51025 standard; Peptide; 10 AA.  
 CC AAB51025;  
 CC  
 CC 21-MAR-2002 (first entry)  
 CC  
 CC IgE peptide #3.  
 CC Vaccine; immunoglobulin E; IgE; anti-allergy.  
 CC Mammalia.  
 CC WO2000074716 A2.  
 CC 14-DEC-2000.  
 CC 06-JUN-2000; 2000WO-EP0516A.  
 CC 08-JUN-1999; 93GB-0013327.  
 CC (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 CC Prieels J;  
 CC WPI; 2001-091150/10.  
 CC New vaccine comprising allergy peptides linked by an inert carrier, useful for boosting an anti-allergy immune response in an individual susceptible to an allergic response.  
 CC Claim 5; Page 20; 26pp; English.  
 CC The present invention relates to a composition comprising allergy peptides linked by an inert carrier. The allergy peptides are derived from immunoglobulin E (IgE) or IgE receptor. The present peptide is one such peptide from IgE. The composition is useful as a vaccine or for

CC manufacturing a medicament for the prophylaxis or treatment of allergy. CC In particular, for boosting an anti-allergy immune response in an individual susceptible to an allergic response.  
 CC  
 CC Sequence 10 AA;  
 SQ  
 Query Match 100.0%; Score 57; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0025;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQKHWSLSDRT 10  
 DB 1 SQKHWSLSDRT 10  
 RESULT 5  
 ABJC0219  
 ID ABJC0219 standard; Peptide; 10 AA.  
 CC ABJC0219;  
 CC 02-SEP-2002 (first entry)  
 CC Human IgE immunogenic peptide SEQ ID NO: 3.  
 CC Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage; vaccine; anti-allergic.  
 CC Homo sapiens.  
 CC WO200216403-A2.  
 CC 28-FEB-2002.  
 CC 17-AUG-2001; 2001WO-EP09576.  
 CC 22-AUG-2000; 2000GB-0020717.  
 CC (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 CC (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 CC Friede M, Mason S, Turnell WG, Vinals Bassols YC;  
 CC WPI; 2002-489648/52.  
 CC Conjugate for use in vaccine for treatment of allergy, comprises disulfide bridge cyclized peptide and immunogenic carrier.  
 CC Claim 4; Page 9; 45pp; English.  
 CC The present invention relates to conjugates suitable for use in vaccines, where the conjugate comprises a disulphide bridge cyclized peptide and an immunogenic carrier. The vaccines can be used in the treatment of allergies. The present sequence is a peptide immunogen derived from human immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
 CC  
 CC Sequence 10 AA;  
 SQ  
 Query Match 100.0%; Score 57; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0025;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQKHWSLSDRT 10  
 DB 1 SQKHWSLSDRT 10  
 RESULT 6  
 AAY42608  
 ID AAY42608 standard; peptide; 8 AA.  
 CC AAY42608;  
 CC

DT 10-JAN-2000 (first entry);  
 XX Human IgE peptide fragment.  
 DE  
 XX Immunoglobulin E; IgE; antagonist; FcεpsilonR1 receptor; human; Fcεs;  
 KW receptor-binding; binding determinant sequence; anti-IgE antibody;  
 KW allergic disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US9565709 A.  
 XX  
 PD 12-OCT-1999.  
 XX  
 XX 21-APR-1994; 94US 0232539.  
 XX  
 XX 14-AUG-1991; 91US-0744768.  
 PR 27-JAN-1994; 94US-0178583.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Cardieu PM, Presta LG;  
 XX WPI; 1999-579541/49.  
 DR  
 XX Immunoglobulin E variants as peptide antagonists useful for raising and  
 PT screening anti-immunoglobulin E (IgE) antibodies, in the isolation and  
 PT purification of FcεpsilonR1 receptor and in the treatment of allergic  
 PT diseases.  
 XX  
 PS Example 1; Column 37-38; 37pp; English.  
 XX  
 CC The invention provides immunoglobulin E (IgE) antagonists comprising one  
 CC or more of the FcεpsilonR1 receptor-binding determinant sites of human  
 CC IgE. The antagonists include IgE variants comprising an immunoglobulin  
 CC template and binding determinant sequences (bds); CDRs, EFBDs and the  
 CC sequence shown in AAY42561. The CDRs (CD-loop binding determinant  
 CC sequence) are selected from the sequences shown in AAY42567 Y42577 and  
 CC the EFBDs (EF loop binding determinant sequence) are selected from  
 CC sequences shown in AAY42578-Y42580. The variants are useful in raising  
 CC and screening anti-IgE antibodies, in the isolation and purification of  
 CC FcεpsilonR1 receptor and in the treatment and prophylaxis of allergic  
 CC diseases.  
 XX  
 SQ Sequence 8 AA:  
 Query Match 84.2%; Score 48; IP 200; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QKHLSLSDR 9  
 DB 1 QKHLSLSDR 8  
 RESULT 7  
 AAY85217  
 ID AAY85217 standard; protein; 8 AA.  
 XX  
 AC AAY85217;  
 XX  
 DT 29-JUN-2000 (first entry)  
 XX  
 DE Human IgE mutant #15 fragment amino acid sequence.  
 XX  
 KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FcεL; FcεH;  
 KW low affinity binding receptor; high affinity binding receptor; allergy;  
 KW diagnosis; treatment; histamine release; heavy chain; prevent.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6037453-A.  
 XX

PD 14-MAR-2000.  
 XX  
 PF 06-JUN-1995; 95US-0466151.  
 XX  
 PR 15-MAR-1995; 95US-0405617.  
 PR 14-AUG-1992; 92WO-US06860.  
 PR 26-JAN-1994; 94US-0184899.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Presta LG, Jardieu PM;  
 XX WPI; 2000-269913/23.  
 DR  
 XX New bispecific antibodies, useful for treating immunoglobulin  
 PT E-mediated disease, binds to IgE, but only when on the low affinity  
 PT receptor, and to an antigen other than IgE.  
 XX  
 PS Example 2; Column 33; 48pp; English.  
 XX  
 CC This sequence represents a fragment of an amino acid sequence encoding a  
 CC mutant human immunoglobulin E (IgE). The mutant IgE is used to test the  
 CC binding of IgE to its receptors. The invention relates to a bispecific  
 CC antibody that binds specifically to IgE when IgE is bound to its low  
 CC affinity receptor (FcεL), but does not bind to IgE. When IgE is bound to  
 CC its high affinity receptor (FcεH). The bispecific antibody comprises an  
 CC IgE-binding arm with human framework residues of a recipient human  
 CC antibody and donor murine CDR (complementarity determining region)  
 CC residues, but with at least one human CDR residue replacing the analogous  
 CC murine residue. The antibody also comprises an Fv that is specific for a  
 CC predetermined antigen other than IgE. The antibodies work by displacing  
 CC bound IgE from its receptor, or via competitive inhibition of its  
 CC binding. The bispecific antibodies are used for diagnosis, treatment and  
 CC prevention of allergy and other IgE-mediated diseases, also, when  
 CC immobilised for the isolation of FcεL from cells (for research or  
 CC therapy). The bispecific antibodies of the invention do not cause  
 CC granulation or release of histamine from mast cells.  
 XX  
 SQ Sequence 8 AA:  
 Query Match 84.2%; Score 48; D9 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QKHLSLSDR 9  
 DB 1 QKHLSLSDR 8  
 RESULT 8  
 AAY85250  
 ID AAY85250 standard; peptide; 8 AA.  
 XX  
 AC AAY85250;  
 XX  
 DT 29-JUN-2000 (first entry)  
 XX  
 DE Human IgE mutant #31 fragment amino acid sequence.  
 XX  
 KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FcεL; FcεH;  
 KW low affinity binding receptor; high affinity binding receptor; allergy;  
 KW diagnosis; treatment; histamine release; heavy chain; prevent.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6037453-A.  
 XX  
 PD 14-MAR-2000.  
 XX  
 PF 06-JUN-1995; 95US-0466151.  
 XX  
 PR 15-MAR-1995; 95US-0405617.  
 PR 14-AUG-1992; 92WO-US06860.

PR 26-JAN-1994; 94US-0185899.  
 XX (GETH) GENENTECH INC.  
 PA  
 PT Presta LG, Jardieu PX;  
 PI  
 XX WPI; 2800-269913/23.  
 DR  
 XX  
 XX New bispecific antibodies, useful for treating immunoglobulin  
 PT E-mediated disease, binds to IgE, but only when on the low affinity  
 PT receptor, and to an antigen other than IgE.  
 PT  
 PS Example 5; Column 43; 49pp; English.  
 XX  
 CC This sequence represents a fragment of an amino acid sequence encoding a  
 CC mutant human immunoglobulin E (IgE). The mutant IgE is used to test the  
 CC binding of the anti-IgE antibodies of the invention. The invention  
 CC relates to a bispecific antibody that binds specifically to IgE when IgE  
 CC is bound to its low affinity receptor (FcεR1), but does not bind to IgE,  
 CC when IgE is bound to its high affinity receptor (FcεR2). The bispecific  
 CC antibody comprises an IgE-binding arm with human framework residues of a  
 CC recipient human antibody and donor murine CDR (complementarity  
 CC determining region) residues, but with at least one human CDR residue  
 CC replacing the analogous murine residue. The antibody also comprises an Fc  
 CC that is specific for a predetermined antigen other than IgE. The  
 CC antibodies work by displacing bound IgE from its receptor, or via  
 CC competitive inhibition of its binding. The bispecific antibodies are used  
 CC for diagnosis, treatment and prevention of allergy and other IgE-mediated  
 CC diseases, also, when immobilised, for the isolation of FcεR1 from cells  
 CC (for research or therapy). The bispecific antibodies of the invention do  
 CC not cause granulation or release of histamine from mast cells.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 84.2%; Score 48; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9,3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QKHWSLR 9  
 Db 1 QKHWSLR 8  
 |||||  
 |||||  
 RESULT 9  
 ID AAE35074 standard; peptide; 9 AA.  
 XX  
 AC AAE35074;  
 XX  
 DT 25-MAY-2003 (first entry)  
 XX  
 DE Human immunoglobulin E (IgE) HLA A2 peptide motif #100  
 XX  
 KW Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;  
 KW lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis;  
 KW psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever;  
 KW inflammatory bowel disease; insulin dependent diabetes; cell therapy;  
 KW Crohn's disease; allergic rhinitis; graft versus host disease; asthma;  
 KW transplant rejection; human; immunoglobulin E; IgE.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200292773-A2.  
 XX  
 PD 21-NOV-2002.  
 XX  
 FF 13-MAY-2002; 2002WO-US15341.  
 XX  
 PR 15-MAY-2001; 2001US-291300P.  
 XX  
 PA (CRTH) CRTHO-MCNEL PHARM INC.  
 XX  
 PI Cai Z, Jackson MR, Peterson PA, Shi W, Kong Y, Leqraw J;

XX WPI; 2003-120673/11.  
 XX  
 PT Producing cytotoxic T lymphocytes for treating e.g. autoimmune  
 PT diseases, comprises culturing CD8+ T cells with antigen presenting  
 PT cells to activate precursor CD8+ T cells specific for T the cell  
 PT epitopes.  
 XX  
 PS Example 3; Column 47; 49pp; English.  
 XX  
 CC The invention relates to a method of producing cytotoxic T lymphocytes  
 CC (CTLs) specific for one or more non-tumour self antigen T cell epitopes.  
 CC The method involves loading antigen presenting cells (APCs) having class  
 CC I major histocompatibility complex molecules with the T cell epitopes,  
 CC and culturing the CD8+ T cells with the APCs to activate precursor CD8+  
 CC T cells specific for the T cell epitopes. The invention is useful for  
 CC treating autoimmune disease including rheumatoid arthritis, psoriasis,  
 CC lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,  
 CC insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
 CC graft versus host disease and transplant rejection and/or allergic  
 CC disease such as food allergy, hay fever, allergic rhinitis, allergic  
 CC asthma and venom allergy. The invention is also useful in cell therapy.  
 CC The present sequence is human immunoglobulin E (IgE) HLA-A2 peptide  
 CC motif. This peptide is used in the exemplification of the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 64.9%; Score 37; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9,3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQKHWSL 6  
 Db 4 SQKHWSL 9  
 |||||  
 |||||  
 RESULT 10  
 ID ABP96578 standard; peptide; 9 AA.  
 XX  
 AC ABP96578;  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE Human immunoglobulin E related peptide SEQ ID NO:17.  
 XX  
 KW Immune response; IgE; cytotoxic T lymphocyte response;  
 KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;  
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;  
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
 KW urticaria hives.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO2003015716-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 08-AUG-2002; 2002WO-US26986.  
 XX  
 PR 13-AUG-2001; 2001US-312120P.  
 XX  
 PA (IGET-) IGE THERAPEUTICS INC.  
 XX  
 PI Chen SA, Yang Y, Barankiewicz T, Chen Z;  
 XX WPI; 2003-268242/26.  
 XX  
 PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
 PT against IgE, by identifying peptide eliciting CTL response to IgE

PT peptides naturally presented by major histocompatibility complex class  
 PT I protein  
 XX  
 ts Example 5; Page 70; 187pp; English.  
 XX  
 CC The present invention describes a method (M1) for identifying peptides  
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
 CC E (IgE), comprising providing a test peptide (T1) suspected of being able  
 CC to bind to major histocompatibility complex (MHC) class I molecule, and  
 CC evaluating (T1) for ability to elicit in a mammal a CTL response to  
 CC naturally processed and presented IgE peptides, where a peptide that  
 CC induces such a response is identified. Also described are compositions:  
 CC (C1) comprising at least one immunogenic peptide (I1) identified by (M1);  
 CC (C2) comprising at least one isolated polynucleotide encoding (I1); and  
 CC (C3) comprising antigen-presenting cells that recognize at least one (I1).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC IgE peptides, C1-3 have anti-allergic, anti-asthmatic, immunosuppressive,  
 CC vasotropic, dermatological, anti-inflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against IgE, and in  
 CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as  
 CC IgE mediated atopic hypersensitivity condition, IgE-mediated non-atopic  
 CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
 CC hives). The present sequence represents a peptide which is used in an  
 CC example from the present invention.

XX Sequence 9 AA;

Query Match 64.9%; Score 37; DB 24; Length 9;  
 Best Local Similarity 120.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQRWL: 6  
 |||||  
 Db 4 SQRWL: 9

RESULT 11  
 AAR33325  
 ID AAR33325 standard; peptide; 8 AA.  
 AC AAR33325;  
 XX  
 D7 25-MAR-2003 (updated);  
 D7 05-JUL-1993 (first entry);  
 XX  
 DE IgE Kabat residue no. 329-336.  
 XX  
 KW High affinity; FCEH; low affinity; FCEH; Padlan;  
 KW IgE receptor; Fc; IgG1.

CS Homo sapiens.  
 XX  
 PN WC9304173-A1.  
 XX  
 PC C4-MAR-1993.  
 XX  
 PF 14-AUG-1992; 92WO-006860.  
 XX  
 PR 14-AUG-1991; 91US-0744768.  
 PR 07-MAY-1992; 92US-0879495.  
 XX  
 PA (GETH) GENENTECH INC.

XX Jardies PX; Presta LG;  
 XX  
 DR WPI; 1993-094024/11.  
 XX

PT Polypeptide(s) binding to specific Fc epsilon receptors act as

PT IgE antagonists; useful for treating and preventing IgE-mediated  
 PT disorders e.g. allergies  
 XX  
 PS Disclosure; Page 57; 113pp; English.  
 XX  
 CC Based on the model of IgE Fc by Padlan & Davies (Mol. Immun.,  
 CC 23:1063-1075 (1986)), which is based on the crystal structure of  
 CC human IgG1Fc (Deisenhofer, Biochem. 20:2361-2370 (1981)), a series  
 CC of mutants were designed which could be used to test the binding of  
 CC human IgE to its receptors. These mutants are designated Emut 1-13.  
 CC The sequence of AAR33325 (amino acids 329-336 of IgE - numbering  
 CC according to Kabat) was replaced by the sequence of AAR33326 to give  
 CC mutant 13. Mutant 13 shows +ve and +ve binding to Fc epsilon RI.  
 CC The mutant IgEs were transiently expressed in human kidney 293 cells,  
 CC purified on a mouse anti-human IgE antibody affinity column and samples  
 CC run using SDS-PAGE to ascertain that the mutant proteins were of the  
 CC proper mol. wt.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 8 AA;

Query Match 61.4%; Score 35; DB 14; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QKHWLSDR 9  
 |||||  
 Db 1 QKHQLSDR 8

RESULT 12

AAR35054  
 ID AAR35054 standard; peptide; 9 AA.

XX AAR35054;

D7 28-MAY-2003 (first entry);

DE Immunoglobulin E (IgE) antigenic peptide, IgE 185.

XX Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;  
 XX lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis;  
 XX psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever;  
 XX inflammatory bowel disease; insulin dependent diabetes; cell therapy;  
 XX Crohn's disease; allergic rhinitis; graft versus host disease; asthma;  
 XX transplant rejection; immunoglobulin 5; IgE; antigen.

XX Unidentified.

XX WC202292773-A2.

XX 21-NOV-2002.

XX 13-MAY-2002; 2002WC-US15341.

XX 15-MAY-2001; 2001US-29130CP.

XX (ORTH) ORTHO-MCNEIL PHARM INC.

XX Cai Z, Jackson MR, Peterson PA, Shi W, Kong Y, Degraw J;

XX WPI; 2003-120673/11.

XX Producing cytotoxic T lymphocytes for treating e.g. autoimmune  
 PT diseases, comprises culturing CD8+ T cells with antigen presenting  
 PT cells to activate precursor CD8+ T cells specific for T cell  
 PT epitopes

XX Example 4; Column: 52; 49pp; English.

XX The invention relates to a method of producing cytotoxic T lymphocytes  
 CC (CTLs) specific for one or more non-tumour self antigen T cell epitopes.  
 CC The method involves loading antigen presenting cells (APCs) having class

CC I major histocompatibility complex molecules with the T cell epitopes,  
 CC and culturing the CD8+ T cells with the APCs to activate precursor CD8+  
 CC T cells specific for the T cell epitopes. The invention is useful for  
 CC treating autoimmune disease including rheumatoid arthritis, psoriasis,  
 CC lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,  
 CC insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
 CC graft versus host disease and transplant rejection and/or allergic  
 CC disease such as food allergy, hay fever, allergic rhinitis, allergic  
 CC asthma and venom allergy. The invention is also useful in cell therapy.  
 CC The present sequence is immunoglobulin E (IgE) antigenic peptide.  
 CC This peptide is used in the exemplification of the invention.

XX  
 XX  
 SQ Sequence 9 AA;

Query Match 61.4%; Score 35; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 WLSRDT 10  
 | : : : : |  
 Db 1 WLSRDT 6

RESULT 13  
 ID AAE35063 standard; peptide; 9 AA.  
 XX AAE35063;  
 AC  
 XX  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX Human immunoglobulin E (IgE) HLA-A2 peptide motif #1.  
 DE  
 XX Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;  
 KW lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis;  
 KW psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever;  
 KW inflammatory bowel disease; insulin dependent diabetes; cell therapy;  
 KW Crohn's disease; allergic rhinitis; graft versus host disease; asthma;  
 KW transplant rejection; human; immunoglobulin E; IgE.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200292773-A2.  
 PN  
 XX 21-NOV-2002.  
 PD  
 XX 13-MAY-2002; 2002WO-US:5341.  
 PF  
 XX 15-MAY-2001; 2001US-29:300P.  
 PR  
 XX (CITE) ORTHO-McNEIL PHARM INC.  
 PA Cai Z, Jackson MR, Peterson PA, Shi W, Komi Y, Legraw G;  
 PI  
 XX WPI; 2003-123673/11.  
 DR  
 XX Producing cytotoxic T lymphocytes for treating end. autoimmune  
 PT diseases, comprises culturing CD8+ T cells with antigen presenting  
 PT cells to activate precursor CD8+ T cells specific for T the cell  
 PT epitopes -  
 XX  
 XX Example 3; Column 47; 49pp; English.

CC The invention relates to a method of producing cytotoxic T lymphocytes  
 CC (CTLs) specific for one or more non-tumour self antigen T cell epitopes.  
 CC The method involves loading antigen presenting cells (APCs) having class  
 CC I major histocompatibility complex molecules with the T cell epitopes,  
 CC and culturing the CD8+ T cells with the APCs to activate precursor CD8+  
 CC T cells specific for the T cell epitopes. The invention is useful for  
 CC treating autoimmune disease including rheumatoid arthritis, psoriasis,  
 CC lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,  
 CC insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
 CC graft versus host disease and transplant rejection and/or allergic  
 CC disease such as food allergy, hay fever, allergic rhinitis, allergic  
 CC asthma and venom allergy. The invention is also useful in cell therapy.  
 CC The present sequence is immunoglobulin E (IgE) antigenic peptide.  
 CC This peptide is used in the exemplification of the invention.

CC disease such as food allergy, hay fever, allergic rhinitis, allergic  
 CC asthma and venom allergy. The invention is also useful in cell therapy.  
 CC The present sequence is human immunoglobulin E (IgE) HLA-A2 peptide  
 CC motif. This peptide is used in the exemplification of the invention.

XX  
 XX  
 SQ Sequence 9 AA;

Query Match 61.4%; Score 35; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 WLSRDT 10  
 | : : : : |  
 Db 1 WLSRDT 6

RESULT 14  
 ID ABP96567 standard; peptide; 9 AA.  
 XX ABP96567;  
 AC  
 XX  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX Human immunoglobulin E related peptide SEQ ID NO:6.  
 DE  
 XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;  
 KW immune response; major histocompatibility complex; MHC; immunogenic;  
 KW anti-allergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;  
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;  
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
 KW urticaria hives.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO2003015716-A2.  
 PN  
 XX 27-FEB-2003.  
 PD  
 XX 08-AUG-2002; 2002WO-US26986.  
 PF  
 XX 13-AUG-2001; 2001US-312120P.  
 PR  
 XX (IGET-) IGE THERAPEUTICS INC.  
 PA Chen SA, Yang Y, Barankiewicz T, Chen Z;  
 PI  
 XX WPI; 2003-268242/26.  
 DR  
 XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
 PT against IgE, by identifying peptide eliciting CTL response to IgE  
 PT peptides naturally presented by major histocompatibility complex class  
 PT I protein -  
 XX  
 XX Example 5; Page 70; 187pp; English.

CC The present invention describes a method (M1) for identifying peptides  
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
 CC E (IgE), comprising providing a test peptide (T) suspected of being able  
 CC to bind to major histocompatibility complex (MHC) class I molecule, and  
 CC evaluating (T) for ability to elicit in a mammal a CTL response to  
 CC naturally processed and presented IgE peptides, where a peptide that  
 CC induces such a response is identified. Also described are compositions:  
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC IgE peptides. C1-3 have anti-allergic, antiasthmatic, immunosuppressive,  
 CC vasotropic, dermatological, antiinflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against IgE, and in



CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as  
 CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic  
 CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
 CC (ives)). The present sequence represents a peptide which is used in an  
 CC example from the present invention.

SQ Sequence 9 AA;

Query Match 61.4%; Score 35; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WLSRDT 10  
 |||||  
 DB : WLSRDT 6

# RESULT 15

ABR18853  
 ID ABR18853 standard; Peptide; 9 AA.

XX ABR18853;

DT 19 MAY-2003 (first entry)

DE Human cancer-related protein 184P3G10 HLA peptide #48

XX Human; Cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX Homo sapiens.

CS WC200283921-A2.

PN 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

PR 10-APR-2002; 2001US-282739P.

PR 10-APR-2002; 2001US-283112P.

XX 25-APR-2002; 2001US-286630P.

PA (AGN-); AGENSYS INC.

PI Jakobovits A, Chailita-Eid PM, Faris M, Ge W, Hestert PS;

PI Morrison K, Morrison RK, Raitano AB;

XX WP; 2003 075555/07.

XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients.

PS Claim 13; Page 304; 1021pp; English.

XX The present invention relates to novel human cancer related genes and  
 CC proteins (AB278120-AB278168 and ABR01789-ABR01861); the genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

SQ Sequence 9 AA;

Query Match 52.6%; Score 30; DB 24; Length 9;  
 Best Local Similarity 80.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 HWLSD 8  
 |||||  
 DB 4 HWLSD 8

Search completed: November 5, 2003, 17:32:29  
 Job time : 34.3333 secs

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OM protein - protein search, using sw model

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without alignment  
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Title: US-09-914-088-3  
Perfect score: 57  
Sequence: 1 SQKWLSDRT 10

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 644079 seqs, 171749292 residues

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Minimum DB seq length: 0  
Maximum DB seq length: 10

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Maximum Match 100%  
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- 2: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pep.
- 3: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pep.
- 4: /cgn2\_6/ptodata/2/pubaa/US06\_PUSCOMB.pep.
- 5: /cgn2\_6/ptodata/2/pubaa/US07\_NEW\_PUB.pep.
- 6: /cgn2\_6/ptodata/2/pubaa/PCTUS\_PUSCOMB.pep.
- 7: /cgn2\_6/ptodata/2/pubaa/US08\_NEW\_PUB.pep.
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- 9: /cgn2\_6/ptodata/2/pubaa/US09A\_PUSCOMB.pep.
- 10: /cgn2\_6/ptodata/2/pubaa/US09B\_PUSCOMB.pep.
- 11: /cgn2\_6/ptodata/2/pubaa/US09C\_PUSCOMB.pep.
- 12: /cgn2\_6/ptodata/2/pubaa/US09\_NEW\_PUB.pep.
- 13: /cgn2\_6/ptodata/2/pubaa/US10A\_PUSCOMB.pep.
- 14: /cgn2\_6/ptodata/2/pubaa/US10B\_PUSCOMB.pep.
- 15: /cgn2\_6/ptodata/2/pubaa/US10C\_PUSCOMB.pep.
- 16: /cgn2\_6/ptodata/2/pubaa/US10\_NEW\_PUB.pep.
- 17: /cgn2\_6/ptodata/2/pubaa/US0C\_NEW\_PUB.pep.
- 18: /cgn2\_6/ptodata/2/pubaa/US06\_PUB.pep.

Pred. No. is the number of results predicted by BLAST to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARY:

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2	48	84.2	8	9	US-09-802-077-24
3	48	84.2	8	9	US-09-802-077-24
4	48	84.2	8	9	US-09-802-077-24
5	48	84.2	8	11	US-09-925-179-24
6	48	84.2	8	11	US-09-925-179-24
7	37	64.9	9	15	US-10-214-524-17
8	35	61.4	9	12	US-10-144-588-52
9	35	61.4	9	15	US-10-214-524-17
10	28	49.1	7	10	US-09-884-767A-14
11	26	45.6	7	12	US-10-285-457-40
12	26	45.6	10	10	US-09-751-378-455
13	26	45.6	10	10	US-09-851-138-193
14	25	43.9	9	15	US-10-301-644-3
15	24	42.1	5	9	US-09-817-661-34

16	24	42.1	7	12	US-10-193-764-20
17	24	42.1	8	9	US-09-848-164-78
18	24	42.1	8	9	US-09-848-164-86
19	24	42.1	8	10	US-09-900-379-78
20	24	42.1	8	10	US-09-900-379-86
21	24	42.1	9	12	US-10-177-725-110
22	24	42.1	9	12	US-10-221-984-4
23	24	42.1	9	12	US-10-286-457-440
24	24	42.1	9	12	US-10-144-188-53
25	24	42.1	10	12	US-10-190-082-565
26	24	42.1	10	12	US-10-353-929-142
27	24	42.1	10	12	US-10-353-929-154
28	24	42.1	10	12	US-10-200-708-260
29	24	42.1	10	14	US-10-054-552-2
30	23	40.4	5	12	US-10-205-110-42
31	23	40.4	6	9	US-09-735-995-102
32	23	40.4	6	9	US-09-735-995-103
33	23	40.4	6	9	US-09-735-995-106
34	23	40.4	6	9	US-09-735-995-107
35	23	40.4	7	10	US-09-884-767A-15
36	23	40.4	7	12	US-10-052-578-167
37	23	40.4	7	12	US-10-205-110-43
38	23	40.4	7	12	US-10-193-082-476
39	23	40.4	7	12	US-10-053-520-167
40	23	40.4	7	12	US-10-053-498B-167
41	23	40.4	8	12	US-10-044-896-12
42	23	40.4	8	15	US-10-193-768-21
43	23	40.4	9	9	US-09-765-527-200
44	23	40.4	9	9	US-09-881-490-168
45	23	40.4	9	12	US-10-205-110-27

## ALIGNMENTS

### RESULT 1

US-09-802-077-24  
 ; Sequence 24, Application US/09802077  
 ; Patent No. US20010033842A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jardiou, Paula M.  
 ; APPLICANT: Presta, Leonard G.  
 ; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)  
 ; FILE REFERENCE: P0718P2C2US  
 ; CURRENT APPLICATION NUMBER: US/09/802.077  
 ; CURRENT FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: US 08/425,617  
 ; PRIOR FILING DATE: 1995-03-15  
 ; PRIOR APPLICATION NUMBER: US 08/185,899  
 ; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR APPLICATION NUMBER: PCT/US92/06860  
 ; PRIOR FILING DATE: 1992-08-14  
 ; PRIOR APPLICATION NUMBER: US 07/879,495  
 ; PRIOR FILING DATE: 1992-05-07  
 ; PRIOR APPLICATION NUMBER: US 07/744,768  
 ; PRIOR FILING DATE: 1991-08-14  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SEQ ID NO 24  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-802-077-24

Query Match 84.2% Score 48; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QKHW:SDR 9

Db 1 QKHW:SDR 9

### RESULT 2

```
US-09-802-096-57
; Sequence 57, Application US/09802096
; Patent No. US2001003839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 57
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-57

Query Match      84.2%; Score 48; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QKHWSLDR 9
      : |||||
Db      1 QKHWSLDR 8

RESULT 3
US-09-802-096-57
; Sequence 57, Application US/09802096
; Patent No. US2001003839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 57
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-57

Query Match      84.2%; Score 48; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QKHWSLDR 9
      : |||||
Db      1 QKHWSLDR 8

US-09-925-179-24
; Sequence 24, Application US/09925179
; Publication No. US20010044858A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IGE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-04-08
; PRIOR APPLICATION NUMBER: US 08/465,163
; PRIOR FILING DATE: 1995-06-04
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/195,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-179-24

Query Match      84.2%; Score 48; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QKHWSLDR 9
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Db      1 QKHWSLDR 8
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Db      2 QKHWLSDR 8

RESULT 6
US-09-925-179-57
; Sequence 57, Application US/09925179
; Publication No. US20030044958A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1JS
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/0656C
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 57
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-179-57

Query Match      84.2%; Score 46; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2 QKHWLSDR 9
Db      1 QKHWLSDR 8

RESULT 7
US-10-214-524-17
; Sequence 17, Application US/0214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: ICE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human (Homo sapiens)
US-10-214-524-17

Query Match      64.9%; Score 37; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 SCXHWL 6
Db      4 SCXHWL 9

RESULT 8
US-10-144-188-52
; Sequence 52, Application US/10144188
; Publication No. US20030170212A1
; GENERAL INFORMATION:
; APPLICANT: Cai, Zeling
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; APPLICANT: Shi, Weixing
; APPLICANT: Kong, Yan
; APPLICANT: Degraw, Juli
; TITLE OF INVENTION: Ex-Vivo Priming For Generating Cytotoxic T Lymphocytes Specific
; FILE REFERENCE: P10010 ORT-1627
; CURRENT APPLICATION NUMBER: US/10/144,188
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/292,300
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide antigen
US-10-144-188-52

Query Match      61.4%; Score 35; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      5 WLSDR 10
Db      1 WLSDR 6

RESULT 9
US-10-214-524-6
; Sequence 6, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: ICE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human (Homo sapiens)
US-10-214-524-6

Query Match      61.4%; Score 35; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      5 WLSDR 10
Db      1 WLSDR 6

RESULT 10
US-09-884-767A-43
; Sequence 43, Application US/09884767A
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; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DVAX Corp.
; APPLICANT: Jey, Arthur C.
; APPLICANT: Lunau, Christopher J.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: NOVEL ENZYMOLOGICAL SEQUENCES
; FILE REFERENCE: DEX-012.1 US, DEX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US 09-884 767A-143

Query Match 49.1%; Score 28; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 58405;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 WLSDR 9
Db 2 WLSDR 6

RESULT 11
US-10-286-457-40
; Sequence 40, Application US/10286457
; Publication No. US2003016604A:
; GENERAL INFORMATION:
; APPLICANT: JENC GYRIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/284,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequences designed to bind to endothelial cells
US-10-286-457-40

Query Match 45.6%; Score 26; DB 12; Length 7;
Best Local Similarity 66.7%; Pred. No. 58405;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HWLSDR 9
Db 2 HWASPR 7

RESULT 12
US-09-791-378-455
; Sequence 455, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: SCHIZOPHRENIA
; CURRENT APPLICATION NUMBER: US/09/791,378

; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: Jey, Arthur C.
; APPLICANT: Lunau, Christopher J.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: NOVEL ENZYMOLOGICAL SEQUENCES
; FILE REFERENCE: DEX-012.1 US, DEX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-455

Query Match 45.6%; Score 26; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 58402;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QXWLSDR 9
Db 3 QYHYLLDR 10

RESULT 13
US-09-851-138-193
; Sequence 193, Application US/09851138
; Publication No. US20020183508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DUNKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <UNKNOWN>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-09-851-138-193

Query Match 45.6%; Score 26; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 58402;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOKHW 5
Db 2 SRRHW 6
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Search completed: November 5, 2003, 17:46:07  
Job time : 22 secs

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RESULT 14
US-10-301-644-9
; Sequence 9, Application US/0301644
; Publication No. US2003012413A1
; GENERAL INFORMATION:
; APPLICANT: Phalipot, Armelle
; APPLICANT: Sansonetti, Philippe
; APPLICANT: Felici, Franco
; APPLICANT: Cortese, Riccardo
; APPLICANT: Kraehenbuhl, Jean Pierre
; TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDES THAT MIXED A SURFACE
; TITLE OF INVENTION: POLYSACCHARIDE ANTIGEN OF A PATHOGENIC MICROORGANISM,
; TITLE OF INVENTION: METHOD FOR OBTAINING THE SAME, AND THEIR USE IN VACCINE
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 03495-0176
; CURRENT APPLICATION NUMBER: US/10/301,644
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: 60/057,906
; PRIOR FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide used to induce an immune response against
; OTHER INFORMATION: pathogenic microorganisms
US-10-301-644-9

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Query Match 43.9%; Score 25; DB 15; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 2 QXWLSDR 9
DB 1 KRFLSOR 8

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RESULT 15
US-09-917-661-34
; Sequence 34, Application US/09917661
; Patent No. US20020276692A1
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane
; APPLICANT: Holst, Thor
; TITLE OF INVENTION: Improvements to ribosome display
; FILE REFERENCE: 84633
; CURRENT APPLICATION NUMBER: US/09/917,661
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/193,822
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutagenized
; OTHER INFORMATION: sequence
US-09-917-661-34

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Query Match 42.1%; Score 24; DB 9; Length 5;
Best Local Similarity 60.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 4 HWLSD 8
DB 1 HWQTD 5

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:30:40 ; Search time 12.333 Seconds  
(without alignments)  
34.396 Million cell updates/sec

Title: US-09-914-088-3  
Perfect score: 57  
Sequence: 1 SQKWLSDRT 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 10054

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/prodata/1/1aa/backlist.pept.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	84.2	8	2	US-08-469-141A-60
2	48	84.2	8	2	US-08-469-141A-60
3	48	84.2	8	3	US-08-469-141A-60
4	48	84.2	8	3	US-08-469-141A-60
5	48	84.2	8	4	US-08-469-141A-60
6	48	84.2	8	4	US-08-469-141A-60
7	26	45.6	10	3	US-08-469-141A-60
8	25	43.9	8	2	US-08-469-141A-60
9	25	43.9	9	4	US-08-469-141A-60
10	24	42.1	4	3	US-08-469-141A-60
11	24	42.1	5	1	US-07-973-205A-19
12	24	42.1	5	2	US-08-469-141A-60
13	24	42.1	6	1	US-08-469-141A-60
14	24	42.1	6	2	US-08-469-141A-60
15	24	42.1	6	4	US-08-469-141A-60
16	24	42.1	7	3	US-08-469-141A-60
17	24	42.1	7	4	US-09-206-942-20
18	24	42.1	7	5	PCT-US95-13794-62
19	24	42.1	8	2	US-08-596-387R-78
20	24	42.1	8	2	US-08-596-387R-78
21	24	42.1	8	3	US-08-596-387R-78
22	24	42.1	8	4	US-08-596-387R-78
23	24	42.1	8	4	US-09-567-615-86
24	24	42.1	8	5	PCT-US95-09816A-78
25	24	42.1	8	5	PCT-US95-09816A-86
26	24	42.1	8	5	PCT-US95-13794-61
27	24	42.1	9	2	US-08-350-262A-153

Sequence 3, Appli  
Sequence 60, Appli  
Sequence 353, App  
Sequence 59, Appl  
Sequence 59, Appl  
Sequence 59, Appl  
Sequence 3, Appli  
Sequence 60, Appli  
Sequence 2, Appli  
Sequence 10, Appli  
Sequence 10, Appli  
Sequence 160, App  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 67, Appli  
Sequence 68, Appli  
Sequence 71, Appli  
Sequence 72, Appli

ALIGNMENTS

RESULT 1  
US-08-232-539D-42  
; Sequence 42, Application US/08232539D  
; Patent No. 5965709  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Jardieu, Paula N.  
; TITLE OF INVENTION: Ige Antagonists  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DCS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232.539D  
; FILING DATE: 31-Apr-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/179583  
; FILING DATE: 07-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: PCT:8P3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-232-539D-42

Query Match 84.2% Score 48; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 QKWLSDR 9





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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-163B-57

Query Match      84.2%, Score 48; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QXHWLSDR 9
DB      1 QXHWLSDR 8

RESULT 5
US-08-466-163B-24
; Sequence 24, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-466-163B-24

Query Match      84.2%, Score 48; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QXHWLSDR 9
DB      1 QXHWLSDR 8

RESULT 6
US-08-466-163B-57
; Sequence 57, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
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; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 57
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-466-163B-57

Query Match      84.2%, Score 48; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QXHWLSDR 9
DB      1 QXHWLSDR 8

RESULT 7
US-08-836-075A-193
; Sequence 193, Application US/08836075A
; Patent No. 6180768
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; TITLE OF INVENTION: AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-075A-193
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Query Match 45.6%; Score 26; DB 3; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.7e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 SOKHW 5  
DB 2 SHRW 6

RESULT 8  
US-08-669-284B-20  
; Sequence 20, Application US/08669284B  
; Patent No. 5939534  
; GENERAL INFORMATION:  
; APPLICANT: Iroue, Makoto  
; APPLICANT: Kikuchi, Kaoru  
; APPLICANT: Ishige, Yoko  
; APPLICANT: Ito, Akira  
; APPLICANT: Kimura, Toru  
; APPLICANT: Nakayama, Chikao  
; APPLICANT: No. 5939534uchi, Hiroshi  
; TITLE OF INVENTION: NOVEL HUMAN CELLULAR NEUROTROPHIC FACTORS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.10  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,284B

FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/02269  
FILING DATE: 27-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 06-268281  
FILING DATE: 05-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 06-261564  
FILING DATE: 02-AUG-1994  
APPLICATION NUMBER: JP 05-150344  
FILING DATE: 29-DEC-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Dean H.  
REGISTRATION NUMBER: 33,981  
REFERENCE/DOCKET NUMBER: G-42041  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-669-284B-20

Query Match 43.9%; Score 25; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 5 WLSDR 10  
DB 2 WLDXT 7

RESULT 9  
US-09-144-280-9  
; Sequence 9, Application US/09144280A  
; Patent No. 6528061  
; GENERAL INFORMATION:  
; APPLICANT: Thalipon, Armelle  
; APPLICANT: Sansonetti, Philippe  
; APPLICANT: Felici, Franco  
; APPLICANT: Cortese, Riccardo  
; APPLICANT: Kraehenbuhl, Jean-Pierre  
; TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDES THAT MIMIC A SURFACE  
; TITLE OF INVENTION: POLYSACCHARIDE ANTIGEN OF A PATHOGENIC MICROORGANISM,  
; TITLE OF INVENTION: METHOD FOR OBTAINING THE SAME, AND THEIR USE IN VACCINE  
; TITLE OF INVENTION: COMPOSITIONS  
; FILE REFERENCE: 03495-0176  
; CURRENT APPLICATION NUMBER: US/09/144,280A  
; CURRENT FILING DATE: 1998-08-31  
; EARLIER APPLICATION NUMBER: 60/057,906  
; EARLIER FILING DATE: 1997-09-04  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 9  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide used to induce an immune response against  
; OTHER INFORMATION: pathogenic microorganisms  
US-09-144-280-9

Query Match 43.9%; Score 25; DB 4; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CY 2 QKWLSDR 9  
DB 1 KRHFLSR 8

RESULT 10  
US-08-904-446A-10  
; Sequence 10, Application US/08904446A  
; Patent No. 6029114  
; GENERAL INFORMATION:  
; APPLICANT: Sharovsky, Igor L.  
; APPLICANT: Ross, Gregory M.  
; APPLICANT: Riopelle, Richard J.  
; APPLICANT: Weaver, Donald F.  
; TITLE OF INVENTION: Molecular Modelling of Neurotrophin-Receptor  
; TITLE OF INVENTION: Binding  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dowell & Dowell, P.C.  
; STREET: 1215 Jefferson Davis Highway, Suite 309  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: United States of America  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/904,446A  
; FILING DATE: 31-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9616105.4  
; FILING DATE: 31-JUL-1996  
; ATTORNEY/AGENT INFORMATION:

```

1 NAME: RALPH A. DOWELL
2 REGISTRATION NUMBER: 26868
3 TELECOMMUNICATION INFORMATION:
4 TELEPHONE: (703) 415-2555
5 TELEFAX: (703) 415-2559
6 INFORMATION FOR SEQ ID NO: 10:
7 SEQUENCE CHARACTERISTICS:
8 LENGTH: 4 amino acids
9 TYPE: amino acid
10 STRANDEDNESS: single
11 TOPOLOGY: linear
12 MOLECULE TYPE: peptide
13 FEATURES:
14 NAME/KEY: Peptide
15 LOCATION: 1..4
16 OTHER INFORMATION: /note= "Residues 74-77 of human
17 NGF, mouse NGF or Delta 3 9 mutant of mouse NGF"
18 US 08-904-446A-10
19
20 Query Match 42.18; Score 24; DB 3; Length 4;
21 Best Local Similarity 100.0%; Pred. No. 2.5e+5;
22 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
23
24 QY 3 KHW 5
25
26 Db 1 KHW 3
27
28 RESULT 1:
29 US-07-973-235A-19
30 : Sequence 19, Application US/07973235A
31 : Patent No. 5491130
32 : GENERAL INFORMATION:
33 : APPLICANT: David D. Roberts, et al.
34 : TITLE OF INVENTION: Peptide Inhibitors of Fibronectin and
35 : TITLE OF INVENTION: Related Collagen-Binding Proteins
36 : NUMBER OF SEQUENCES: 30
37 : CORRESPONDENCE ADDRESS:
38 : ADDRESSEE: Lowe, Price, LeBlanc & Becker
39 : STREET: Suite 300, 99 Canal Center Plaza
40 : CITY: Alexandria
41 : STATE: Virginia
42 : ZIP: 22314
43 : COUNTRY: USA
44 : MEDIUM TYPE: Floppy Disk
45 : COMPUTER: IBM PC Compatible
46 : OPERATING SYSTEM: PC-DOS/MS-DOS
47 : SOFTWARE: Word Perfect, Version 4.1
48 : CURRENT APPLICATION DATA:
49 : APPLICATION NUMBER: US/07/973,235A
50 : FILING DATE: 19921110
51 : CLASSIFICATION: 514
52 : ATTORNEY/AGENT INFORMATION:
53 : NAME: Robert L. Price
54 : REGISTRATION NUMBER: 22,685
55 : REFERENCE/DOCKET NUMBER:
56 : TELECOMMUNICATION INFORMATION:
57 : TELEPHONE: (703)684-1111
58 : TELEFAX: (703)684-1124
59 : INFORMATION FOR SEQ ID NO: 19:
60 : SEQUENCE CHARACTERISTICS:
61 : LENGTH: 5 amino acids
62 : TYPE: AMINO ACIDS
63 : TOPOLOGY: linear
64 : MOLECULE TYPE: peptide
65 : US-07-973-235A-19
66
67 Query Match 42.18; Score 24; DB 3; Length 5;
68 Best Local Similarity 100.0%; Pred. No. 2.5e+5;
69 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
70
71 QY 3 KHW 5

```

```

Db      3 KHW 5

RESULT 12
US-08-462-720-19
; Sequence 19, Application US/58462720
; Patent No. 5849701
; GENERAL INFORMATION:
; APPLICANT: Roberts, David D.
; APPLICANT: Krutzsch, Henry C.
; APPLICANT: Sipes, John M.
; APPLICANT: Guo, Neng-hua
; APPLICANT: Negre, Eric
; TITLE OF INVENTION: Peptide Inhibitors of Fibronectin and
; TITLE OF INVENTION: Related Collagen-Binding Proteins
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,720
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 0:5280-023110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2430
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO. 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MO-ECULE TYPE: peptide
US-08-462-720-19

Query Match 42.14; Score 24; DB 2; Length 5;
Best Local Similarity 100.00; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Cy      3 KHW 5
Db      3 KHW 5

RESULT 13
US-08-487-006-67
; Sequence 67, Application US/0847006
; Patent No. 5641861
; GENERAL INFORMATION:
; APPLICANT: Dooley, Colette T.
; APPLICANT: Houghten, Richard A.
; TITLE OF INVENTION: NO. 5641861: Mu Opioid Receptor Ligands:
; TITLE OF INVENTION: Agonists and Antagonists
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4170 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California

```

COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,066  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/SOCKET NUMBER: P-TP 1706  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 6  
OTHER INFORMATION: /note= "Amino acid is amidated at the C-terminal."  
US-08 487-006-67

Query Match 42.1%; Score 24; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
DB 4 KHW 6

RESULT 14  
US 08 488-659A 67  
Sequence 67, Application US/08488659A  
Patent No. 5919897  
GENERAL INFORMATION:  
APPLICANT: Dooley, Colette T.  
TITLE OF INVENTION: Mu Opioid Receptor Agonists  
TITLE OF INVENTION: Agonists and Antagonists  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4876 La Jolla Village Drive, Suite 100  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,659A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/SOCKET NUMBER: P-TP 1706  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 6  
OTHER INFORMATION: /note= "Amino acid is amidated at the C-terminal."  
US-08-488-659A-67

Query Match 42.1%; Score 24; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHW 5  
DB 4 KHW 6

RESULT 15  
US-08-877-605-172  
Sequence 172, Application US/08877605  
Patent No. 6582965  
GENERAL INFORMATION:  
APPLICANT: Robert Townsend  
APPLICANT: Raj Parekh  
APPLICANT: Sally Prime  
APPLICANT: Nick Webb  
TITLE OF INVENTION: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION  
FILE REFERENCE: 9195-004  
CURRENT APPLICATION NUMBER: US/08/877,605  
CURRENT FILING DATE: 1997-06-18  
NUMBER OF SEQ ID NOS: 353  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 172  
LENGTH: 6  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide X Library  
US-08-877-605-172

Query Match 42.1%; Score 24; DB 4; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 HMLSDR 9  
DB 1 HPIADR 6

Search completed: November 5, 2003, 17:36:11  
Job time : 13.333 secs

GenCore version 5.1.6  
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OM protein: protein search, using sw model

Run on: November 5, 2003, 17:29:45 : Search time 11 seconds  
(without alignment)  
27,426 Million cell updates/sec

Title: US-09 914-088-4  
Perfect score: 55  
Sequence: 1 GHTFEDSTKK 10  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0  
Maximum DB seq length: 10  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:  
1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	38.2	10	2 A60476	S-layer protein -
2	19	34.5	9	2 A31576	xylose isomerase (
3	17	30.9	8	2 S43971	tumor-associated a
4	17	30.9	8	2 S43972	tumor-associated a
5	17	30.9	8	2 I54812	transferrin
6	17	30.9	10	2 A27613	transferrin
7	16	29.1	5	2 S73615	transferrin
8	16	29.1	10	2 XGHE	transferrin
9	15	27.3	5	2 A26830	transferrin
10	15	27.3	8	2 A28719	transferrin
11	15	27.3	8	2 S69165	transferrin
12	15	27.3	9	2 A60427	transferrin
13	15	27.3	10	2 GXHJ1	transferrin
14	15	27.3	10	2 A59272	transferrin
15	15	27.3	10	2 A43977	transferrin
16	14	25.5	3	3 GXHJ	transferrin
17	14	25.5	4	2 PL0142	transferrin
18	14	25.5	4	2 I38888	transferrin
19	14	25.5	5	2 D6274	transferrin
20	14	25.5	6	2 A61419	transferrin
21	14	25.5	6	2 B56979	transferrin
22	14	25.5	7	2 S42407	transferrin
23	14	25.5	7	2 S68004	transferrin
24	14	25.5	8	2 D61512	transferrin
25	14	25.5	8	2 PH0803	transferrin
26	14	25.5	9	2 A24244	transferrin
27	14	25.5	9	2 S07205	transferrin
28	14	25.5	9	2 S07205	transferrin
29	14	25.5	9	2 S07241	transferrin

leader peptide - p  
Ig heavy chain CRD  
peptidylglycine mo  
D-amino-acid oxida  
leucosulfakinin-II  
streptopain (EC 3.  
neurotensin C - lau  
neurotensin C - bov  
cardioexcitatory n  
leucosulfakinin I;  
neurotensinpressin  
bothrostoxin - ja  
T-cell receptor be  
nuclease Bn1 (EC 3  
Fc epsilon RIIB -  
hypothalamic hepta

30 14 25.5 9 2 JQ1202  
31 14 25.5 9 2 PT0315  
32 14 25.5 9 2 A42266  
33 14 25.5 9 2 S39437  
34 14 25.5 10 1 GMRO12  
35 14 25.5 10 2 A61289  
36 14 25.5 10 2 PQ0177  
37 14 25.5 10 2 A60647  
38 14 25.5 10 2 A32543  
39 14 25.5 10 2 B60656  
40 14 25.5 10 2 A56633  
41 14 25.5 10 2 A30823  
42 14 25.5 10 2 PH0895  
43 14 25.5 10 2 A59173  
44 14 25.5 6 2 A46474  
45 14 23.6 7 1 NYPG7

RESULT 1  
A60476  
S-layer protein - Bacillus thuringiensis (fragment)  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1993 #sequence\_revision: 20-Feb-1993 #text\_change 12-Mar-1993  
C:Accession: A60476  
J. Lucke, M.D.; Beveridge, T.J.  
J. Lucke, M.D.; Beveridge, T.J.  
A:Title: Characterization of a dynamic S layer on Bacillus thuringiensis.  
A:Reference number: A60476; MIMD:90078111; PMID:2592346  
A:Accession: A60476  
A:Molecule type: protein  
A:Residues: 1-10 <LTC>  
C:Comment: The S-layer, or surface array, is the outermost component of several archae

# ALIGNMENTS

Query Match 38.2% Score 21; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. NC. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GHTFED 6  
DB 2 GHTFED 7

RESULT 2  
A31576  
xylose isomerase (EC 5.3.1.5), intracellular - Streptomyces sp. (fragment)  
C:Species: Streptomyces sp.  
C:Date: 31-Mar-1990 #sequence\_revision: 31-Mar-1990 #text\_change 28-Apr-1993  
C:Accession: A31576  
R. Pawar, H.S.; Kannan, K.; Srinivasan, M.C.; Vartak, H.G.  
Biochem. Biophys. Res. Commun. 155, 411-417, 1988  
A:Title: Purification and characterization of glucose (xylose) isomerase from Chainia  
A:Reference number: A31576; MIMD:88326335; PMID:3415697  
A:Contents: Chainia sp. NCL 82-5-1  
A:Accession: A31576  
A:Molecule type: protein  
A:Residues: 1-9 <PAW>  
C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 34.5% Score 19; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. NO. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 HTF 4  
DB 7 HTP 9

RESULT 3  
S43971  
tumor-associated antigen MUT1 - mouse

```

C:Species: Mus musculus (house mouse)
C>Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
C:Accession: S43971
R:Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.
Nature 369, 67-71, 1994
A:Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine
A:Reference number: S43971; PMID:8421781; PMID:8164742
A:Accession: S43971
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <MAK>
C:Superfamily: unassigned animal peptides

Query Match 30.9%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 FEQST 8
DB 1 FEQNT 5

RESULT 4
S43972
tumor-associated antigen MUT2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
C:Accession: S43972
R:Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.
Nature 369, 67-71, 1994
A:Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine
A:Reference number: S43971; PMID:9427811; PMID:8164742
A:Accession: S43972
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <XAN>
C:Superfamily: unassigned animal peptides

Query Match 30.9%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 FEQST 8
DB 1 FEQNT 5

RESULT 5
164832
Ca2+-transporting ATPase (EC 3.6.3.8) - rat thymus
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 19-Apr-2002
C:Accession: 164832
R:Yu, K.
Am. J. Physiol. 264, 333-341, 1993
A:Title: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase 1
A:Reference number: 151892
A:Accession: 164832
A>Status: preliminary; translated from GB/EWH/0062
A:Molecule type: mRNA
A:Residues: 1-8 <RES>
A:Cross-references: GB:M99223; NID:9203644; PID:MAA409001; PID:9203646
C:Genetics:
A:Gene: SERCA1b
C:Keywords: hydrolase

Query Match 30.9%; Score 17; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 EDSTKK 10
DB 3 EDENRR 8

RESULT 6
A27617
triase-phosphate isomerase (EC 5.3.1.1) - curled-leaved tobacco (fragment)
C:Species: Nicotiana glauca (curled-leaved tobacco)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 28-Apr-1993
C:Accession: A27617
R:Bauw, G.; De Loose, W.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4866-4870, 1987
A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino aci-
A:Reference number: A94167
A:Accession: A27617
A:Molecule type: protein
A:Residues: 1-10 <BAU>
C:Keywords: gluconeogenesis; glycolysis; intramolecular oxidoreductase; isomerase; pen-

Query Match 30.9%; Score 17; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHTF 4
DB 1 GRTP 4

RESULT 7
S70615
endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (fragm
N:Alternate names: xylanase
C:Species: Streptomyces sp.
A:Variety: Chainia sp. NCL 82.5.1
C>Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S70615
R:Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.
Biochem. J. 316, 771-775, 1996
A:Title: Structural environment of an essential cysteine residue of xylanase from Chai
A:Reference number: S70615; PMID:96265041; PMID:8670151
A:Accession: S70615
A:Molecule type: protein
A:Residues: 1-5 <RAO>
A:Experimental source: Chainia sp. strain NCJ 82.5.1
A>Note: the source is designated as Chainia sp.
C:Function:
A:Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans
A:Pathway: fermentation of hemicellulose into ethanol
C:Keywords: glycosidase; hydrolase

Query Match 29.1%; Score 16; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TFED 6
DB 2 TFSD 5

RESULT 8
XGHUE
erythrocyte membrane glycopeptide - human
C:Species: Homo sapiens (man)
C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A03187
R:Weiss, J.B.; Lote, C.J.; Bobinski, H.
Nature New Biol. 234, 25-26, 1971
A:Title: New low molecular weight glycopeptide containing triglycosylcysteine in humar
A:Reference number: A03187; PMID:72034940; PMID:528658
A:Accession: A03187
A:Molecule type: protein
A:Residues: 1-10 <WEI>
C:Comment: The identity of the glycoprotein from which this peptide is derived is unkn
found (see PIR:XGHJEC).
C:Superfamily: unassigned animal peptides

```

C:Keywords: glycoprotein  
F:1/Binding site: carbohydrate (Cys) (covalent: #status experimental:

Query Match 29.1%; Score 16; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.7e+03;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY : GHTE 5  
DB : 3 GHSHD ?

## RESULT 9

A6830  
metosis inhibiting peptide - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Nov-1988 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C:Accession: A6830  
R:Reichelt, K.; Elgjo, K.; Edmonson, P.D.;  
Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987  
A:Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.  
A:Reference number: A26830; MUID:87298602; PMID:3619940  
A:Accession: A26830  
A:Molecule type: protein  
A:Residues: 1-5 <REL>  
C:Superfamily: unassigned animal peptides  
C:Keywords: blocked amino end; pyroglutamic acid  
F:1/Modified site: pyroglutamic acid (Gln) #status experimental:

Query Match 27.3%; Score 15; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EDS 7  
DB 2 EDS 4

## RESULT 10

A28719  
thymic humoral factor gamma-2 - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1999 #text\_change 18-Jun-1993  
C:Accession: A28719  
R:Burstein, Y.; Buchner, V.; Pecht, M.; Trainin, N.;  
Biochemistry 27, 4066-4071, 1988  
A:Title: Thymic humoral factor gamma-2: purification and amino acid sequence of an immun  
A:Reference number: A28719; MUID:88326320; PMID:3261994  
A:Accession: A28719  
A:Molecule type: Protein  
A:Residues: 1-8 <PUR>

Query Match 27.3%; Score 15; DB 2; Length 3;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 EDSK 9  
DB 2 EDGPK 6

## RESULT 11

S69165  
ferredoxin a2 - Japanese radish (fragment)  
C:Species: Kaiware daikon (Japanese radish)  
C:Date: 10-Mar-1998 #sequence\_revision 10-Mar-1998 #text\_change 17-Apr-1998  
C:Accession: S69165  
R:Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shim, M.;  
Arch. Biochem. Biophys. 316, 797-802, 1995  
A:Title: Four ferredoxins from Japanese radish leaves.  
A:Reference number: S69164; MUID:95168667; PMID:7864635  
A:Accession: S69165  
A:Molecule type: protein

A:Residues: 1-8 <OBA>

C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 27.3%; Score 15; DB 2; Length 8;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HTFED 6  
DB 2 HREED 6

## RESULT 12

A60427  
macrophage cytotoxicity-inducing factor, 29K - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Jun-1993  
C:Accession: A60427  
R:Jones, C.M.; Prince, C.A.; Williams, J.S.;  
Exp. Hematol. 19, 704-709, 1991  
A:Title: Purification and amino acid analysis of a human macrophage cytotoxicity-induc  
A:Reference number: A60427; MUID:91372335; PMID:1909970  
A:Accession: A60427  
A:Molecule type: protein  
A:Residues: 1-9 <JON>  
A:Note: the sequence from the text on page 706 is inconsistent with that from page 708  
C:Keywords: cytokine

Query Match 27.3%; Score 15; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EDS 7  
DB 6 EDS 8

## RESULT 13

GXHU:  
gastric juice peptide - human  
C:Species: Homo sapiens (man)  
C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C:Accession: A01628  
R:Heathcote, J.G.; Washington, R.J.;  
Int. J. Protein Res. 2, 117-126, 1970  
A:Title: Peptides of normal human gastric juice.  
A:Reference number: A01628; MUID:75150968; PMID:5538395  
A:Accession: A01628  
A:Molecule type: protein  
A:Residues: 1-10 <HEA>  
A:Note: a second peptide lacking 1-Leu, but otherwise identical in composition with th  
C:Superfamily: unassigned animal peptides  
C:Keywords: stomach

Query Match 27.3%; Score 15; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EDS 7  
DB 7 EDS 9

## RESULT 14

A59272  
peptide-N4- (N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, large chain  
N:Alternate names: peptide N-glycosidase  
C:Species: Prunus dulcis var. sativa (sweet almond)  
C:Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 19-May-2000  
C:Accession: A59272  
R:Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.;  
Eur. J. Biochem. 252, 118-123, 1998  
A:Title: Characterisation of peptide-N4- (N-acetyl-beta-glucosaminyl) asparagine amidase

A:Reference number: A59272; MUID:98181894; PMID:9523720

A:Accession: A59272

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <ALT>

C:Keywords: hydrolase

Query Match 27.3%; Score 15; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 1e+04;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFD 6

DB 6 HSWAD 10

#### RESULT 15

A43977

PMRFamide-like protein - tobacco hornworm

C:Species: Manduca sexta (tobacco hornworm)

C>Date: 11-Feb-1993 #sequence\_revision 11-Feb-1993 #text change 17-Mar-1999

C:Accession: A43977

R:Kingsan, T.G.; Teplow, D.B.; Phillips, J.M.; Rehm, J.P.; Rao, K.R.; Hildebrand, J.G.;

Peptides 11, 849-856, 1990

A:Title: A new peptide in the PMRFamide family isolated from the CNS of the hawkmoth, Ma

A:Reference number: A43977; MUID:91045350; PMID:2235684

A:Accession: A43977

A:Molecule type: protein

A:Residues: 1-10 <K1N>

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyroglutamic acid (Gln); #status experimental

F:10/Modified site: amidated carboxyl end (Pro); #status experimental

Query Match 27.3%; Score 15; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HTF 4

DB 5 HSF 7

Search completed: November 5, 2003, 17:35:21

^Gb time : 11 secs



GenCore version 5.1.6  
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QM protein: protein search, using sw mode:

Run on: November 5, 2003, 17:23:40 : Search time 7.3343 seconds  
(without alignments)  
64.127 Million cell updates/sec

Title: US-09-914-088-4

Perfect score: 55

Sequence: 1 GHTFEDSTKK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scatched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 1:2

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	21	38.2	1	SLAP_BACTG
2	19	34.5	9	XYLA_STRSQ
3	17	30.9	10	TPIS_NICPL
4	17	30.9	10	UPA7_HUMAN
5	16	29.1	10	GLEM_HUMAN
6	15	27.3	10	FARP_VANSE
7	15	27.3	10	GATJ_HUMAN
8	15	27.3	10	SPI_EALRC
9	14	25.5	3	GRAM_HUMAN
10	14	25.5	4	DMPL_PSECH
11	14	25.5	9	LITO_LITAU
12	14	25.5	9	LITR_PHYRC
13	14	25.5	9	NSKI_SABRU
14	14	25.5	10	AVEN_BELAY
15	14	25.5	10	FARP_LOCM
16	14	25.5	10	GRP_FANRC
17	14	25.5	10	LCMS_LEIMA
18	14	25.5	10	LSK2_LEIMA
19	13	23.6	7	HV7_PIG
20	13	23.6	7	UC22_VAIZE
21	13	23.6	8	ALL5_CYDPO
22	13	23.6	8	ANG2_SOTTA
23	13	23.6	9	FLA2_TREHY
24	13	23.6	9	PPK1_PERRA
25	13	23.6	10	ANG1_BCTJA
26	13	23.6	10	ANGT_BOVIN
27	13	23.6	10	ANGT_CHICK
28	13	23.6	10	ESTA_SCHGA
29	13	23.6	10	TKNK_FIG
30	13	23.6	10	UPA9_HUMAN
31	12	21.8	8	RT34_BOVIN
32	12	21.8	9	FARP_VANSE
33	12	21.8	10	COXO_RAT

P42560 mytilus edu  
P81545 dictyosteli  
P30090 homo sapien  
P35904 achatina fu  
P13071 citrobacter  
P80628 zea mays (m  
P41966 moniezia ex  
P14595 tabanus atr  
P04549 periplaneta  
P81152 mycobacteri  
P30096 homo sapien  
P83195 perkinsus a

ALIGNMENTS

RESULT 1  
SLAP\_BACTG STANDARD; PRT: 10 AA.  
ID SLAP\_BACTG  
AC P49325;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE S-layer Protein (Surface layer protein) (Fragment).  
OS Bacillus thuringiensis (Subsp. Gallieriae).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
CX NCBI\_TaxID=23338;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=NPRL 4045;  
RX MEDLINE=90078111; PubMed=2592346;  
RA Luckeivich M.D., Beveridge T.J.;  
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";  
RL J. Bacteriol. 171:6656-6667(1989).  
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.  
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH OBLIQUE (P2) SYMMETRY.  
DR P.R. A60476; A60476.  
KW Cell wall; S-layer.  
FT NON TER  
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;  
Query Match 38.2%; Score 21; DB 1; Length 10;  
Best Loca: Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY : GHTFED 5  
Db 2 GHTFED 7

RESULT 2  
XYLA\_STRSQ STANDARD; PRT: 9 AA.  
ID XYLA\_STRSQ  
AC P19149;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Xylose isomerase (EC 5.3.1.5) (Fragment).  
GN XYLA.  
OS Streptomyces sp. (strain NC 82-5-1).  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycetaceae; Streptomycetaceae; Streptomyces.  
CX NCBI\_TaxID=1931;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=88126315; PubMed=3415697;  
RA Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.;  
RT "Purification and characterisation of glucose (xylose) isomerase from  
RT Chaetia sp. (NC 82-5-1)."  
RL Biochem. Biophys. Res. Commun. 155:411-417(1989).

CC 1 FUNCTION: Involved in D-xylose catabolism.  
 CC 2 CATABOLIC ACTIVITY: D-xylose = D-xv:ulose.  
 CC 3 COFACTOR: Binds 2 magnesium ions per subunit (Parental).  
 CC 4 SUBUNIT: Homotrimer.  
 CC 5 SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.  
 DR PIR: A11576; A11576.  
 DR HAMAP: MF02455; 1.  
 DR InterPro: IPR001998; Xylose isom.  
 DR PROSITE: PS01721; XYLOSE\_ISOMERASE\_1; PARTIAL.  
 DR PROSITE: PS01731; XYLOSE\_ISOMERASE\_2; PARTIAL.  
 KW Isomertase; Pentose shunt; Xylose metabolism; Metal binding; Vaguestum.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 983 MW; F64BA1BDC5897D1 CRC64;

Query Match 34.5%; Score 19; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HTF 4

DB 7 HTF 9

RESULT 3  
 TP15\_NICPL STANDARD; PRT: 10 AA;  
 AC P19418;  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Triosephosphatase)  
 OS Nicotiana glaucaefolia (Leadwort-leaved tobacco)  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 CC Asteridae; Lamiaceae; Solanaceae; Solanaceae; Nicotiana  
 FT NON\_TER 11  
 SQ SEQUENCE 10 AA; 1140 MW; 82E9D1362C099D CRC64;  
 RA Baw G., de Loose M., Inze D., van Montagu M., Van der Krieke J.  
 RE "Alterations in the phenotype of plant cells studied by NMR terminal  
 RE amino acid-sequence analysis of proteins electroeluted from two  
 RE dimensional gel-separated total extracts."  
 RI Proc. Natl. Acad. Sci. U.S.A. 84:4896-4899 (1987)  
 CC 1 CATABOLIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate  
 CC 2 PATHWAY: Plays an important role in several metabolic pathways.  
 CC 3 SUBUNIT: Homotrimer.  
 CC 4 SUBCELLULAR LOCATION: Cytoplasm; Plastid.  
 CC 5 MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TIM: CYTOSOLIC AND PLASTID.  
 CC 6 SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.  
 DR PIR: A27617; A27617.  
 DR InterPro: IPR000652; Triosephosphatase  
 DR PROSITE: PS01717; TIM; PARTIAL.  
 KW Isomertase; Glycolysis; Gluconeogenesis; Early glycolysis/synthesis;  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1140 MW; 82E9D1362C099D CRC64;

Query Match 30.9%; Score 17; DB 1; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HTF 4

DB 1 HTF 4

RESULT 4  
 URAT\_HUMAN STANDARD; PRT: 10 AA;  
 AC P14931;  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DE Uracilase  
 OS Homo sapiens (Human)  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1140 MW; 82E9D1362C099D CRC64;

DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of red blood cells (Spot 2D-036HC)  
 DE (fragment)  
 OS Homo sapiens (Human)  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Erythrocyte;  
 RA Goiaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,  
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer G.,  
 RA Balant L., Hochstrasser D.F.;  
 RL Submitted (FEB-1994) to the SWISS PROT data bank  
 CC 1 MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN  
 CC PROTEIN IS: 4.77, ITS MW IS: 26 KDa.  
 DR SWISS-2DPAGE; P34990; HUMAN  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1161 MW; F72D82E9C44B1871 CRC64;

Query Match 30.9%; Score 17; DB 1; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HTFED 6

DB 4 GENPXD 9

RESULT 5  
 GLEM\_HUMAN STANDARD; PRT: 10 AA;  
 ID P02728;  
 AC P02728;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Erythrocyte membrane glycoprotein  
 OS Homo sapiens (Human)  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE:72014940; PubMed:5256858;  
 RA Weiss C.B., Lote C.C., Borinski H.;  
 RE "New low molecular weight glycoprotein containing triglucoylcysteine  
 RE in human erythrocyte membrane."  
 RL Nature New Biol. 244:25-26 (1973)  
 CC 1 MISCELLANEOUS: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS  
 CC PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN  
 CC ATTRIBUTED.  
 DR PIR: A01187; XGHUE.  
 DR Glycoprotein; Erythrocyte.  
 FT CARBOHYD 1  
 SQ SEQUENCE 10 AA; 1049 MW; 235EFEEA1F581E8 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 10;  
 Best Local Similarity 40.0%; Pred. No. 2.4e+03;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HTF 5

DB 3 GRSHD 7

RESULT 6  
 FARP\_MANSE STANDARD; PRT: 10 AA;  
 AC F14931;  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DE Farp  
 OS Homo sapiens (Human)  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1140 MW; 82E9D1362C099D CRC64;



AT 119016;  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (AA)  
 DR Cofactor: NAD<sup>+</sup> (Fragment)  
 GN CytC  
 GS Pseudomonas carboxydhydrogena  
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 CC Bradyrhizobiaceae  
 CC NCBI\_TaxID=229;  
 RN  
 RP SEQUENCE  
 RX MEDLINE=90055478; PubMed=2819128;  
 RA Kraut M., Hugendrick L., Herwig S., Meyer G.,  
 PT "Homology and distribution of CO dehydrogenase structural genes in  
 PT carboxydotrophic bacteria."  
 RI Arch. Microbiol. 152:335-341(1999)  
 CC  
 CC FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
 CC dioxide.  
 CC CATALYTIC ACTIVITY: CO + H<sub>2</sub>O + acceptor + CO<sub>2</sub> + reduced  
 CC acceptor.  
 CC COFACTOR: Molybdenum (polypyrroline)  
 CC SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND  
 CC SMALL.  
 DR PIR: P01410; P01410.  
 KW Oxidoreductase, Molybdenum.  
 FT MCD RES 4  
 FT NCN TER 4  
 SQ SEQUENCE 4 AA; 441 MW; 776187650000000 CRC64;  
  
 Query Match: 25.5%; Score 14; DB 1; Length 4;  
 Best local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 CH 2  
 DB 1 CH 3  
  
 RESULT 11  
 LITR PHVRO STANDARD; PRT; 9 AA  
 AC P08975;  
 DT 01-NOV-1999 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Litorin.  
 OS Litoria aurea (Green and golden bell frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Anura; Batrachia;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 CC Pelodytidae; Litoria.  
 CC NCBI\_TaxID=8377  
 RN  
 RP SEQUENCE  
 RX MEDLINE=75187311; PubMed=1140241;  
 RA Anastasi A., Erspamer V., Endeat P.  
 PT "Amino acid composition and sequence of litorin, a neuropeptide-like  
 PT nonapeptide from the skin of the Australian leopards frog  
 PT Litoria aurea."  
 RI Experientia 31:1259-1269(1977)  
 CC  
 CC FUNCTION: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 CC TISSUE: Skin secretion;  
 CC MEDLINE=78053546; PubMed=908397;  
 RA Anastasi A., Montecucci P.C., Angelelli P., Erspamer V., Endeat P.,  
 PT "Glu(Glu)litorin, the second bombesin-like peptide identified in the  
 PT carboxyl extracts of the skin of the Australian leopards frog  
 PT Litoria aurea."  
 RI Experientia 31:1259-1269(1977)  
 CC  
 CC SUBCELLULAR LOCATION: Secreted.  
 CC TISSUE SPECIFICITY: Skin.  
 CC SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.

PIR: S07204; S07204;  
 DR InterPro: IPR000874; Bombesin.  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 KW Amphibian defense peptide; Bombesin family; Amidation; Methylation;  
 KW Pyroglutamate carboxylic acid; Pyroglutamate carboxylic acid.  
 FT MCD RES 1  
 FT MCD RES 2  
 FT MCD RES 9  
 FT AMIDATION.  
 SQ SEQUENCE 9 AA; 1103 MW; D7CC01862C0C366 CRC64;  
  
 Query Match: 25.5%; Score 14; DB 1; Length 9;  
 Best local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 CH 2  
 DB 6 CH 7  
  
 RESULT 12  
 LITR PHVRO STANDARD; PRT; 9 AA  
 AC P08975;  
 DT 01-NOV-1999 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Rhodelitorin.  
 OS Phyllomedusa rohdei (Rohde's leaf frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 CC Phyllomedusinae; Phyllomedusa.  
 CC NCBI\_TaxID=8394;  
 RN  
 RP SEQUENCE  
 RX MEDLINE=95127565; PubMed=3838283;  
 RA Bairra D., Erspamer G.F., Simpraco M., Bossa F., Melchiorri P.,  
 RA Erspamer V.  
 RT "Rhodelitorin: a new peptide from the skin of Phyllomedusa rohdei".  
 RL FEBS Lett. 362:53-56(1995).  
 CC  
 CC SUBCELLULAR LOCATION: Secreted.  
 CC TISSUE SPECIFICITY: Skin.  
 CC SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 CC PIR: S07241; S07241.  
 DR InterPro: IPR000874; Bombesin.  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 KW Amphibian defense peptide; Bombesin family; Amidation;  
 KW Pyroglutamate carboxylic acid; Pyroglutamate carboxylic acid.  
 FT MCD RES 1  
 FT MCD RES 9  
 FT AMIDATION.  
 SQ SEQUENCE 9 AA; 1092 MW; 4ECC01861AC377 CRC64;  
  
 Query Match: 25.5%; Score 14; DB 1; Length 9;  
 Best local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 CH 2  
 DB 6 CH 7  
  
 RESULT 13  
 NSKI SARPBU STANDARD; PRT; 9 AA  
 ID NSKI SARPBU  
 AC P41492;  
 DT 01-NOV-1995 (Rel. 42, Created)  
 DT 01-NOV-1995 (Rel. 42, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Neosulfakian I. (NSK-I).  
 CC Salicetraga bullata (Grey fleshy) (Neobellieria bullata).

CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Cecidomyiidae;  
 CC Sarcophagidae; Sarcophaga.  
 CX NCBI TaxID:7186;  
 RN 1-1  
 RP SEQUENCE  
 RC TISSUE=Heart;  
 RX MEDLINE=3308111; PubMed=1350367;  
 RA Faculty A., Schoofs L., Proost P., Van Damme D., de Loof A.;  
 RT "Isolation and primary structure of two sulfakinin-like peptides from  
 the housefly, *Musca domestica* L.";  
 PI Comp. Biochem. Physiol. 133C:135-142(1992).  
 CC 1- FUNCTION: MYOTROPIC PEPTIDE  
 CC 1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLESTYRILIN FAMILIES  
 CC INTERFERON (PEPTIDIC); Gastrin.  
 DR PROSITE: PS00259; GASTRIN, 1.  
 KW Neuropeptide; 4 4 SULFATION (POTENTIAL)  
 FT XIC RES 9 9 AMIDATION (POTENTIAL)  
 SQ SEQUENCE 9 AA; 1197 MW; 880AC691E8E6AAA CRC64;

Query Match 25.5%; Score 14; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1 GH 2  
 DB 5 GH 6

RESULT 14  
 AMPN HELAM STANDARD; PRT: 10 AA  
 AC F81731;  
 DT 30 MAY 2000 (Rel. 39, Last sequence update);  
 DT 30 MAY 2000 (Rel. 39, Last annotation update);  
 DT 28-FEB-2001 (Rel. 41, Last annotation update);  
 LE Aminopeptidase N (EC 3.4.11.2) (CYP1A1) receptor fragment;  
 CS Helicoverpa armigera (cotton bollworm);  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Noctuidae;  
 CC Noctuidae; Heliothinae; Helicoverpa.  
 CX NCBI TaxID:29056;  
 RN 1-1  
 RP SEQUENCE  
 RC TISSUE=Midgut;  
 RA Indle S.S., Tripathi N., Prasad R., Rao K.K., Chaitan R.S.;  
 PT "Aminopeptidase N as a receptor for *Battus thurinus* Cytine  
 toxin from *Helicoverpa armigera*.";  
 RI Submitted (MAR-1999) to the SWISS PRO database;  
 CC 1- FUNCTION: ACTS AS A RECEPTOR FOR BUTTERFLY CYPINE  
 CC 1- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa,  
 Xbb from a peptide, amide or amide, and is followed by Ala, Ser  
 may be most amino acids including proline which when a  
 terminal hydrophobic residue is followed by a phenyl residue, the  
 two may be released as an intact Xaa-pro dipeptide;  
 CC 1- COFACTOR: Binds 1 zinc ion (5% similarity);  
 CC 1- SIMILARITY: Belongs to peptidase family M;  
 DR InterPro: IPR006295; Zn\_MTPeptide;  
 DR PROSITE: PS0142; ZINC\_PROTEASE; PARTIAL;  
 KW Hydrolase; Metalloprotease; Aminopeptidase, Zinc;  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1093 MW; 05042E8B7B11F1F8A CRC64;

Query Match 25.5%; Score 14; DB 1; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 5.8e-03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 2 HTFDS 7  
 DB 3 YTHEGS 8

RESULT 15  
 FARP LOCMI STANDARD; PRT: 10 AA  
 AC P38553;  
 DT 01-OCT-1994 (Rel. 30, Created);  
 DT 01-OCT-1994 (Rel. 30, Last sequence update);  
 DT 30-MAY-2003 (Rel. 39, Last annotation update);  
 DE Schistoflavinamide (FVDFHFLRF-amide, [cardioexcitatory neuropeptide];  
 CS Locusta migratoria migratoria locust), and  
 CS Schistocerca gregaria (Desert locust);  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthoptera; Acrididae; Caelifera; Acridomorpha;  
 CC Acridoidea; Acrididae; Caelifera; Caelifera; Acridomorpha;  
 CX NCBI TaxID:7004; M10;  
 RN 1-1  
 RP SEQUENCE  
 RC SPECIES=Locust; TISSUE=Brain;  
 RX MEDLINE=9324430; PubMed=7487352;  
 RA Schoofs L., Roelofs G.M., Faemken H., Veelaert D., Amelinkx M.,  
 RA de Loof A.;  
 RT "Isolation, identification, and synthesis of FVDFHFLRFamide  
 (Schistoflavinamide) in *Locusta migratoria* and its association with the  
 male accessory glands, the salivary glands, the heart, and the  
 oviduct.";  
 RL Peptides 14:409-421(1993).  
 RN 1-1  
 RP SEQUENCE  
 RC SPECIES=S. gregaria; TISSUE=Thoracic nervous system;  
 RX MEDLINE=9324433; PubMed=2719702;  
 RA Robb S., Packman J.C., Evans P.D.;  
 RT "Isolation, primary structure and bioactivity of schistoflavinamide, a  
 FMRF-amide-like neuropeptide from the locust, *Schistocerca*  
 gregaria.";  
 RL Biochem. Biophys. Res. Commun. 163:850-856(1989).  
 CC 1- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL  
 CC OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND  
 CC OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.  
 CC 1- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS,  
 CC THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.  
 CC 1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR PIR: A32543; A32543;  
 KW Neuropeptide; Amidation.  
 FT MOD RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 25.5%; Score 14; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 5.8e-03;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 2 HCF 4  
 DB 5 HVF 7

Search completed: November 5, 2003, 17:33:04  
 Job time : 7.3333 secs

GenCore version 5.1.6  
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Query protein protein search, using sw mode:

Run on: November 5, 2003, 17:33:05 / Search time 26 Seconds  
Without alignments:  
99.251 Million cell updates/sec

Title: US-09-914-088-4  
Perfect score: 55  
Sequence: 1 GHTFADSTK 10

Scoring table: E-6SJM62  
Gapop 10.0, Gapext 0.5

Searched: 83525 seqs, 25852604 residues

Total number of hits satisfying chosen parameters: 1319

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mbs.\*
- 8: sp\_organalle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertibrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. Num is the number of results predicted by chosen parameters  
score greater than or equal to the score of the best hit being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	length	DB	ID	Description
1	20	36.4	7	10	P82445	P82445 nicotiana t
2	18	32.7	10	2	Q93002	Q93002 escherichia
3	18	32.7	10	15	Q8UT83	Q8UT83 human immun
4	17	30.9	9	12	Q93622	Q93622 muray val
5	16	29.1	8	2	Q95950	Q95950 bacillus su
6	16	29.1	8	13	Q90204	Q90204 tulica leuc
7	16	29.1	9	2	Q93E20	Q93E20 streptococc
8	16	29.1	9	4	Q96F97	Q96F97 homo sapien
9	16	29.1	10	2	Q8VN85	Q8VN85 helicobacte
10	15	27.3	8	2	Q93SH0	Q93SH0 staphylococ
11	15	27.3	8	4	Q93J50	Q93J50 homo sapien
12	15	27.3	8	4	Q92PK3	Q92PK3 homo sapien
13	15	27.3	8	11	Q62034	Q62034 ratius norv
14	15	27.3	9	11	Q8CG34	Q8CG34 bacillus norv
15	15	27.3	10	2	Q42561	Q42561 escherichia
16	15	27.3	10	5	P82445	P82445 nicotiana t

17	15	27.3	10	6	Q9TU33	Q9TU33 canis fami
18	15	27.3	10	10	P81899	P81899 prunus dulc
19	15	27.3	10	13	Q9PRY8	Q9PRY8 triakis scy
20	14	25.5	9	2	Q51349	Q51349 pseudomonia
21	14	25.5	9	2	Q47410	Q47410 escherichia
22	14	25.5	9	4	Q14277	Q14277 homo sapien
23	14	25.5	9	11	Q89799	Q89799 mus musculu
24	14	25.5	10	2	Q9R7J9	Q9R7J9 helicobacte
25	14	25.5	10	3	Q9UW42	Q9UW42 schizopyl
26	14	25.5	10	4	Q81Z42	Q81Z42 homo sapien
27	14	25.5	10	6	Q9TRS3	Q9TRS3 sus scrofa
28	14	25.5	10	6	Q95NB1	Q95NB1 eulemur fu
29	14	25.5	10	6	Q95MR0	Q95MR0 eulemur fu
30	14	25.5	10	6	Q8M552	Q8M552 eulemur fu
31	14	25.5	10	8	P82136	P82136 spinacia o
32	14	25.5	10	10	Q9FS93	Q9FS93 silene pent
33	14	25.5	10	10	Q95936	Q95936 beta vulgar
34	14	25.5	10	10	P82434	P82434 nicotiana t
35	14	25.5	10	11	Q8V118	Q8V118 mus musculu
36	13	23.6	6	10	P82541	P82541 spinacia o
37	13	23.6	7	2	P70804	P70804 azotobacter
38	13	23.6	8	2	Q45615	Q45615 bacillus su
39	13	23.6	8	2	Q9SL7	Q9SL7 clostridium
40	13	23.6	8	2	P83156	P83156 anabaena sp
41	13	23.6	8	4	Q9HCQ3	Q9HCQ3 homo sapien
42	13	23.6	8	6	Q9T778	Q9T778 canis fami
43	13	23.6	8	8	Q36898	Q36898 nicotiana p
44	13	23.6	8	11	Q9ER32	Q9ER32 mus musculu
45	13	23.6	9	11	Q8CJ03	Q8CJ03 mus musculu

## ALIGNMENTS

RESULT 1  
P82445 PRELIMINARY: PPT: 7 AA.  
AC P82445  
DT 01-JUN-2000 (TREMBUREL, 14, Created)  
DT 01-JUN-2000 (TREMBUREL, 14, last sequence update)  
DT 01-JUN-2000 (TREMBUREL, 14, last annotation update)  
DE 10 kDa cell wall protein (Fragment)  
OS Nicotiana tabacum (Common tobacco)  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.  
OX NCBI TaxID=4037;  
RN 1;  
RP SEQUENCE.  
RC STRAIN: CV, PETIT HAVANA,  
RA Pile K.A., Borth V.A., Marchell G.P., Robertson D., Slabas A.P.,  
RA Wotaszek P., Bolwell G.P.;  
PT "Proteomic study of secondary cell wall proteins from transformed  
RT tobacco culture";  
RL Plantae CO-022001;  
CC 11- SUPPLEMENTARY LOCATION: CELL, WALL.  
CC 11- ISSUE SPECIFICITY: XYLEM.  
KW Cell wall.  
FT NON TER  
SC SEQUENCE 7 AA; 758 MW; 637231EH62D1E2AC CRC64;

Query Match: 36.4%; Score 20; DB 10; Length 7;  
Best Local Similarity: 75.0%; Pred. No. 8.3e+05;  
Matches: 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHTF 4

DB 4 GHTF 7

RESULT 2

Q93002 PRELIMINARY: PPT: 10 AA.  
ID Q93002

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AC Q93072.
BT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae
OX NCBI_TaxID 93344
RN [1]
RP SEQUENCE FROM N.A.
RA Miyamoto T., Ichioika N., Sasaki T., Koyashi H., Hagan A., Ito M.,
RA Harano S.
RT "PCR assay using primers amplify the DNA region specific to
RT Escherichia coli O157:H7."
RL Submitted (MAY 2001) to the EMBL/GenBank/CDL databases
DR EMBL: AB061018, SRA047190.1; F04408A404D5A6 (F044)
SQ SEQUENCE 10 AA; 1216 MW; 5F34408A404D5A6 (F044)

Query Match 32.7% Score 18; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 4; 05;
Matches 3; Conservative 2; Mismatches 2; Indels 1; Gaps 0;

QY 4 TRDSTK 3
DB 4 SPDSPE 10

RESULT 5
Q939E0 PRELIMINARY; PRT; 10 AA
AC Q939E0;
DT 01-MAY-2003 (TREMBlrel. 20, Created)
DT 01-MAY-2003 (TREMBlrel. 20, Last sequence update)
DT 01-MAY-2003 (TREMBlrel. 22, Last annotation update)
DE Stage V sporulation protein E (Fragment)
GN SPOVE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=168;
RX MEDLINE=93004529; PubMed:1391353;
RA Henriques A.C., de Lencastre H., Piguet P.C.;
RA "A Bacillus subtilis morphogene cluster that includes spoVE is
RT homologous to the mia region of Escherichia coli."
RL Biochimie 74:735-748(1992)
DR EMBL: X64256; CAA45561.1;
FT NCN CTR 8
SQ SEQUENCE 8 AA; 893 MW; E875A1A13521B1A6 (C6C64);

Query Match 35.1% Score 16; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4; 05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 STKK 10
DB 2 TTKK 5

RESULT 6
Q90ZV5 PRELIMINARY; PRT; 8 AA
AC Q90ZV5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Adenylate kinase (Fragment)
OS Fulica leucoptera.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Rallidae; Fulica.
OX NCBI_TaxID=156755;
RN [1]
RP SEQUENCE FROM N.A.
RA Shapiro L.H., Durracher J.P.;
RA "Adenylate kinase action by a new nuclear locus for avian
RT systematics."

```

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OX NCBI_TaxID=11079;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88118912; PubMed:2828633;
RA Hahn C.S., Hahn Y.S., Rice C.M., Lee E., Dalgarno L., Strauss E.G.,
RA Strauss C.H.;
RT "Conserved elements in the 3' untranslated region of flavivirus RNAs
RT and potential cyclization sequences."
RL C. Mol. Biol. 168:33-41(1997)
DR EMBL: M35172; AAA66627.1;
KW Hypothetical protein.
FT NONTER 1
SQ SEQUENCE 9 AA; 1055 MW; FF36D40AAB05A2C1 (C6C64);

Query Match 30.9% Score 17; DB 12; Length 9;
Best Local Similarity 62.0%; Pred. No. 4; 05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 HIFEC 6
DB 2 HVSEC 6

RESULT 5
Q9R9E0 PRELIMINARY; PRT; 8 AA
AC Q9R9E0;
DT 01-MAY-2003 (TREMBlrel. 13, Created)
DT 01-MAY-2003 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2003 (TREMBlrel. 13, Last annotation update)
DE Stage V sporulation protein E (Fragment)
GN SPOVE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=168;
RX MEDLINE=93004529; PubMed:1391353;
RA Henriques A.C., de Lencastre H., Piguet P.C.;
RA "A Bacillus subtilis morphogene cluster that includes spoVE is
RT homologous to the mia region of Escherichia coli."
RL Biochimie 74:735-748(1992)
DR EMBL: X64256; CAA45561.1;
FT NCN CTR 8
SQ SEQUENCE 8 AA; 893 MW; E875A1A13521B1A6 (C6C64);

Query Match 35.1% Score 16; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4; 05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 STKK 10
DB 2 TTKK 5

RESULT 6
Q90ZV5 PRELIMINARY; PRT; 8 AA
AC Q90ZV5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Adenylate kinase (Fragment)
OS Fulica leucoptera.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Rallidae; Fulica.
OX NCBI_TaxID=156755;
RN [1]
RP SEQUENCE FROM N.A.
RA Shapiro L.H., Durracher J.P.;
RA "Adenylate kinase action by a new nuclear locus for avian
RT systematics."

```

RL AAK116248-255(2001);  
 DR EMBL: AF307898; AAK41537.1; --  
 KW Kinase.  
 FT NON TER 1  
 FI NFN TER 8

SQ SEQUENCE 9 AA; 994 MW; 9633300CELE1966 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 9;  
 Best Local Similarity 42.9%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

CY 1 GHTPE 5  
 DB 2 GHTPE 6

## RESULT 7

ID Q91E20 PRELIMINARY; PRT; 9 AA.  
 AC Q91E20 (TREMUREL. 19, Created)  
 DT 01-DEC-2001 (TREMUREL. 19, Last sequence update)  
 DE ScpB (Fragment).  
 GN SCpB.  
 OS Streptococcus agalactiae.  
 CC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 CC Streptococcus.  
 CX NCBI\_TaxID:1311;  
 RN [1]  
 PP SEQUENCE FROM N.A.  
 RC STRAIN=6907;  
 RX MEDLINE:21454698; PubMed:1532154;  
 RA Franken C., Haase G., Brandt C., Weber-Heymann J., Martin S.,  
 Lamber C., Podilelski A., Lutticken R., Spellerberg H.,  
 RT "Horizontal gene transfer and host specificity of beta-haemolytic  
 ST streptococci: the role of a putative composite transposon containing  
 FT scpB and lmb." 4:925-935(2001).  
 RL NCBI\_Microbiol. 4:925-935(2001).  
 DR EMBL: AF327852; AAL10713.1; --  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 1146 MW; 54371AB1326C401 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 9;  
 Best Local Similarity 50.3%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 5 DSTKK 10  
 DB 4 QSTTK 9

## RESULT 8

ID Q96P97 PRELIMINARY; PRT; 9 AA.  
 AC Q96P97 (TREMUREL. 19, Created)  
 DT 01-DEC-2001 (TREMUREL. 19, Last sequence update)  
 DE Reptin52 protein (Fragment).  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID:9606;  
 RN [1]  
 PP SEQUENCE FROM N.A.  
 RA Kang H.S., Park Y.C., Jung H.M., Jun D.Y., Suh T.H., Kim Y.H.;  
 RT "Characterization of TPA-responsive genes in U937 cells using ordered  
 PL differential display PCR.";  
 DR EMBL: AF401216; AALC2172.1; --  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 961 MW; 5CDDAA651A1187A CRC64;

Query Match 29.1%; Score 16; DB 4; Length 9;  
 Best Local Similarity 42.9%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

CY 1 GHTPDS 7  
 DB 3 GHTPDS 9

## RESULT 9

ID Q8VN85 PRELIMINARY; PRT; 10 AA.  
 AC Q8VN85 (TREMUREL. 20, Created)  
 DT 01-MAR-2002 (TREMUREL. 20, Last sequence update)  
 DE Urease accessory protein.  
 GN UREP.  
 OS Helicobacter pylori (Campylobacter pylori).  
 CC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 CC Helicobacteraceae; Helicobacter.  
 CX NCBI\_TaxID:210;  
 RN [1]  
 PP SEQUENCE FROM N.A.  
 RC STRAIN=NQ267;  
 RX MEDLINE:21625040; PubMed:11742075;  
 RA Falush D., Kraft C., Taylor N.S., Correa P., Fox J.G., Achtman M.,  
 RA Suerbaum S.;  
 RT "Recombination and mutation during long term gastric colonization by  
 RT Helicobacter pylori: Estimates of clock rates, recombination size and  
 RT transmission age." 1:1-11(2001).  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:15056-15061(2001).  
 DR EMBL: AJ418329; CAD1229.1; --  
 SQ SEQUENCE 10 AA; 1329 MW; 81E8C04C332411 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 10;  
 Best Local Similarity 60.3%; Pred. No. 1.6e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 6 DSTKK 10  
 DB 2 DTRKK 6

## RESULT 10

ID Q93SR0 PRELIMINARY; PRT; 8 AA.  
 AC Q93SR0 (TREMUREL. 19, Created)  
 DT 01-DEC-2001 (TREMUREL. 19, Last sequence update)  
 DE Beta lactamase repressor Blai (Fragment).  
 GN BLAI.  
 OS Staphylococcus epidermidis.  
 OG Plasmid pST6.  
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 CX NCBI\_TaxID:1282;  
 RN [1]  
 PP SEQUENCE FROM N.A.  
 RC STRAIN=6;  
 RA Sidhu M.S., Heir E., Sorum H., Hoick A.L.;  
 RT "Genetic linkage between quaternary ammonium compound and beta-lactam  
 RT resistance in Staphylococci isolated from food.";  
 DR EMBL: AY028779; AAK38453.1; --  
 FT NON TER 1  
 SQ SEQUENCE 8 AA; 930 MW; 4F3325H05AA4472C CRC64;

Query Match 27.3%; Score 15; DB 2; Length 8;  
 Best Local Similarity 60.3%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;



Best Local Similarity 60.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PEDST 8  
DB 4 PGDKT 8

RESULT 13  
Q62933 PRELIMINARY; PRT: 9 AA.  
ID Q62933  
AC Q62933  
DT 01-NOV-1996 (TRENBLREL: 01, Created;  
DT 01-NOV-1996 (TRENBLREL: 01, Last sequence update;  
DE Histone H2.0 (Fragment)  
DE Histone H2.0 (Fragment)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]\_TaxID=10116;  
RP SEQUENCE FROM N.A.  
RC STRAIN:Wistar; TISSUE:Testis;  
RA Khochbin S., Peretti V.P., Girardot V.;  
RT "The structure of differentiation specific histone H2c gene basal  
RT promoter."  
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U49737; AAA592724.1;  
FT NON TER  
SQ SEQUENCE 8 AA; 850 MW; F4C77B5B44B01A6 CRC64;

Query Match 27.3%; Score 15; DB 11; Length 8;  
Best Local Similarity 75.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PDST 8  
DB 2 ENST 6

RESULT 14  
Q8CG39 PRELIMINARY; PRT: 9 AA.  
ID Q8CG39  
AC Q8CG39  
DT 01-MAR-2003 (TRENBLREL: 23, Created;  
DT 01-MAR-2003 (TRENBLREL: 23, Last sequence update;  
DT 01-MAR-2003 (TRENBLREL: 23, Last annotation update;  
DE Histamine N-tele-methyltransferase (Fragment)  
OS Rattus norvegicus (Rat)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]\_TaxID=10116;  
RP SEQUENCE FROM N.A.  
RC STRAIN:Sprague Dawley; TISSUE=Liver;  
RX MEDLINE=96342418; PubMed=8750786;  
RA Takemura M., Yamachi K., Yamatodani A.;  
RT "Structural analysis of histamine N-methyltransferase gene."  
RL Methods find. Exp. Clin. Pharmacol. 17;1:141995;  
DR EMBL: S82579; AA86745.1;  
KW Transferase; Methyltransferase;  
FT NON TER  
SQ SEQUENCE 9 AA; 1060 MW; 4223B1E042EB053 CRC64;

Query Match 27.3%; Score 15; DB 11; Length 9;  
Best Local Similarity 56.7%; Pred. No. 8.3e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HTF 4  
DB 7 NSF 9

Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 PEDST 7  
DB 1 YEN 4

RESULT 12  
Q9PCK3 PRELIMINARY; PRT: 9 AA.  
ID Q9PCK3  
AC Q9PCK3  
DT 01-OCT-2000 (TRENBLREL: 15, Created;  
DT 01-OCT-2000 (TRENBLREL: 15, Last sequence update;  
DT 01-OCT-2000 (TRENBLREL: 15, Last annotation update;  
DE cAMP specific phosphodiesterase PDE5A (Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99153747; PubMed=1030676;  
RA White G.R.M., Varley J.M., Helgway J.;  
RT "Genomic structure and expression profile of PDE5A, a cGMP dep-  
RT variably expressed in breast cancer cell lines."  
RL Biochim. Biophys. Acta 1491:75-92(2000);  
DR EMBL: AJ244509; CAB60204.1;  
FT NON TER  
SQ SEQUENCE 8 AA; 1025 MW; 4D53D763344AACC CRC64;

Query Match 27.3%; Score 15; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 PEDST 7  
DB 1 YEN 4

RESULT 12  
Q9PCK3 PRELIMINARY; PRT: 9 AA.  
ID Q9PCK3  
AC Q9PCK3  
DT 01-OCT-2000 (TRENBLREL: 15, Created;  
DT 01-OCT-2000 (TRENBLREL: 15, Last sequence update;  
DT 01-OCT-2000 (TRENBLREL: 15, Last annotation update;  
DE cAMP specific phosphodiesterase PDE5A (Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20145478; PubMed=10679249;  
RA Jin C.H., Lau A., Tu R., Jue T.F.;  
RT "Identification of three alternative first exons in an intronic  
RT promoter of human PDE5A gene."  
RL Biochem. Biophys. Res. Commun. 268:596-603(2000);  
DR EMBL: AF551953; AAF40302.1;  
FT NON TER  
SQ SEQUENCE 9 AA; 908 MW; EBA3AAB7879E926 F0C4;

Query Match 27.3%; Score 15; DB 4; Length 8;

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RESULT 15
Q4756:
ID Q4756: PRELIMINARY: PRT: 10 AA
AC Q4756:
DT 01-NOV-1996 (TRENBLrel: 01, Created)
DE 01-NOV-1996 (TRENBLrel: C1, Last sequence update)
DI 01-JAN-1999 (TRENBLrel: C9, Last annotation update)
DE Hypothetical: 1.1 kDa protein (fragment).
CS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID:562;
RN [1]
RP SEQUENCE FROM NIA
RC STRAIN:K 12;
RX MEDLINE:94162733; PubMed:9764507;
RA Yamada M., Yanai S., Talkner A.;
RT "Analysis of products of the Escherichia coli genomic genes and
RT regulation of their expressions: an applicable procedure for genomic
RT analysis of other microorganisms."
RD Biosci. Biotechnol. Biochem. 58:117-120(1994).
DR EMBL: D21431; BAA04679.1; -.
KW Hypothetical protein.
FT NON-TER 1
FT NON-TER 10 13
SQ SEQUENCE 10 AA: 1109 MW; 2D1B5B5B5F87D2D33 CRC64.
Query March 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 66.7%; Pred No. 2.5e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY : GHZ 3
QB : 6 GHS 8

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Search completed: November 5, 2003, 17:34:37  
 Job time: 17 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM Protein - protein search, using sw model

Run on: November 5, 2003, 17:23:00 / Search time: 31.013 seconds  
(without alignments)  
47,618 Million cell updates/sec

Title: us-09-914-088-4

Perfect score: 65

Sequence: 1 GHTFELSTRK 10

Scoring table:

Gapop 12.0, Gapext 2.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 11420

Minimum DB seq length: 3

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1 Geneseq\_19Jun01.\*  
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2: /S:DS1/gcgdata/geneseq/geneseq-emb/AA1981.DAT.\*  
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24: /S:DS1/gcgdata/geneseq/geneseq-emb/AA2003.DAT.\*

Prod. No. is the number of results predicted by choice to have a score greater than or equal to the score of the hit it being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	55	100.0	10	21	AA825910		IGF C-peptide 2 domain surface exposed epitope peptide P4 SEQ ID NO:4.
2	55	100.0	10	22	AAU16035		Epitope: mimotope; Human; Immunoglobulin E; IGE: C-epsilon-2 domain; allergic disease; immunophylaxis; immunotherapy; anti-allergic;c;
3	58	100.0	10	23	AB023220		Human IgE mimotope
4	28	50.9	8	22	AA089420		Human IgE supermotif
5	27	49.1	9	23	AB034507		Human IgE supermotif
6	27	49.1	9	23	AB034507		Human IgE supermotif
7	27	49.1	9	23	AB034507		Human IgE supermotif
8	27	49.1	9	23	AB034507		Human IgE supermotif
9	26	47.3	8	13	AA027994		Human IgE supermotif

10	26	47.3	9	23	AB046949		Human BlyS binding
11	26	47.3	10	22	AA086567		Saccharomyces cere
12	26	47.3	10	23	ABB94538		CTE epitope HLA pe
13	25	45.5	7	23	AAU181553		Enterokinase recog
14	25	45.5	9	15	AA047316		Human IgE supermotif
15	25	45.5	9	20	AA045502		Human IgE supermotif
16	25	45.5	9	22	AAU26670		Human Leukocyte An
17	25	45.5	9	22	AAU27003		Human Leukocyte An
18	25	45.5	10	15	AA047316		Human Leukocyte An
19	25	45.5	10	19	AA045740		Fibronectin bindin
20	25	45.5	10	19	AA045741		Fibronectin bindin
21	25	45.5	10	22	ABP20812		HIV A33 motif gag
22	25	45.5	10	22	ABP20812		HIV A33 motif gag
23	25	45.5	10	22	ABP20812		HIV A33 motif gag
24	24	43.6	7	20	AA042578		Vpr-binding peptid
25	24	43.6	8	22	AA042578		Vpr-binding peptid
26	24	43.6	9	22	AA042578		Vpr-binding peptid
27	24	43.6	9	22	AA042578		Vpr-binding peptid
28	24	43.6	9	22	AA042578		Vpr-binding peptid
29	24	43.6	9	23	AB013412		Human Leukocyte An
30	24	43.6	9	24	ABR21659		Human 125P5C8 epit
31	24	43.6	10	18	AA042711		Human 125P5C8 epit
32	24	43.6	10	19	AA042711		Human 125P5C8 epit
33	24	43.6	10	19	AA042711		Human 125P5C8 epit
34	24	43.6	10	20	AA042711		Human 125P5C8 epit
35	24	43.6	10	22	AA042711		Human 125P5C8 epit
36	24	43.6	10	22	AA042711		Human 125P5C8 epit
37	24	43.6	10	22	AA042711		Human 125P5C8 epit
38	24	43.6	10	22	AA042711		Human 125P5C8 epit
39	24	43.6	10	23	ABJ14186		Human 125P5C8 epit
40	24	43.6	10	23	ABJ14186		Human 125P5C8 epit
41	24	43.6	10	24	ABR21556		Human 125P5C8 epit
42	24	43.6	10	24	ABR21556		Human 125P5C8 epit
43	24	43.6	10	24	ABR21556		Human 125P5C8 epit
44	24	43.6	10	24	ABR21556		Human 125P5C8 epit
45	23	41.8	7	23	AAU1560		Human 125P5C8 epit

## ALIGNMENTS

RESULT 1  
ID AA825910 standard; Peptide: 10 AA  
XX AA825910;  
XX AA825910;  
XX 95-JAN-2003 (first entry);  
XX IGF C-peptide 2 domain surface exposed epitope peptide P4 SEQ ID NO:4.

XX Epitope: mimotope; Human; Immunoglobulin E; IGE: C-epsilon-2 domain; allergic disease; immunophylaxis; immunotherapy; anti-allergic;c;  
XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
XX allergy; atopy.

XX Homo sapiens.

XX WC3C0050460-AA1.

XX 31-AUG-2003.

XX 22-FEB-2003; 2003WC EP01455.

XX 25-FEB-1999; 99GB-C004425.

XX 29-MAR-1999; 99GB-C007151.

XX 07-MAY-1999; 99GB-C010537.

XX 07-MAY-1999; 99GB-C010538.

XX 07-AUG-1999; 99GB-C018594.

XX 07-AUG-1999; 99GB-C018603.

XX 07-SEP-1999; 99GB-C021046.

XX 07-SEP-1999; 99GB-C021047.

XX 29-OCT-1999; 99GB-C025613.



XX Claim 4: Page 9: 45pp; English.  
 XX The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulphide bridge cyclised peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a peptide immunogen derived from human  
 CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
 XX  
 XX Sequence 10 AA;  
 SQ  
 Query Match 100.0%; Score 55; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00687;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GHTFEDSTKK 10  
 DB 1 GHTFEDSTKK 10  
 RESULT 4  
 AA389420  
 ID AAG59420 standard; Peptide; 8 AA.  
 XX  
 AC AAG59420;  
 XX  
 DT 11-SEP 2001 (first entry)  
 XX  
 DE p53 DR supermotif binding peptide core sequence #16.  
 XX  
 KW Human; p53, tumor suppressor; human leukocyte antigen; HLA; CTL;  
 KW cytotoxic T lymphocyte; T cell; immune response; tumor; cancer;  
 KW vaccine; epitope; cytostatic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FN WO2001/4789-A1.  
 XX  
 DT 14 JUN 2001.  
 XX  
 PF 11-DEC-2001; 2000W3-US33629.  
 XX  
 PR 10 DEC 1999; 99US-0458297.  
 XX  
 PA (EPIM) EPIMUNE INC.  
 XX  
 PI Fikes J, Sette A, Sidney J, Southwood S, Chishti R, Levin E,  
 PI Keohavong E.  
 XX  
 WP17 2001-391493/40.  
 XX  
 PT Epitope based vaccines comprising p53 epitope having a modified  
 PT sequence, useful for treating and preventing cancer, the epitope  
 PT peptide is useful as diagnostic agents and for evaluating immune  
 PT response.  
 XX  
 PS Disclosures: Page 111, 138pp; English.  
 XX  
 CC The present invention describes isolated prepared epitopes (I). Also  
 CC described are: (i) a cytotoxic T lymphocyte (CTL) that is cultured  
 CC in vivo and binds to a complex of (i); (2) a peptide (ii) comprising (i)  
 CC and a second epitope and has less than 50 contiguous amino acids; (3) a  
 CC vaccine composition comprising (ii); a unit dose of a peptide with less  
 CC than 50 contiguous amino acids with 100% identity to the native peptide  
 CC sequence of p53; and a pharmaceutical excipient; (4) an isolated nucleic  
 CC acid encoding (i); and (5) an isolated nucleic acid encoding (ii). (i)  
 CC has cytostatic activity and can be used in vaccines. The vaccine  
 CC composition is useful for treating or preventing cancer. (i) and (ii)  
 CC are useful as diagnostic agents and for evaluating immune responses.  
 CC Unlike conventional epitopes, immunosuppressive epitopes that may be  
 CC present in whole antigens can be avoided with the use of the vaccine  
 CC composition of (i). The ability to combine selected epitopes and

CC further, to modify the composition of the epitopes enhances the  
 CC immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigens, which might have their own  
 CC intrinsic biological activity, are eliminated. AAG59363 to AAG59747  
 CC represent amino acid sequences used in the exemplification of the  
 CC present invention.  
 XX  
 XX Sequence 8 AA;  
 SQ  
 Query Match 50.9%; Score 28; DB 22; Length 8;  
 Best Local Similarity 83.3%; Pred. No. 9.3e-05;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 HTFEDS ?  
 DB 3 HTLEDS 8  
 RESULT 5  
 ABB94507  
 ID ABB94507 standard; Peptide; 9 AA.  
 XX  
 AC ABB94507;  
 XX  
 DT 17-JUN 2002 (first entry)  
 XX  
 DE CTL epitope HLA peptide SEQ ID NO:36.  
 XX  
 KW Human; 158P1H4; chromosome 8q22q23, 158P1H4; chromosome 8q23; cancer;  
 KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
 KW human leukocyte antigen; helper T lymphocyte; HTL.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FN WO2002/6598-A2.  
 XX  
 DT 28-FEB 2002.  
 XX  
 PF 22-AUG 2001; 2001W3-US26411.  
 XX  
 PR 22-AUG-2000; 2000US-227098P.  
 PR 10-APR-2001; 2001US-282739P.  
 XX  
 PA (AGEN) AGENSYS INC.  
 XX  
 PI Chaitin-Eid PM, Hubert RS, Kaitaro AB, Afar DEH, Levin E,  
 PI Faris M, Ge W, Jakubovits A;  
 XX  
 WP1 2002 269357/31.  
 XX  
 PT Monitoring 158P1H4 gene products in biological sample from patient who  
 PT has or is suspected of having cancer, useful for treating cancer,  
 PT comprises identifying presence of aberrant 158P1H4 gene products in  
 PT biological sample.  
 XX  
 PS Claim 64; Page 143; 209pp; English.  
 XX  
 CC The present invention describes a method for monitoring 158P1H4 gene  
 CC products in a biological sample from a patient who has or is suspected  
 CC of having cancer. The method comprises determining the status of 158P1H4  
 CC gene products in a tissue sample from an individual, comparing the  
 CC status to the status of 158P1H4 gene products in a normal sample, and  
 CC identifying the presence of aberrant 158P1H4 gene products in the sample.  
 CC 158P1H4 sequences have cytostatic activity and can be used in vaccine  
 CC production. 158P1H4 polynucleotides may be used in monitoring genetic  
 CC abnormalities. The 158P1H4 proteins may be used in assessing the status  
 CC of 158P1H4 gene products in normal versus cancerous tissues and so  
 CC elucidating the malignant phenotype, in generating and characterising  
 CC domain-specific antibodies, for identifying agents or cellular factors  
 CC that bind to 158P1H4 or its particular domain, and for generating  
 CC cancer vaccines. Antibodies against 158P1H4 are useful in diagnostic  
 CC and prognostic assays, in treating patients with cancer, in generating

CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
 CC and as immunological reagents for detecting 158p1H4-expressing cells.  
 CC The antibodies are particularly useful in bladder cancer diagnostic and  
 CC prognostic assays, and imaging methodologies. The 158p1H4 gene has been  
 CC located to chromosome 8q22-q23, and the 158p1H4 gene also described in  
 CC the present invention has been located to chromosome 8q23. ABL50429 to  
 CC ABL50429 and ABB94468 to ABB95188 represent sequences used in the  
 CC exemplification of the present invention.  
 XX Sequence 9 AA:  
 SQ

Query Match 49.18; Score 27; CR 23; Length 9;  
 Best Local Similarity 55.68; Pred. No. 9.3e+05;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFEDSTKK 10  
 DQ 1 NTFEDATKK 9

RESULT 6  
 ABB94683  
 ID ABB94683 standard; Peptide; 9 AA.  
 XX  
 AC ABB94683;  
 DT 17 JUN 2002 (first entry);  
 DE CTL epitope HLA peptide SEQ ID NO:212.  
 XX  
 KW Human; 158p1H4; chromosome 8q22q23, 158p1F4; chromosome 8q23; cancer;  
 KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
 KW human leukocyte antigen; helper T lymphocyte; HTL.  
 XX  
 OS Homo sapiens  
 GS Synthetic.  
 XX  
 TN WC200214598 A2.  
 XX  
 FD 28-FEB-2002.  
 XX  
 PF 22-AUG-2001; 2001NO-US26411.  
 XX  
 PR 22 AUG 2000; 2000US-227098P.  
 PR 10 APR 2001; 2001US-282739P.  
 XX  
 PA (AGEN: AGENSYS INC.  
 PI Chaitin-Eld PM, Hubert RS, Raitano AR, Afar DEH, Levin E;  
 PI Faris M, Ge W, Jakubovits A;  
 XX  
 DR WPI; 2002-269357/31.  
 XX  
 PT Monitoring 158p1H4 gene products in biological sample from patient who  
 PT has or is suspected of having cancer, useful for treating cancer,  
 PT comprises identifying presence of aberrant 158p1H4 gene products in  
 PT biological sample  
 XX  
 PS Claim 64; Page 149; 209pp; English.  
 XX  
 PS The present invention describes a method for monitoring 158p1H4 gene  
 CC products in a biological sample from a patient who has or is suspected  
 CC of having cancer. The method comprises determining the status of 158p1H4  
 CC gene products in a tissue sample from an individual, comparing the  
 CC status to the status of 158p1H4 gene products in a normal sample, and  
 CC identifying the presence of aberrant 158p1H4 gene products in the sample.  
 CC 158p1H4 sequences have cytostatic activity and can be used in vaccine  
 CC production. 158p1H4 polynucleotides may be used in monitoring genetic  
 CC abnormalities. The 158p1H4 proteins may be used in assessing the status  
 CC of 158p1H4 gene products in normal versus cancerous tissues and so  
 CC elucidating the malignant phenotype, in generating and characterizing  
 CC domain specific antibodies, for identifying agents or cellular factors  
 CC that bind to 158p1H4 or its particular domain, and for generating

CC cancer vaccines. Antibodies against 158p1H4 are useful in diagnostic  
 CC and prognostic assays, in treating patients with cancer, in generating  
 CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
 CC and as immunological reagents for detecting 158p1H4-expressing cells.  
 CC The antibodies are particularly useful in bladder cancer diagnostic and  
 CC prognostic assays, and imaging methodologies. The 158p1H4 gene has been  
 CC located to chromosome 8q22-q23, and the 158p1H4 gene also described in  
 CC the present invention has been located to chromosome 8q23. ABL50400 to  
 CC ABL50429 and ABB94469 to ABB95189 represent sequences used in the  
 CC exemplification of the present invention.  
 XX Sequence 9 AA:  
 SQ

Query Match 49.18; Score 27; CR 23; Length 9;  
 Best Local Similarity 55.68; Pred. No. 9.3e+05;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFEDSTKK 10  
 DQ 1 NTFEDATKK 9

RESULT 7  
 ABB94777  
 ID ABB94777 standard; Peptide; 9 AA.  
 XX  
 AC ABB94777;  
 DT 17-JUN-2002 (first entry);  
 DE CTL epitope HLA peptide SEQ ID NO:306.  
 XX  
 KW Human; 158p1H4; chromosome 8q22q23, 158p1F4; chromosome 8q23; cancer;  
 KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
 KW human leukocyte antigen; helper T lymphocyte; HTL.  
 XX  
 OS Homo sapiens  
 GS Synthetic.  
 XX  
 TN WC200216598-A2.  
 XX  
 FD 28-FEB-2002.  
 XX  
 PF 22-AUG-2001; 2001WO-US26411.  
 XX  
 PR 22-AUG-2000; 2000US-227098P.  
 PR 10-APR-2001; 2001US-282739P.  
 XX  
 PA (AGEN: AGENSYS INC.  
 PI Chaitin-Eld PM, Hubert RS, Raitano AR, Afar DEH, Levin E;  
 PI Faris M, Ge W, Jakubovits A;  
 XX  
 DR WPI; 2002-269357/31.  
 XX  
 PT Monitoring 158p1H4 gene products in biological sample from patient who  
 PT has or is suspected of having cancer, useful for treating cancer,  
 PT comprises identifying presence of aberrant 158p1H4 gene products in  
 PT biological sample  
 XX  
 PS Claim 64; Page 152; 209pp; English.  
 XX  
 PS The present invention describes a method for monitoring 158p1H4 gene  
 CC products in a biological sample from a patient who has or is suspected  
 CC of having cancer. The method comprises determining the status of 158p1H4  
 CC gene products in a tissue sample from an individual, comparing the  
 CC status to the status of 158p1H4 gene products in a normal sample, and  
 CC identifying the presence of aberrant 158p1H4 gene products in the sample.  
 CC 158p1H4 sequences have cytostatic activity and can be used in vaccine  
 CC production. 158p1H4 polynucleotides may be used in monitoring genetic  
 CC abnormalities. The 158p1H4 proteins may be used in assessing the status  
 CC of 158p1H4 gene products in normal versus cancerous tissues and so  
 CC elucidating the malignant phenotype, in generating and characterising

CC domain specific antibodies, for identifying agents or cellular factors  
 CC that bind to 158PIH4 or its particular domain, and for generating  
 CC cancer vaccines. Antibodies against 158PIH4 are useful in diagnostic  
 CC and prognostic assays, in treating patients with cancer, in generating  
 CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
 CC and as immunological reagents for detecting 158PIH4-expressing cells.  
 CC The antibodies are particularly useful in bladder cancer diagnostic and  
 CC prognostic assays, and imaging methodologies. The 158PIH4 gene has been  
 CC located to chromosome 8q22-q23, and the 158PIH4 gene also described in  
 CC the present invention has been located to chromosome 8q23. ABL50420 to  
 CC ABL50429 and ABB94468 to ABB95188 represent sequences used in the  
 CC exemplification of the present invention.

XX Sequence 9 AA;  
 SQ

Query Match 49.1%; Score 27; DB 23; Length 3;  
 Best Local Similarity 55.6%; Pred. No. 9.3e+06;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFEDSTKK 10  
 : : : : :  
 DB 1 NTFDIATKK 9

RESULT 9  
 ID ABB94466 standard; Peptide; 10 AA.  
 AC ABB94466;  
 DT 17 JUN-2002 (first entry;  
 DE CTL epitope HLA peptide SEQ ID NO:395.  
 KW Human; 158PIH4; chromosome 8q220q23, 158PIH4; chromosome 8q23; Cancer;  
 KW bladder cancer; immune response; cytotoxic T lymphocyte; HTL; HLA;  
 KW human leukocyte antigen; Helper T lymphocyte; HTL.  
 XX Homo sapiens.  
 CS Synthetic.  
 XX WO200215598 A1.  
 XX 28 FEB. 2002.  
 XX 22-AUG-2001; 2001WO US26411.  
 XX 22-AUG-2000; 2001US 227598P.  
 XX 10-APR 2001; 2001US-282739P.  
 XX (AGEN-1) AGENSYS INC.  
 XX Chailita-Rid PM, Hubert RS, Rattato AB, Atlas LEH, Lavin EJ,  
 PI Faris M, Ge W, Jakobovits A;  
 XX WPI; 2002-269357/31.  
 XX Monitoring 158PIH4 gene products in biological sample from patient who  
 PT has or is suspected of having cancer, useful for treating cancer,  
 PT comprises identifying presence of aberrant 158PIH4 gene products in  
 PT biological sample -  
 XX Claim 64; Page 155; 209pp; English

CC The present invention describes a method for monitoring 158PIH4 gene  
 CC products in a biological sample from a patient who has or is suspected  
 CC of having cancer. The method comprises determining the status of 158PIH4  
 CC gene products in a tissue sample from an individual, comparing the  
 CC status to the status of 158PIH4 gene products in a normal sample, and  
 CC identifying the presence of aberrant 158PIH4 gene products in the sample.  
 CC 158PIH4 sequences have cytostatic activity and can be used in vaccine  
 CC production. 158PIH4 polynucleotides may be used in monitoring genetic  
 CC abnormalities. The 158PIH4 proteins may be used in assessing the status

CC of 158PIH4 gene products in normal versus cancerous tissues and so  
 CC elucidating the malignant phenotype, in generating and characterising  
 CC domain-specific antibodies, for identifying agents or cellular factors  
 CC that bind to 158PIH4 or its particular domain, and for generating  
 CC cancer vaccines. Antibodies against 158PIH4 are useful in diagnostic  
 CC and prognostic assays, in treating patients with cancer, in generating  
 CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
 CC and as immunological reagents for detecting 158PIH4-expressing cells.  
 CC The antibodies are particularly useful in bladder cancer diagnostic and  
 CC prognostic assays, and imaging methodologies. The 158PIH4 gene has been  
 CC located to chromosome 8q22-q23, and the 158PIH4 gene also described in  
 CC the present invention has been located to chromosome 8q23. ABL50400 to  
 CC ABL50429 and ABB94468 to ABB95188 represent sequences used in the  
 CC exemplification of the present invention.

XX Sequence 10 AA;  
 SQ

Query Match 49.1%; Score 27; DB 23; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFEDSTKK 10  
 : : : : :  
 DB 2 NTFDIATKK 10

RESULT 9  
 ID AAR27999 standard; peptide; 6 AA.  
 AC AAR27999;  
 DT 25-MAR-2003 (updated;  
 DT 17 MAR-1993 (first entry;  
 DE Tryptic peptide fragment #17.  
 XX Insulin receptor substrate-1; IRS 1; antibody; proteolytic cleavage;  
 KW ID-SDS PAGE.  
 XX Rattus rattus.  
 XX WO9211083 A1.  
 XX 06-AUG-1992; 92WO US00437.  
 XX 17-JAN-1992; 92WO US00437.  
 XX 18-JAN-1991; 91US-0643982.  
 XX (JOSL-1) JOSLIN DIABETES CENT INC.  
 XX Kahn CR, Rotherberg PL, White MF;  
 XX WPI; 1992-365881/44.  
 XX Purified nucleic acid encoding Insulin Receptor Substrate - used  
 PT to prepare IRS-1, for diagnosis and treatment of insulin related  
 PT diseases and abnormal cellular proliferation  
 XX Disclosure; Page 26; 128pp; English.

CC The sequences given in AAR27993-8000 and AAR28044 are fragments from  
 CC insulin receptor substrate-1 (IRS-1). These fragments were used to  
 CC determine the sequence of IRS-1 and to distinguish it from proteins  
 CC which are co-purified with it. Antibodies were raised against the  
 CC IRS-1 proteins and were used to remove them from the reaction media.  
 CC These peptides were formed by proteolytic cleavage of proteins  
 CC isolated by 1D-SDS PAGE to be approx. 185 kD.  
 CC (Updated on 25-MAR 2003 to correct PN field.)  
 XX Sequence 8 AA;  
 SQ

Query Match 47.3%, Score 26, DB 13, Length 8;  
Best Local Similarity 62.5%; Pred. No. 9,Je+05;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 TERTSTKX 10  
DB 1 TERTSTKX 8

RESULT 10  
ABP46946  
ID ABP46946 standard; peptide: 9 AA.  
XX  
AC ABP46946;  
PT 19-AUG-2002 (first entry)  
DE Human HLA binding scFv VH CDR3 SEQ ID 2359.  
XX  
KW BLYS; B lymphocyte stimulator; TNF superfamily; human, cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; anti-infective;  
KW anti-HIV; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; HIV; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
GO Homo sapiens.  
XX  
FN W02002064; A1.  
XX  
PD 10 JAN 2002.  
XX  
PF 15-JUN-2001; 2001WC JS13110.  
XX  
PR 14-JUN-2000; 2000US 212210P.  
XX  
PR 17-OCT-2000; 2000US 240816P.  
XX  
PR 16 MAR 2001; 2001US-276248P.  
XX  
PR 21 MAR 2001; 2001US-277379P.  
XX  
PR 25 MAY-2001; 2001US-293499P.  
XX  
PA RUWA : RUWAN GEN-WE SCI INC.  
PA (CAVE) : CAVRIDGE ANTIBODY TECHNOLOGY  
XX  
PI Ruben AM, Barash SC, Choi GH, Vardhan T, Halperin E,  
XX  
XX WPI: 2002 114799415.  
XX  
XX Antibodies against B lymphocyte stimulator (BlyS) are useful in the diagnosis and treatment of cancer and autoimmune diseases.  
XX  
XX Claim 1, Page 308; 3148pp; English.  
XX  
XX This invention describes novel antibodies that recognize and bind to B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitumouric and anti-AIDS activity and can be used in vaccines to inhibit the expression and activity of BlyS. The antibodies bind to BlyS and so may be used to detect and quantify the presence of BlyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BlyS. They may also be administered to treat diseases associated with aberrant BlyS expression and activity such as cancer, tumor, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVI)) and acquired immunodeficiency syndrome (AIDS). ABP46946 represents the antibodies and fragments of the antibodies described in the method of the invention.  
XX  
XX Sequence 9 AA,  
XX  
XX Query Match 47.3%, Score 26, DB 13, Length 8;

Best Local Similarity 71.4%; Pred. No. 9,Je+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GRTFES 7  
DB 3 GRTFES 9

RESULT 11  
AAG86567  
ID AAG86567 standard; peptide: 10 AA.  
XX  
AC AAG86567;  
XX  
XX 11-SEP-2001 (first entry)  
XX  
XX Saccharomyces cerevisiae peptide, SEQ ID NO: 1516.  
XX  
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;  
KW drug discovery; drug design.  
XX  
OS Saccharomyces cerevisiae.  
XX  
FN W0200142276 A1.  
XX  
PD 14 JUN-2001.  
XX  
PF 13-DEC-2000; 2000WC GB04773.  
XX  
PR 13-DEC-1999; 99GB-0129471.  
XX  
XX (PROT-) PROTEOM LTD.  
XX  
XX Roberts GW, Heal JR;  
XX  
XX WPI: 2001 367863/38.  
XX  
XX Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design.  
XX  
XX Example 3; Page 239; 488pp; English.  
XX  
XX The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from Saccharomyces cerevisiae.  
XX  
XX Sequence 10 AA;  
XX  
XX Query Match 47.3%, Score 26; DB 22; Length 10;  
XX  
XX Best Local Similarity 50.0%; Pred. No. 2,Je+02;  
XX  
XX Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GHTFEDSTKX 10  
DB 1 GHTFEDSTKX 10

RESULT 12  
ABB94536  
ID ABB94536 standard; peptide: 10 AA.  
XX  
AC ABB94536;  
XX  
XX 17-JUN-2002 (first entry)  
XX  
XX CTL epitope HLA peptide SEQ ID NO: 57.  
XX  
XX Hu-60; 156P144; chromosome Hq20q123, 156P14; chromosome 4q21; cancer;  
XX  
XX



KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
 KW human leukocyte antigen; helper T lymphocyte; HTL.  
 XX  
 CS Homo sapiens.  
 CS Synthetic.  
 XX  
 PN WO2002/6593-A2.  
 XX  
 PD 28 FEB 2002.  
 XX  
 PF 22-AUG 2001; 2001WO-US26411.  
 XX  
 PF 22-AUG 2000; 2000US-2270982.  
 XX  
 PR 10-APR-2001; 2001US-2827392.  
 XX  
 XX  
 DA TAGEN; AGENSYS INC.  
 PI Chailita-Eid FN, Subert RS, Raitano AS, Astar UEH, Levin E;  
 PI Faris M, Ge W, Jakobovits A.  
 XX  
 DR WP; 2002-269357/11.  
 XX  
 XX Monitoring 158P1H4 gene products in biological sample from patient who  
 PT has or is suspected of having cancer, useful for treating cancer.  
 PT comprises identifying presence of aberrant 158P1H4 gene products in  
 PT biological sample  
 XX  
 XX Claim 64; Page 144; 209pp; English.  
 XX  
 CC The present invention describes a method for monitoring 158P1H4 gene  
 CC products in a biological sample from a patient who has or is suspected  
 CC of having cancer. The method comprises determining the status of 158P1H4  
 CC gene products in a tissue sample from an individual, comparing the  
 CC status to the status of 158P1H4 gene products in a normal sample, and  
 CC identifying the presence of aberrant 158P1H4 gene products in the sample.  
 CC 158P1H4 sequences have cytostatic activity and can be used in vaccine  
 CC production. 158P1H4 polynucleotides may be used in monitoring genetic  
 CC abnormalities. The 158P1H4 proteins may be used in assessing the status  
 CC of 158P1H4 gene products in normal versus cancerous tissues and so  
 CC elucidating the malignant phenotype, in generating and characterizing  
 CC domain-specific antibodies, for identifying agents or cellular factors  
 CC that bind to 158P1H4 or its particular domain, and for generating  
 CC cancer vaccines. Antibodies against 158P1H4 are useful in diagnostic  
 CC and prognostic assays, in treating patients with cancer, in generating  
 CC cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
 CC and as immunological reagents for detecting 158P1H4 expressing cells.  
 CC The antibodies are particularly useful in diagnosing cancer, prognosis and  
 CC prognostic assays, and in aging methods. The invention has been  
 CC located to chromosome 8q24-q25, and the 158P1H4 gene has been found  
 CC in the present invention has been located to chromosome 8p11. ABL5C429  
 CC ABL5C429 and ABB94468 to ABB95188 represent sequences found in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 1C AA;  
 Query Match 47.34; Score 26; DB 1; Length 10;  
 Best Local Similarity 62.54; Pred. No. 2; Mismatches 1; Indels 0;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

XX  
 KW Enterokinase recognition sequence; protein isolation;  
 KW enterokinase cleavage sequence.  
 XX  
 CS Synthetic.  
 XX  
 PN WO200198366-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 19-JUN-2001; 2001WO-US19533.  
 XX  
 PF 19-JUN 2000; 2000US-0597121.  
 XX  
 PA (DYAX-1) DYAX CORP.  
 XX  
 PI Ley AC, Lureau CT, Cadner RC;  
 XX  
 DR WP; 2002-110791/17.  
 XX  
 XX New polypeptide comprising an enterokinase recognition sequence for  
 PT isolating and purifying a protein of interest or its fragment.  
 XX  
 PS Claim 13; Page 35; 110pp; English.  
 XX  
 CC The present invention relates to novel enterokinase recognition  
 CC sequences and methods for rapid isolation of a protein of interest  
 CC present in a fusion protein construct including a novel enterokinase  
 CC cleavage sequence of the invention and a ligand recognition sequence  
 CC for capturing the fusion construct on a solid substrate. The  
 CC enterokinase recognition sequence is useful for isolating and purifying  
 CC a protein of interest or its fragment. The enterokinase recognition  
 CC sequences are highly specific and can be rapidly cleaved.  
 CC AAJ81543-AAJ81729 represent enterokinase recognition sequences of the  
 CC invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 45.54; Score 23; DB 23; Length 7;  
 Best Local Similarity 80.04; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFED 6  
 DB 1 HTFED 5  
 ID AAR47316 standard; Protein: ) AA.  
 XX AAR47316;  
 AC AAR47316;  
 XX  
 DT 14-MAY-2003 (updated;  
 DT 25-MAR-2003 (updated;  
 DT 31-AUG-1994 (first entry;  
 DE HLA-A1 HPV18.E6 antigen peptide fragment 4-12.  
 XX  
 XX Immunogenic; HLA A1.2; HLA-A1; HLA A1; binding motif; MHC molecule;  
 KW immune response; viral infection; cancer; prostate cancer; lymphoma;  
 KW hepatitis; AIDS; antibody; diagnosis.  
 XX  
 OS Human papilloma virus 18.  
 XX  
 PN WC9433205-A1.  
 XX  
 PD 17-FEB 1994.  
 XX  
 PF 06-AUG 1993; 93WC-US07421.  
 XX  
 XX 07-AUG 1992; 92US-5925666.  
 PR 05-MAR-1993; 92US-0027741.

XX CYTEC CYTEC CORP.  
 XX Cells A. Grey HX. Kube RT. Sette A;  
 XX WPI: 1994-065403/0A.  
 XX Peptide which specifically binds selected MHC alleles, used to  
 XX induce an immune response for treatment or prevention of viral  
 XX infection or cancer, or for diagnosis  
 XX Example 6; Page 51; 150pp; English  
 XX The sequences given in AAR4304-13 and AAR4301-14 are immunoprecip-  
 XX peptides which have a HLA-A1.2, HLA-A1 or a HLA-A11 binding motif.  
 XX These peptides may be used in the composition of the invention.  
 XX These peptides are capable of binding selected MHC molecules and  
 XX inducing an immune response. They can be used to treat and/or  
 XX prevent viral infection and cancer, eg. prostate cancer, lymphoma,  
 XX hepatitis or AIDS. They can also be used to produce antibodies for  
 XX use as diagnostic or therapeutic agents. The peptides can also be  
 XX used as diagnostic agents.  
 XX (Updated on 25-MAR-2003 to correct EN field.)  
 XX (Updated on 14-MAY-2003 to correct ES field.)  
 XX  
 XX Sequence 9 AA:  
 SQ  
 Query Match 45.5%; Score 25; DB 15; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 FEDSTK IC  
 H 1 FEDSTK P  
 PEPTIDE IS  
 ID AAY5502  
 AA AAY5502 standard; peptide: 9 AA.  
 AA AAY5502  
 XX 22-SEP-1999 (first entry)  
 XX Insulin-like growth factor binding protein fragment 100  
 XX Insulin-like growth factor binding protein (IGFBP) fragment 100  
 XX antiproliferative, anti-inflammatory, growth inhibitory, muscle mass,  
 XX shrinkage, wound healing, osteoporosis, diabetes, myasthenia gravis,  
 XX neoplasia, inflammation, cancer, lung and prostate cancer, muscle mass,  
 XX muscle, bone apparatus; wound healing, bone growth, bone therapy,  
 XX diabetes; nervous system; lymph glands, stomach, intestinal tract.  
 XX Unidentifed.  
 XX DEL3757250 A1.  
 XX 01-JUL-1999.  
 XX 22-DEC-1997; 97DE-1057250.  
 XX 22-DEC-1997; 97DE-1057250.  
 XX (FORS) FORSMANN W.  
 XX Forsmann W, Kling L, Mostafavi H, Gwendolf V. (1998),  
 XX Staendker L;  
 XX WPI: 1999-372233/12.  
 XX An insulin-like growth factor binding protein  
 XX Claim 12; Page 19, 26pp; German.

XX This invention describes a novel, insulin-like growth factor binding  
 XX protein (IBP) constructed using the formula R1-C-X1-PNC-X2-CC-X3-CWCY  
 XX X4-C-R2 where cyclic, glycosylated, phosphorylated, acetylated, amidated,  
 XX sulphated derivatives and fragments of these with the physiological  
 XX ability of IBP are included and R1NH2 - an amino acid or peptide with a  
 XX sequence of up to 41 amino acid residues, X1 = a peptide consisting of  
 XX 24-31 amino acids, X2 = a peptide consisting of 9 amino acids, X3 = a  
 XX peptide consisting of 10 amino acids, X4 = a peptide consisting of 18-24  
 XX amino acids, R2CCOH = CONH2 or a peptide with up to 12 amino acids. The  
 XX products of the invention have immunoprotective, antiproliferative,  
 XX anti-inflammatory and cytostatic activity. The IBP peptides, complexes,  
 XX antibodies, inhibitors and antisense nucleic acids are all useful in  
 XX the treatment of muscle loss/shrinkage/wasting, osteoporosis, diabetes,  
 XX amyloid lateral sclerosis, peripheral and central neuropathies,  
 XX inflammatory processes, cancer, inflammatory and neoplastic diseases,  
 XX growth disturbances, diseases of the muscles, diseases of the bone  
 XX apparatus and wound or bone healing. The nucleic acids and antisense  
 XX oligonucleotides can be used in somatic or non-somatic gene therapy. The  
 XX peptides, etc., can be used in diagnosis of functional deficiencies in  
 XX bones, muscles, nervous systems, lymph glands, stomach/intestinal tracts,  
 XX immune systems, for diabetes, inflammatory and neoplastic processes and  
 XX also as a marker for cancer. This sequence represents a specific claimed  
 XX example of a peptide which can occupy the R2 position of the IBP of the  
 XX invention.  
 XX  
 XX Sequence 9 AA:  
 SQ  
 Query Match 45.5%; Score 25; DB 20; Length 9;  
 Best Local Similarity 56.7%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 HTFDS 7  
 H 1 HTFDS 6  
 HTFDS 6

Search completed: November 5, 2003, 17:12:30  
 Job time : 34.333 secs

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QX protein: protein search, using sw model

Run on: November 5, 2003, 17:14:46 Search time 21 seconds  
(without alignments)  
81.79% Million cell of hits/sec

Query: US-09-914-088-4  
Perfect score: 55  
Sequence: 1 GHTFEDSTKK 10

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 644279 seqs, 171749294 residues

Total number of hits satisfying chosen parameters: 81026

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: Published Applications AA\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCP\_NEW\_PUB.pep\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCPUS\_PUBCOMB.pep\*
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- 8: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_NEW\_PUB.pep\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_NEW\_PUB.pep\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US10F\_PUBCOMB.pep\*

Pred. No. is the number of results identified by the search engine  
score greater than or equal to the score of the best result printed,  
and is derived by analysis of the total set of hits in the DB.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	55	100.0	10	12	US-10-082-014-275
2	55	100.0	10	12	US-10-372-076-129
3	27	49.1	9	12	US-09-935-384-136
4	27	49.1	9	12	US-09-935-384-137
5	27	49.1	9	12	US-09-935-384-138
6	27	49.1	10	12	US-09-935-384-139
7	26	47.3	9	11	US-09-880-748-2354
8	26	47.3	10	12	US-09-935-384-140
9	25	45.5	7	10	US-09-884-767A-20
10	25	45.5	10	12	US-09-755-630A-222
11	24	43.6	7	11	US-09-281-495-18
12	24	43.6	10	11	US-09-572-434P-1991
13	24	43.6	10	15	US-10-268-551-7
14	23	41.8	7	10	US-09-884-767A-27
15	23	41.8	9	12	US-10-190-082-150

Query Match 100.0% Score 55; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00072;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV : GHTFEDSTKK 10  
| | | | |  
DB 1 GHTFEDSTKK 10

RESULT 2  
US-10-372-076-129  
; Sequence 129, Application US/10372076  
; Publication No. US20030198645A;  
; GENERAL INFORMATION:  
; APPLICANT: Page, Mark  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS

Sequence 9, Appli  
Sequence 45, Appl  
Sequence 497, App  
Sequence 1, Appli  
Sequence 147, App  
Sequence 176, Appl  
Sequence 38, Appl  
Sequence 2, Appli  
Sequence 21, Appl  
Sequence 146, App  
Sequence 1601, Ap  
Sequence 2303, Ap  
Sequence 12, App  
Sequence 95, Appl  
Sequence 253, App  
Sequence 361, App  
Sequence 138, App  
Sequence 209, App  
Sequence 219, App  
Sequence 63, Appl  
Sequence 757, Ap  
Sequence 1905, Ap  
Sequence 3735, Ap  
Sequence 2, Appli  
Sequence 3740, Ap  
Sequence 2, Appli  
Sequence 116, App  
Sequence 201, App

## ALIGNMENTS

RESULT 1  
US-10-082-014-275  
; Sequence 275, Application US/10082014  
; Publication No. US2003018588A1  
; GENERAL INFORMATION:  
; APPLICANT: Birckett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N TERMINAL C  
; FILE REFERENCE: ICC-130-C 4564/85-24  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/930,915  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 275  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014 275

FILE REFERENCE: 4564/87179  
 CURRENT APPLICATION NUMBER: US/10/172,076  
 PRIOR FILING DATE: 2003-02-21  
 PRIOR APPLICATION NUMBER: 10/580,299  
 PRIOR FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 10/582,014  
 PRIOR FILING DATE: 2002-02-22  
 NUMBER OF SEQ ID NOS: 308  
 SOFTWARE: Patent in version 3.2  
 SEQ ID NO 129  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-172-076-129

Query Match: 100.0%; Score 35; DB 12; Length 9;  
 Best Local Similarity: 100.0%; Pred. No. 5.8e+05;  
 Matches: 10; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY : GTFEDSTKK 10  
 : |||||  
 DB 1 GTFEDSTKK 10

RESULT 3  
 US-09-935-384-306  
 Sequence 36, Application US/09935384  
 Publication No. US20030166526A1  
 GENERAL INFORMATION:

APPLICANT: CHALLITA-EID, PIA  
 APPLICANT: HUBERT, RENE  
 APPLICANT: RAITANO, ARTHUR  
 APPLICANT: AFAR, DANIEL  
 APPLICANT: LEVIN, ELANA  
 APPLICANT: AFAR, DANIEL  
 APPLICANT: HUBERT, RENE  
 APPLICANT: JAKBOVITZ, AYA  
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
 TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 TITLE OF INVENTION: OTHER CANCERS  
 FILE REFERENCE: 51158-22033-30  
 CURRENT APPLICATION NUMBER: US/09/935,384  
 CURRENT FILING DATE: 2001-08-22  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: 60/227,099  
 NUMBER OF SEQ ID NOS: 783  
 SOFTWARE: Patent in Ver. 2.1  
 SEQ ID NO 36  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-935-384-306

Query Match: 49.1%; Score 27; DB 12; Length 9;  
 Best Local Similarity: 55.6%; Pred. No. 5.8e+05;  
 Matches: 5; Conservative: 3; Mismatches: 1; Indels: 0; Gaps: 0;

QY : 2 HTFEDSTKK 10  
 : |||||  
 DB : NTFDIATKK 9

RESULT 4  
 US-09-935-384-395  
 Sequence 395, Application US/09935384  
 Publication No. US20030166526A1  
 GENERAL INFORMATION:

APPLICANT: CHALLITA-EID, PIA  
 APPLICANT: HUBERT, RENE  
 APPLICANT: RAITANO, ARTHUR  
 APPLICANT: AFAR, DANIEL  
 APPLICANT: LEVIN, ELANA  
 APPLICANT: HUBERT, RENE  
 APPLICANT: RAITANO, ARTHUR

APPLICANT: GE, WANGMAO  
 APPLICANT: JAKBOVITZ, AYA  
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
 TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 TITLE OF INVENTION: OTHER CANCERS  
 FILE REFERENCE: 51158-22033-30  
 CURRENT APPLICATION NUMBER: US/09/935,384  
 CURRENT FILING DATE: 2001-08-22  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: 60/227,098  
 NUMBER OF SEQ ID NOS: 783  
 SOFTWARE: Patent in Ver. 2.1  
 SEQ ID NO 212  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-935-384-212

Query Match: 49.1%; Score 27; DB 12; Length 9;  
 Best Local Similarity: 55.6%; Pred. No. 5.8e+05;  
 Matches: 5; Conservative: 3; Mismatches: 1; Indels: 0; Gaps: 0;

QY : 2 HTFEDSTKK 10  
 : |||||  
 DB 1 NTFDIATKK 9

RESULT 5  
 US-09-935-384-306  
 Sequence 306, Application US/09935384  
 Publication No. US20030166526A1  
 GENERAL INFORMATION:

APPLICANT: CHALLITA-EID, PIA  
 APPLICANT: HUBERT, RENE  
 APPLICANT: RAITANO, ARTHUR  
 APPLICANT: AFAR, DANIEL  
 APPLICANT: LEVIN, ELANA  
 APPLICANT: FARIS, MARY  
 APPLICANT: GE, WANGMAO  
 APPLICANT: JAKBOVITZ, AYA  
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
 TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 TITLE OF INVENTION: OTHER CANCERS  
 FILE REFERENCE: 51158-22033-30  
 CURRENT APPLICATION NUMBER: US/09/935,384  
 CURRENT FILING DATE: 2001-08-22  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: 60/227,098  
 NUMBER OF SEQ ID NOS: 783  
 SOFTWARE: Patent in Ver. 2.1  
 SEQ ID NO 306  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-935-384-306

Query Match: 49.1%; Score 27; DB 12; Length 9;  
 Best Local Similarity: 55.6%; Pred. No. 5.8e+05;  
 Matches: 5; Conservative: 3; Mismatches: 1; Indels: 0; Gaps: 0;

QY : 2 HTFEDSTKK 10  
 : |||||  
 DB 1 NTFDIATKK 9

RESULT 6  
 US-09-935-384-395  
 Sequence 395, Application US/09935384  
 Publication No. US20030166526A1  
 GENERAL INFORMATION:

APPLICANT: CHALLITA-EID, PIA  
 APPLICANT: HUBERT, RENE  
 APPLICANT: RAITANO, ARTHUR

```

; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 1-8P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158 2003.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,096
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 395
; LENGTH: 10
; TYPE: FRT
; ORGANISM: Homo sapiens
US-09-935-384-395

Query Match      49.1%; Score 27; DB 12; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 HTFEDSTKK 10
DB 2 HTFEDATKK 10

RESULT 7
US-09-880-748-2359
; Sequence 2959, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Robert et al.
; TITLE OF INVENTION: Antibodies that Immunorecognitively Bind B2M5
; FILE REFERENCE: IF523
; CURRENT APPLICATION NUMBER: US/09/880,749
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 1239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2959
; LENGTH: 9
; TYPE: FRT
; ORGANISM: Homo sapiens
US-09-880-748-2359

Query Match      47.3%; Score 25; DB 12; Length 9;
Best Local Similarity 71.4%; Pred. No. 5.8e+05;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHTFEDS 7
DB 3 GHTFSDS 9

RESULT 8
US-09-935-384-67
; Sequence 67, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA

```

```

; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158 2003.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,096
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 10
; TYPE: FRT
; ORGANISM: Homo sapiens
US-09-935-384-67

Query Match      47.3%; Score 26; DB 12; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTFEDSTKK 10
DB 1 TTFDIATKK 8

RESULT 9
US-09-884-767A-20
; Sequence 20, Application US/09884767A
; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Lureau, Christopher J.
; APPLICANT: Laderer, Robert C.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-312.1 US, DYX-012.1 ECT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,121
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 7
; TYPE: FRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-20

Query Match      45.5%; Score 25; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFED 6
DB 1 HTFSD 5

RESULT 10
US-09-755-130A-222
; Sequence 222, Application US/09755130A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALISHA, VERTAZA F.
; APPLICANT: ASTWOOD, JAMES D.

```

```

; APPLICANT: SAMPOSON, HUGH A.
; APPLICANT: SCHWARTZ, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DILATED/ORGANIZED PROTEINS AND PEPTIDES
; FILE REFERENCE: 11999-0217 NPS00 (MKT-117)
; CURRENT APPLICATION NUMBER: US/09/756,630A
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: Patent in version 3.0
; SEQ ID NO: 222
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US 09-756-630A-22

Query Match 45.5%; Score 25; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CY 3 TPEEALKR 9
DB 2 TPEEALKR 9

RESULT 11
US 09-756-630A-22
; Sequence 19, Application US/09/281,495
; Publication No. US20030059765A1
; GENERAL INFORMATION:
; APPLICANT: Pomerantz, Roger J
; APPLICANT: Bouhadani, Mohamed
; APPLICANT: Duang, Lara Xin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PREVENTING A PEPTIDE TO A
; FILE REFERENCE: 9809-2501
; CURRENT APPLICATION NUMBER: US/09/281,495
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 60/239,800
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO: 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificially Synthesized Peptide
; OTHER INFORMATION: Polypeptide Binding Mode
US 09-281-495-18

Query Match 43.6%; Score 24; DB 1; Length 7;
Best Local Similarity 66.1%; Pred. No. 8.8e+01;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 2 HTFEDSKR 7
DB 2 HSEFVS 7

RESULT 12
US 09-572-424B-1981
; Sequence 192, Application US/09/572,424B
; Publication No. US20030078394A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide binding to the human p-glyc
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,424B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203

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; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 198:
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Sequence located in CMKRL OR DEZ at 328-337 and may interact w
; OTHER INFORMATION: Sequence 1982 in this patent.
US-09-572-424B 198:

Query Match 43.6%; Score 24; DB 1; Length 10;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

CY 1 GHTFEDSKR 9
DB 1 GHTFEDSKR 9

RESULT 13
US-10-268-501-7
; Sequence 7, Application US/10268501
; Publication No. US20030085924A1
; GENERAL INFORMATION:
; APPLICANT: Silkowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P1
; CURRENT APPLICATION NUMBER: US/10/268,501
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/143,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO: 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 10
; OTHER INFORMATION: unknown amino acid
US-10-268-501-7

Query Match 43.6%; Score 24; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 1 GHTFEDSKR 9
DB 1 GHTFEDSKR 9

RESULT 14
US-09-984-767A-27
; Sequence 27, Application US/0984767A
; Publication No. US2003192789A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Lev, Arthur C.
; APPLICANT: Luneau, Christopher J.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/597,321
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patent in version 3.0
; SEQ ID NO: 27
; LENGTH: 7
; TYPE: PRT

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1 ORGANISM: Artificial Sequence  
2 FEATURE:  
3 OTHER INFORMATION: synthetic enterotoxinase cleavage sequence  
4 US-09-914-088-4

Query Match: 41.8% Score: 237 DE 125 Length: 7  
Best Local Similarity: 57.1% Pct: 5.8e-05  
Matches: 4 Conservative 1 Mismatches 1 Gaps 0

CY 1 GTFERS ?  
DE 1 GTFERS ?

RESULT 15  
US-10-190-082-140  
1 Sequence: 180, Application: US/1019008,  
2 Publication No: US20030148244A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Lusk, Lawrence A.  
5 APPLICANT: Singh, Sachdev S.  
6 APPLICANT: Heid, Heike A.  
7 TITLE OF INVENTION: PHAGE DISPLAYED PVZ DOMAIN LIGAND.  
8 FILE REFERENCE: P1905P.  
9 CURRENT APPLICATION NUMBER: US/10190082  
10 CURRENT FILING DATE: 2002-07-03  
11 PRIOR APPLICATION NUMBER: US 60/301,834  
12 PRIOR FILING DATE: 2001-07-06  
13 NUMBER OF SEQ ID NOS: 683  
14 SEQ ID NO 180  
15 LENGTH: 9  
16 TYPE: PRT  
17 ORGANISM: Artificial sequence  
18 FEATURE:  
19 OTHER INFORMATION: Synthetic  
20 US-10-190-082-140

Query Match: 41.8% Score: 237 DE 125 Length: 7  
Best Local Similarity: 57.1% Pct: 5.8e-05  
Matches: 4 Conservative 1 Mismatches 1 Gaps 0

CY 1 GTFERS ?  
DE 1 GTFERS ?

Search completed: November 5, 2003, 10:45:00  
Job time: 1.11 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2001 CorpuGen Ltd.

QV protein protein search, using sw model

Run on: November 5, 2003, 17:16:40 : Search time 12.1133 seconds  
Without alignment  
14,104 Million cell updates/sec

Title: US 09 914 088-4

Perfect score: 55

Sequence: 1 GTTREDSTKK 10

Scoring table: RASJMK-2

Gapop 10.0 : Gapext 0.5

Searched: 328717 seqs, 423:0858 residues

Total number of hits satisfying chosen parameters: 9:158

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA\*

1: /cgn2\_6/ptodata/1/aa/5A.COMB.pep\*  
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5: /cgn2\_6/ptodata/1/aa/PTCS.COMB.pep\*  
6: /cgn2\_6/ptodata/1/aa/backfiles.pep\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	8	1	US-08-094-948A-21
2	26	47.3	8	5	PCT-US96/0919-21
3	25	45.5	9	3	US-08-159-339A-21
4	25	45.5	9	3	US-08-159-339A-21
5	25	45.5	10	3	US-08-159-339A-21
6	24	43.6	7	4	US-09-281-495-22
7	24	43.6	10	2	US-08-966-348-8
8	24	43.6	10	3	US-09-188-401-8
9	24	43.6	10	3	US-09-188-404-8
10	24	43.6	10	3	US-09-281-259-8
11	24	43.6	10	4	US-09-117-860-8
12	23	41.8	8	2	US-08-424-232-2
13	23	41.8	9	1	US-08-149-809-19
14	23	41.8	9	4	US-09-267-991-9
15	22	40.0	6	4	US-09-081-975-22
16	22	40.0	7	4	US-09-281-495-22
17	22	40.0	8	1	US-08-487-863-61
18	22	40.0	9	1	US-08-149-809-23
19	22	40.0	9	3	US-08-159-339A-21
20	22	40.0	9	3	US-08-159-339A-21
21	22	40.0	9	4	US-09-238-924-31
22	22	40.0	10	1	US-08-235-946-51
23	22	40.0	10	1	US-08-487-863-61
24	22	40.0	10	6	5198347-23
25	21	38.2	5	4	US-09-187-859-1257
26	21	38.2	5	4	US-09-187-859-1255
27	21	38.2	5	4	US-09-187-859-1219

28 21 38.2 5 4 US-09-839-542B-1757 Sequence 1757, Ap  
29 21 38.2 5 4 US-09-839-542B-1905 Sequence 1905, Ap  
30 21 38.2 5 4 US-09-839-542B-3739 Sequence 3739, Ap  
31 21 38.2 6 4 US-09-187-859-3740 Sequence 3740, Ap  
32 21 38.2 6 4 US-08-982-285-2 Sequence 2, App  
33 21 38.2 6 4 US-09-839-542B-3740 Sequence 3740, Ap  
34 21 38.2 6 4 US-08-577-635-72 Sequence 72, App  
35 21 38.2 6 5 PCT-US93-00136-8 Sequence 8, App  
36 21 38.2 7 1 US-08-421-702A-12 Sequence 12, App  
37 21 38.2 7 1 US-08-353-052A-8 Sequence 8, App  
38 21 38.2 7 1 US-08-353-052A-12 Sequence 12, App  
39 21 38.2 7 1 US-08-421-696A-12 Sequence 12, App  
40 21 38.2 7 1 US-08-421-697A-12 Sequence 12, App  
41 21 38.2 7 1 US-08-421-698A-12 Sequence 12, App  
42 21 38.2 7 2 US-08-421-695A-12 Sequence 12, App  
43 21 38.2 7 5 PCT-US95-04741-12 Sequence 12, App  
44 21 38.2 8 1 US-08-346-455B-45 Sequence 45, App  
45 21 38.2 8 2 US-08-686-599A-11 Sequence 11, App

## ALIGNMENTS

RESULT 1  
US-08-094-948A-21  
Sequence 21, Application US/08094948A  
Patent No. 5621075  
GENERAL INFORMATION:  
APPLICANT: Kahn, C. Ronald  
APPLICANT: White, Morris F.  
APPLICANT: Rothenberg, Paul Louis  
TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lahive & Cookfield  
STREET: 63 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/094,948A  
FILING DATE: 21-JULY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/643,982  
FILING DATE: 18-JAN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis (PLM)  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: JDP-013DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-094-948A-21

Query Match: 47.3%; Score 26; DB 1; Length 8;  
Best Local Similarity 62.5%; Pred. No. 2, Seq 05;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 TREDSTKK 10

Dh : TREDSTKK 8



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1  RESULT 2
2  PCT US96-09419-01
3  Sequence 21, Application PC/TUS9609319
4  GENERAL INFORMATION:
5  APPLICANT: Kamm, C. Ronald
6  APPLICANT: White, Morris F.
7  APPLICANT: Rotherberg, Paul, Louis
8  TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRAIE
9  NUMBER OF SEQUENCES: 29
10 CORRESPONDENCE ADDRESS: 29
11 ADDRESSEE: Iahive & Cockfield
12 STREET: 60 State Street, Suite 510
13 CITY: Boston
14 STATE: Massachusetts
15 COUNTRY: U.S.A.
16 ZIP: 02109
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC Compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: PatentIn Release #1.0, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: PCT/US96/09419
24 FILING DATE:
25 PRIORITY APPLICATION DATA:
26 APPLICATION NUMBER: US 08/094,948
27 FILING DATE: 21-JULY-1993
28 APPLICATION NUMBER: US 07/643,982
29 FILING DATE: 18-JAN-1993
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Myers, Louis (PLM)
32 REGISTRATION NUMBER: 35,965
33 REFERENCE/DOCKET NUMBER: JDP-0110V
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (617)227-7400
36 TELEFAX: (617)227-5941
37 INFORMATION FOR SEQ ID NO: 21:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 8 amino acids
40 TYPE: amino acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 MOLECULE TYPE: peptide
44 US-08-159-319A-85
45 Query Match 47.1%, Score 20, DB 3, Length 8;
46 Best Local Similarity 62.5%, Pred. No. 2.5e+05;
47 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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49 QY 3 FEEDSTCK 10
50 DE 1 FEEDSPCK 8
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52 RESULT 3
53 US-08-159-319A-85
54 Sequence 85, Application US/08:59339A
55 Patent No. 6037135
56 GENERAL INFORMATION:
57 APPLICANT: Kubo, Ralph T.
58 APPLICANT: Grey, Howard M.
59 APPLICANT: Sette, Alessandro
60 APPLICANT: Celis, Esteban
61 TITLE OF INVENTION: HLA Binding peptides and Their
62 NUMBER OF SEQUENCES: 1254
63 CORRESPONDENCE ADDRESS:
64 ADDRESSEE: Townsend and Townsend and Crew LLP
65 STREET: Two Embarcadero Center, Eighth Floor
66 CITY: San Francisco
67 STATE: CA
68 COUNTRY: USA
69 ZIP: 94111-3834
70 COMPUTER READABLE FORM:
71 MEDIUM TYPE: Diskette
72 COMPUTER: IBM Compatible
73 OPERATING SYSTEM: DOS
74 SOFTWARE: FastSeq for Windows Version 2.0
75 CURRENT APPLICATION DATA:
76 APPLICATION NUMBER: US/08/159,339A
77 FILING DATE: 29 NOV-1993
78 CLASSIFICATION: 424
79 PRIOR APPLICATION DATA:
80 APPLICATION NUMBER: US 07/926,666

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1  ZIP: 94111-3834
2  COMPUTER READABLE FORM:
3  MEDIUM TYPE: Diskette
4  COMPUTER: IBM Compatible
5  OPERATING SYSTEM: DOS
6  SOFTWARE: FastSeq for Windows Version 2.0
7  CURRENT APPLICATION DATA:
8  APPLICATION NUMBER: US/08/159,339A
9  FILING DATE: 29-NOV-1993
10 CLASSIFICATION: 424
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 07/926,666
13 FILING DATE: 07-AUG-1992
14 APPLICATION NUMBER: US 08/027,746
15 FILING DATE: 05-MAR-1993
16 APPLICATION NUMBER: US 08/103,396
17 FILING DATE: 06-AUG-1993
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Weber, Ellen Lauver
20 REGISTRATION NUMBER: 32,762
21 REFERENCE/DOCKET NUMBER: 019623-0050300US
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (415) 576-0200
24 TELEFAX: (415) 576-0300
25 TELEX:
26 INFORMATION FOR SEQ ID NO: 95:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 9 amino acids
29 TYPE: amino acid
30 STRANDEDNESS: single
31 TOPOLOGY: linear
32 MOLECULE TYPE: peptide
33 US-08-159-319A-85
34 Query Match 45.5%, Score 25, DB 3, Length 9;
35 Best Local Similarity 57.1%, Pred. No. 2.5e+05;
36 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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38 QY 4 FEEDSTCK 10
39 DE 1 FEEDPTRN 7
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41 RESULT 4
42 US-08-159-319A-1004
43 Sequence 1004, Application US/08:59339A
44 Patent No. 6037135
45 GENERAL INFORMATION:
46 APPLICANT: Kubo, Ralph T.
47 APPLICANT: Grey, Howard M.
48 APPLICANT: Sette, Alessandro
49 APPLICANT: Celis, Esteban
50 TITLE OF INVENTION: HLA Binding peptides and Their
51 NUMBER OF SEQUENCES: 1254
52 CORRESPONDENCE ADDRESS:
53 ADDRESSEE: Townsend and Townsend and Crew LLP
54 STREET: Two Embarcadero Center, Eighth Floor
55 CITY: San Francisco
56 STATE: CA
57 COUNTRY: USA
58 ZIP: 94111-3834
59 COMPUTER READABLE FORM:
60 MEDIUM TYPE: Diskette
61 COMPUTER: IBM Compatible
62 OPERATING SYSTEM: DOS
63 SOFTWARE: FastSeq for Windows Version 2.0
64 CURRENT APPLICATION DATA:
65 APPLICATION NUMBER: US/08/159,339A
66 FILING DATE: 29 NOV-1993
67 CLASSIFICATION: 424
68 PRIOR APPLICATION DATA:
69 APPLICATION NUMBER: US 07/926,666

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1 FILING DATE: 07-AUG-1992
2 APPLICATION NUMBER: US 08/027,746
3 FILING DATE: 05-MAR-1993
4 APPLICATION NUMBER: US 08/103,196
5 FILING DATE: 06-AUG-1993
6 ATTORNEY/AGENT INFORMATION:
7 NAME: Weber, Ellen Lauver
8 REGISTRATION NUMBER: 32,762
9 REFERENCE/DOCKET NUMBER: 019623-005030US
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (415) 576-0200
12 TELEFAX: (415) 576-0300
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1 MEDIUM TYPE: Floppy disk  
 2 COMPUTER: IBM PC compatible  
 3 OPERATING SYSTEM: PC-DOS/MS-DOS  
 4 SOFTWARE: Patent In Release #1.0, Version #1.0  
 5 CURRENT APPLICATION DATA:  
 6 APPLICATION NUMBER: US/98/966,488  
 7 FILING DATE:  
 8 CLASSIFICATION: 435  
 9 PRIOR APPLICATION DATA:  
 10 APPLICATION NUMBER: JP 311,235/1996  
 11 FILING DATE: 8-NOV-1996  
 12 PRIOR APPLICATION DATA:  
 13 APPLICATION NUMBER: JP 61,716/97  
 14 FILING DATE: 3-MAR-1997  
 15 ATTORNEY/AGENT INFORMATION:  
 16 NAME: BROWDY, Roger L.  
 17 REGISTRATION NUMBER: 25,618  
 18 REFERENCE/DOCKET NUMBER:  
 19 TELECOMMUNICATION INFORMATION:  
 20 TELEPHONE: 202-628-5197  
 21 TELEFAX: 202-737-3528  
 22 TELEX: 248633  
 23 INFORMATION FOR SEQ ID NO: 8:  
 24 SEQUENCE CHARACTERISTICS:  
 25 LENGTH: 10 amino acids  
 26 TYPE: amino acid  
 27 TOPOLOGY: linear  
 28 MOLECULE TYPE: peptide  
 29 FRAGMENT TYPE: internal fragment  
 30 US-914-966 388 8  
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 32 Query Match: 43.6% Score 24; DB 2; Length 10;  
 33 Best Local Similarity 57.1%; Pred. No. 1.4e+02;  
 34 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
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 36 QV 1 CHUFFEDS 7  
 37 DB 1 CHUFFEDS 7  
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 39 RESULT 8  
 40 US-09-188-424-8  
 41 Sequence 8, Application US/09188404  
 42 Patent No. 6145487  
 43 GENERAL INFORMATION:  
 44 APPLICANT: TOMOYUKI NISHIMOTO  
 45 APPLICANT: MICHIO KUROTA  
 46 APPLICANT: HIROTO CHAEN  
 47 APPLICANT: TOSHIO MIYAKE  
 48 TITLE OF INVENTION: KOLIBRISE PHOSPHORYLASE, ITS PREPARATION AND USES  
 49 NUMBER OF SEQUENCES: 10  
 50 CORRESPONDENCE ADDRESS:  
 51 ADDRESSEE: BROWDY AND NEIMARK  
 52 STREET: 419 Seventh Street, N.W., Suite 300  
 53 CITY: Washington  
 54 STATE: D.C.  
 55 COUNTRY: USA  
 56 ZIP: 20004  
 57 COMPUTER READABLE FORM:  
 58 MEDIUM TYPE: Floppy disk  
 59 COMPUTER: IBM PC compatible  
 60 OPERATING SYSTEM: PC-DOS/MS-DOS  
 61 SOFTWARE: Patent In Release #1.0, Version #1.0  
 62 CURRENT APPLICATION DATA:  
 63 APPLICATION NUMBER: US/09/188,404  
 64 FILING DATE:  
 65 CLASSIFICATION:  
 66 PRIOR APPLICATION DATA:  
 67 APPLICATION NUMBER: 09/966,388  
 68 FILING DATE:  
 69 PRIOR APPLICATION DATA:  
 70 APPLICATION NUMBER: JP 61,716/97  
 71 FILING DATE: 3-MAR-1997  
 72 ATTORNEY/AGENT INFORMATION:  
 73 NAME: BROWDY, Roger L.  
 74 REGISTRATION NUMBER: 25,618  
 75 REFERENCE/DOCKET NUMBER:  
 76 TELECOMMUNICATION INFORMATION:  
 77 TELEPHONE: 202-628-5197  
 78 TELEFAX: 202-737-3528  
 79 TELEX: 248633  
 80 INFORMATION FOR SEQ ID NO: 8:  
 81 SEQUENCE CHARACTERISTICS:  
 82 LENGTH: 10 amino acids  
 83 TYPE: amino acid  
 84 TOPOLOGY: linear  
 85 MOLECULE TYPE: peptide

1 ATTORNEY/AGENT INFORMATION:  
 2 NAME: BROWDY, Roger L.  
 3 REGISTRATION NUMBER: 25,618  
 4 REFERENCE/DOCKET NUMBER:  
 5 TELECOMMUNICATION INFORMATION:  
 6 TELEPHONE: 202-628-5197  
 7 TELEFAX: 202-737-3528  
 8 TELEX: 248633  
 9 INFORMATION FOR SEQ ID NO: 8:  
 10 SEQUENCE CHARACTERISTICS:  
 11 LENGTH: 10 amino acids  
 12 TYPE: amino acid  
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 14 MOLECULE TYPE: peptide  
 15 FRAGMENT TYPE: internal fragment  
 16 US-09-188-403-8  
 17  
 18 Query Match: 43.6% Score 24; DB 3; Length 10;  
 19 Best Local Similarity 57.1%; Pred. No. 1.4e+02;  
 20 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 21  
 22 QV 1 CHUFFEDS 7  
 23 DB 1 CHUFFEDS 7  
 24  
 25 RESULT 9  
 26 US-09-188-424-8  
 27 Sequence 8, Application US/09188404  
 28 Patent No. 6145487  
 29 GENERAL INFORMATION:  
 30 APPLICANT: TOMOYUKI NISHIMOTO  
 31 APPLICANT: MICHIO KUROTA  
 32 APPLICANT: HIROTO CHAEN  
 33 APPLICANT: TOSHIO MIYAKE  
 34 TITLE OF INVENTION: KOLIBRISE PHOSPHORYLASE, ITS PREPARATION AND USES  
 35 NUMBER OF SEQUENCES: 10  
 36 CORRESPONDENCE ADDRESS:  
 37 ADDRESSEE: BROWDY AND NEIMARK  
 38 STREET: 419 Seventh Street, N.W., Suite 300  
 39 CITY: Washington  
 40 STATE: D.C.  
 41 COUNTRY: USA  
 42 ZIP: 20004  
 43 COMPUTER READABLE FORM:  
 44 MEDIUM TYPE: Floppy disk  
 45 COMPUTER: IBM PC compatible  
 46 OPERATING SYSTEM: PC-DOS/MS-DOS  
 47 SOFTWARE: Patent In Release #1.0, Version #1.0  
 48 CURRENT APPLICATION DATA:  
 49 APPLICATION NUMBER: US/09/188,404  
 50 FILING DATE:  
 51 CLASSIFICATION:  
 52 PRIOR APPLICATION DATA:  
 53 APPLICATION NUMBER: 09/966,388  
 54 FILING DATE:  
 55 PRIOR APPLICATION DATA:  
 56 APPLICATION NUMBER: JP 61,716/97  
 57 FILING DATE: 3-MAR-1997  
 58 ATTORNEY/AGENT INFORMATION:  
 59 NAME: BROWDY, Roger L.  
 60 REGISTRATION NUMBER: 25,618  
 61 REFERENCE/DOCKET NUMBER:  
 62 TELECOMMUNICATION INFORMATION:  
 63 TELEPHONE: 202-628-5197  
 64 TELEFAX: 202-737-3528  
 65 TELEX: 248633  
 66 INFORMATION FOR SEQ ID NO: 8:  
 67 SEQUENCE CHARACTERISTICS:  
 68 LENGTH: 10 amino acids  
 69 TYPE: amino acid  
 70 TOPOLOGY: linear  
 71 MOLECULE TYPE: peptide

FRAGMENT TYPE: internal fragment  
US-09-188-404-8

Query Match 43.6% Score 24; DB 1; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHTEFS 7  
DB 1 GHVFWOT 7

RESULT 10

US-09-281-259-8

Sequence 9; Application US/69281259

Patent No. 6204177

GENERAL INFORMATION:

APPLICANT: TOMOYUKI NISHIMOTO

APPLICANT: MICHIO KUBOTA

APPLICANT: HIROO CHAEN

APPLICANT: TOSHIO MIYAKE

TITLE OF INVENTION: KOLIBRIOSE PROSOPHYLASE, ITS PREPARATION AND USES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEWMARK

STREET: 419 Seventh Street, N.W., Suite 800

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS DOS

SOFTWARE: Patent in Release #1.0, Version #1.10

CURRENT APPLICATION DATA: US/09/281-259

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/966,388

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 61,710,797

FILING DATE: 3-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, ROGER L.

REGISTRATION NUMBER: 25,518

REFERENCE/DOCKET NUMBER:

TRICOMMUNICATION INFORMATION:

TELEPHONE: 202 528 5197

TELEFAX: 202 737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal fragment

US-09-281-259-8

Query Match 43.6% Score 24; DB 1; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHTEFS 7  
DB 1 GHVFWOT 7

RESULT 11

US-09-117-860-8

Sequence 8; Application US/09117860A

Patent No. 6338955

GENERAL INFORMATION:

APPLICANT: OGURI, Suguru

APPLICANT: MINOWA, Mari

APPLICANT: YOSHIDA, Arit

APPLICANT: TAKEUCHI, Makoto

TITLE OF INVENTION: NOVEL 1,4-N-ACETYLGLUCOSAMINYLTRANSFERASE AND GENE

TITLE OF INVENTION: ENCODING THE SAME

FILE REFERENCE: 081356/0113

CURRENT APPLICATION NUMBER: US/09/117,860A

CURRENT FILING DATE: 1998-08-12

EARLIER APPLICATION NUMBER: WO 97/2697/04546

EARLIER FILING DATE: 1997-12-10

EARLIER APPLICATION NUMBER: JP 161462/1997

EARLIER FILING DATE: 1997-06-18

EARLIER APPLICATION NUMBER: JP 332411/1996

EARLIER FILING DATE: 1996-12-12

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO 8

LENGTH: 10

TYPE: PRT

ORGANISM: Bovine

US-09-117-860-8

Query Match 43.6% Score 24; DB 4; Length 10;

Best Local Similarity 80.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHTEFS 5

DB 5 GHTEFS 9

RESULT 12

US-08-424-292-2

Sequence 2; Application US/08424292

Patent No. 5939273

GENERAL INFORMATION:

APPLICANT: HAUROSC, Stig

APPLICANT: KJELSEN, John

APPLICANT: KJELSEN, Reid

APPLICANT: JOHANSEN, Tahir M.

APPLICANT: LARSEN, Peter M.

APPLICANT: JENSEN, Ulla A.

APPLICANT: REY, Stephen J.

APPLICANT: BOUTRY, Marc

APPLICANT: REY, Hervé

TITLE OF INVENTION: MARKERS FOR ORGAN REJECTION

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/424,292

FILING DATE: 18-APR-1995

CLASSIFICATION: 535

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1363-1-001

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5803  
 TELEFAX: 201-343-1684  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 DESCRIPTION: Xaa at Position 1 is Gly at Position 2 is Ala  
 HYDROPHILIC: NO

US-08-424-292-2

Query Match 41.8%; Score 23; DB 1; Length 8;  
 Best Local Similarity 80.0%; Pred No. 2.5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GHTFE 5  
 TL 2 GHTFE 4

RESULT 14  
 US-08-149-809-19  
 Sequence 19, Application US/08149809  
 Patent No. 549869  
 GENERAL INFORMATION:  
 APPLICANT: METSALFE, Dean D.  
 APPLICANT: MARTIN, Brian M.  
 APPLICANT: SAC, Pillsbury, V.S.  
 TITLE OF INVENTION: ICE-BINDING PEPTIDES OF A MALE  
 TITLE OF INVENTION: HEAT-STABLE CRUSTACEAN ALLERGEN DERIVED FROM SHRIMP  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 300  
 CITY: Washington, D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/149,809  
 FILING DATE: 10 NOV 1993  
 CLASSIFICATION: 520  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A  
 REGISTRATION NUMBER: 29,769  
 REFERENCE/DOCKET NUMBER: 40399/183/NIH0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 1202-672-5300  
 TELEFAX: 1202-672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

US-08-149-809-19  
 Query Match 41.8%; Score 23; DB 1; Length 9;  
 Best Local Similarity 44.4%; Pred No. 2.5e-05;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HTFEDSTK 10  
 TL 1 HTFEDSTK 9

US-09-267-993-9  
 Sequence 9, Application US/09267993  
 Patent No. 6349692  
 GENERAL INFORMATION:  
 APPLICANT: Jindal, Satish  
 APPLICANT: Regnier, Fred  
 APPLICANT: Evans, David  
 APPLICANT: Williams, Kevin  
 APPLICANT: Afevan, No. 6348624ar  
 APPLICANT: Pallwal, Sandeep  
 APPLICANT: Pingali, Aruna  
 TITLE OF INVENTION: High Speed, automated, continuous flow,  
 FILE OF INVENTION: Multidimensional molecular selection and analysis  
 FILE REFERENCE: SYP 101CN  
 CURRENT APPLICATION NUMBER: US/09/267,993  
 CURRENT FILING DATE: 1999-03-12  
 PRIOR APPLICATION NUMBER: 60/600,518  
 PRIOR FILING DATE: 1995-06-26  
 PRIOR APPLICATION NUMBER: 09/670,670  
 PRIOR FILING DATE: 1996-06-26  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: Patent Ver. 2.0  
 SEQ ID NO 9  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 OTHER INFORMATION: peptide

US-09-267-993-9  
 Query Match 41.8%; Score 23; DB 4; Length 9;  
 Best Local Similarity 80.0%; Pred No. 2.5e-05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHTFE 5  
 TL 4 GHTFE 8

RESULT 15  
 US-09-081-975-2  
 Sequence 2, Application US/09081975  
 Patent No. 6451975  
 GENERAL INFORMATION:  
 APPLICANT: Kaelin, William  
 APPLICANT: Cost, Christine  
 TITLE OF INVENTION: METHODS OF TREATMENT USING  
 TITLE OF INVENTION: NRS 1, ANTIBODIES AND PROTEINS THEREOF, AND USES OF THE  
 TITLE OF INVENTION: ANTIBODIES  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon Peabody LLP  
 STREET: 101 Federal Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FastSeq for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/081,975  
 FILING DATE: 12-MAY-1998  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/946,207  
 FILING DATE: 12-MAY-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Eisenstein, Ronald

US-09-081-975-2  
 Query Match 41.8%; Score 23; DB 4; Length 9;  
 Best Local Similarity 80.0%; Pred No. 2.5e-05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHTFE 5  
 TL 4 GHTFE 8

1 REGISTRATION NUMBER: 30,628  
2 REFERENCE/DOCKET NUMBER: 47400  
3 TELECOMMUNICATION INFORMATION:  
4 TELEPHONE: 617-345-6054  
5 TELEFAX: 617-345-1300  
6 TELEX:  
7 INFORMATION FOR SEQ ID NO: 2:  
8 SEQUENCE CHARACTERISTICS:  
9 LENGTH: 6 amino acids  
10 TYPE: amino acid  
11 STRANDEDNESS: single  
12 TOPOLOGY: linear  
13 US 09 041 973-2

Query Match: 40.0%; Score 22; DB 4; Length 6;  
Best Local Similarity: 100.0%; Pred. No. 2; 50+3;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TFE0 5  
Db 1  
1 TFE0 4

Search completed: November 5, 2003, 17:36:12  
Job time: 13.333 secs

GenCore version 5.1.6  
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OM protein: protein search, using sw model

Run on: November 5, 2003, 17:18:39 ; Search time 13.5 seconds  
(without alignments)  
56.999 Million cell updates/sec

Title: US-09-914-088-5

Perfect score: 51

Sequence: 1 GGGHFFPT 8

Scoring table: BLOSUM62

Gapop 18.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 404

Minimum DB seq length: 0

Maximum DB seq length: 8

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	39.2	7	2 S42407	gramicidin S synth
2	18	35.3	5	2 C53284	T-cell receptor be
3	18	35.3	7	2 B61491	seed protein ws-5
4	18	35.3	8	2 PT0369	T-cell receptor be
5	16	31.4	6	2 PT0369	Ig heavy chain CRD
6	15	29.4	7	2 A61061	tryptophan, bas
7	15	29.4	8	2 PLO184	capid protein VP-
8	14	27.5	3	3 GKHU	growth-modulating
9	14	27.5	4	2 PLO140	carbon-monoxide de
10	14	27.5	4	2 I38898	QCT intrin 16 prot
11	14	27.5	5	2 B37988	acid prorelinase li
12	14	27.5	6	2 A61429	sarcosine dehydrog
13	14	27.5	6	2 B56979	collagen alpha 1(I)
14	14	27.5	7	2 S71299	ICL2 protein - Par
15	14	27.5	7	2 PT0383	Ig heavy chain CRD
16	14	27.5	8	2 S10596	adipokinetic hormo
17	14	27.5	8	2 B39745	endoglycosylseram
18	14	27.5	8	2 S16324	hypothetical prote
19	14	27.5	8	2 S21588	lectin - potato
20	14	27.5	8	2 B47393	neuropeptide cala
21	14	27.5	8	2 S10783	myosin f - bovin
22	14	27.5	8	2 PT0359	T-cell receptor be
23	13	25.5	4	2 S53508	starvation-induced
24	13	25.5	6	2 GNC861	hepatidyl dipeptida
25	13	25.5	6	2 A61049	halo-toxin - Esed
26	13	25.5	6	2 A43129	neuropeptide GRPR
27	13	25.5	7	2 PH1408	Ig heavy chain V r
28	13	25.5	7	2 S58797	serine/threonine-s
29	13	25.5	8	2 A61348	red pigment-conde

30	13	25.5	8	2 S08995	hypertrehalosemic
31	13	25.5	8	2 A49823	adipokinetic hormo
32	13	25.5	8	2 A4960	neuropeptide led-C
33	13	25.5	8	2 A43976	hypertrehalosemic
34	13	25.5	8	2 B43376	hypertrehalosemic
35	13	25.5	8	2 S55310	adipokinetic hormo
36	13	25.5	8	2 A58620	adipokinetic hormo
37	13	25.5	8	2 PH1407	Ig heavy chain V r
38	13	25.5	8	2 A46306	spasmogenic toxin
39	13	25.5	8	2 A05169	neuropeptide M-J
40	13	25.5	8	2 S66646	cardioacceleratory
41	13	25.5	8	2 A14683	aspartate transami
42	13	25.5	9	2 A61328	trypsin (EC 3.4.21
43	12	23.5	3	3 A23751	spinal cord peptid
44	12	23.5	3	3 I78890	tyrosine protein k
45	12	23.5	4	1 ECXAA	antho-RFamide neur

## ALIGNMENTS

### RESULT 1

S42407  
gramicidin S synthetase component II - Bacillus brevis (fragment)  
C:Species: Bacillus brevis  
C:Date: 20-Oct-1994 #sequence\_revision 12-Apr-1996 #text\_change 12-Apr-1996  
C:Accession: S42407  
R:Stein, T.; Vater, J.; Kruff, V.; Wittmann-Liebold, B.; Franke, P.; Panico, M.; Mc Dr  
PEBS Lett. 340, 39-44, 1994  
A:Title: Detection of 4'-phosphopantetheine at the thioester binding site for L-valin  
A:Reference number: S42407; MUID:94164305; PMID:8119405  
A:Accession: S42407  
A:Molecule type: protein  
A:Residues: 1-7 <STE>

Query Match 39.2%; Score 20; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGH 4

DB 2 GGH 4

### RESULT 2

C53284  
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: C53284  
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 891-899, 1991  
A:Title: Evolutionarily conserved organization and sequences of germline diversity an  
A:Reference number: A53284; MUID:91342695; PMID:1678859  
A:Accession: C53284  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-5 <HAR>  
A:Cross-references: DB:S60737; NID:g233916; PIDN:AA19519.1; PID:g233919  
A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60740)  
C:Keywords: T-cell receptor

Query Match 35.3%; Score 18; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3

DB 3 GGG 5

### RESULT 3

E6149:

seed protein ws-5 - winged bean (fragment)

C:Species: Psophocarpus tetragonolobus (winged bean)  
C>Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C:Accession: E61491  
R: Hirano, H.  
A: Protein Chem. 8, 115-130, 1989  
A>Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gels  
A:Reference number: A61491; PMID:89351606; PMID:276119  
A:Accession: E61491  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <R>  
C:Keywords: glycoprotein; seed

Query Match 35.1%; Score 18; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3  
||  
DB 5 GGG 7

#### RESULT 4

P10509  
C:Title: Receptor beta chain V-D-J region (100-4K) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 10-May-1997  
C:Accession: P10509  
R: Feeney, A.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: P10509; PMID:91277601; PMID:711558  
A:Accession: P10509  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-8 <FE>  
A:Experimental source: adult thymus, strain BALB/c  
C:Keywords: T cell receptor

Query Match 35.1%; Score 18; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3  
||  
DB 6 GGG 8

#### RESULT 5

P1280  
C:Title: heavy chain CDR3 region (clone 4 918) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: P1280  
R: Yamada, M.; Kasseran, R.; Reichard, B.A.; Shann, S.; Gaton, A.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J<sub>H</sub> gene segments in the generation of the CDR3 region of the heavy chain of a murine anti-lymphoma antibody  
A:Reference number: P1280; PMID:9104337; PMID:1811102  
A:Accession: P1280  
A:Molecule type: DNA  
A:Residues: 1-6 <YM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotrimer; immunoglobulin

Query Match 31.4%; Score 16; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGHP 6  
||  
DB 1 GGGAP 6

#### RESULT 6

A61081  
C:Title: Phyllomedusa tordei (Rohde's leaf frog)  
C:Species: Phyllomedusa tordei (Rohde's leaf frog)  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Aug-2000  
C:Accession: A61081  
R: Montecucchi, P.C.; Vincenti, M.; Iazzarini, A.M.; Rusconi, L.; Erspamer, V.  
Int. J. Pept. Protein Res. 33, 391-395, 1989  
A:Title: Isolation, structure determination and synthesis of a novel tryptophan-containing peptide from the skin of Phyllomedusa tordei  
A:Reference number: A61081  
A:Accession: A61081  
A:Molecule type: protein  
A:Residues: 1-7 <MON>

C:Comment: The biological activity of this peptide was not determined.  
C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end; hydroxyproline; skin  
F:3/Modified site: 4-hydroxyproline (Pro) #status experimental  
F:7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 29.4%; Score 15; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 PPT 8  
||  
DB 2 PBS 4

#### RESULT 7

P10184  
C:Title: capsid protein VP-1 - murine poliovirus (fragment)  
C:Species: murine poliovirus; Theiler's encephalomyelitis virus  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Feb-1995  
C:Accession: P10184  
R: Zurbriggen, A.; Hogle, J.M.; Fujinami, R.S.  
J. Exp. Med. 170, 2037-2049, 1989  
A:Title: Alteration of amino acid 101 within capsid protein VP-1 changes the pathogen specificity of murine poliovirus  
A:Reference number: P10184; PMID:90063468; PMID:2479706  
A:Accession: P10184  
A:Molecule type: genomic RNA  
A:Residues: 1-8 <ZUR>  
C:Keywords: capsid protein

Query Match 29.4%; Score 15; DB 2; Length 8;  
Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 2 GGG-HFP 6  
||  
DB 2 GGG-HFP 8

#### RESULT 8

GKHU  
C:Title: growth-modulating peptide - human  
C:Species: Homo sapiens (man)  
C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: A01421  
R: Schlesinger, D.H.; Pickart, L.; Thaler, M.M.  
Experientia 33, 324-325, 1977  
A:Title: Growth modulating serum tripeptide is glycyl-histidyl-lysine.  
A:Reference number: A01421; PMID:7762369; PMID:858356  
A:Accession: A01421  
A:Molecule type: protein  
A:Residues: 1-3 <SCH>  
A:Note: this serum tripeptide is found to stimulate growth of some cell types and to inhibit growth of others  
C:Superfamily: unassigned animal peptides

Query Match 27.5%; Score 14; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 3 GH 4  
||  
Db 1 GH 2

## RESULT 9

PL0140  
carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrogena  
C:Species: Pseudomonas carboxydohydrogena  
C:Date: 07-Sep-1990 #sequence\_revision: 07-Sep-1990 #text\_change 28 Apr-1993  
C:Accession: PL0140

R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.

Arch. Microbiol. 152, 335-341, 1989

A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydohydrog

A:Reference number: PL0138; MUID:90056678; PMID:2618128

A:Accession: PL0140

A:Molecule type: protein

A:Residues: 1-4 <KRA>

C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me

C:Keywords: oxidoreductase

Query Match 27.5%; Score 14; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4  
||  
Db 2 GH 3

## RESULT 10

I38888

COI intron 16 protein - Podospora anserina mitochondrion

C:Species: Mitochondrion Podospora anserina

C:Date: 03 Feb-1994 #sequence\_revision 03 Feb-1994 #text\_change 07-Dec-1999

C:Accession: I38888

R:Cummings, D.J.; Michel, F.; McNally, K.L.

Curr. Genet. 16, 381-406, 1989

A:Title: DNA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit I mi

A:Reference number: A18327; MUID:90124722; PMID:2558803

A:Accession: I38888

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-4 <CUM>

A:Cross references: GB:X55026; GB:M15937; GB:X61714

A:Genome: mitochondrion

A:Genetic code: SQ3

C:Keywords: mitochondrion

Query Match 27.5%; Score 14; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4  
||  
Db 3 GH 4

## RESULT 11

B37988

acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)

C:Species: Physarum polycephalum

C:Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993

C:Accession: B37988

J:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Og

J. Biol. Chem. 265, 19898-19903, 1990

A:Title: Purification and characterization of a novel intracellular acid proteinase from

A:Reference number: A37988; MUID:91060608; PMID:2246266

A:Accession: B37988

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 <MUR>

Query Match 27.5%; Score 14; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
||  
Db 3 PP 4

## RESULT 12

A61419

sarcosine dehydrogenase (EC 1.5.99.1) - Pseudomonas sp. (strain WRF) (fragment)

C:Species: Pseudomonas sp.

C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999

C:Accession: A61419

R:Pinto, J.T.; Frisell, W.R.

Arch. Biochem. Biophys. 169, 483-491, 1975

A:Title: Characterization of the peptide-bound flavin of a bacterial sarcosine dehydro

A:Reference number: A61419; MUID:76038634; PMID:241294

A:Accession: A61419

A:Molecule type: protein

A:Residues: 1-6 <PIN>

C:Keywords: FAD; flavoprotein; oxidoreductase; phosphoprotein

F:6/Modified site: 3'-FAD-histidine (His) #status experimental

Query Match 27.5%; Score 14; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4  
||  
Db 5 GH 6

## RESULT 13

B56979

collagen alpha 1(I) chain - bovine (fragment)

N:Alternate names: collagen alpha 3(XI) chain

C:Species: Bos primigenius taurus (cattle)

C:Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 03-Oct-1995

C:Accession: B56979

R:Wu, J.J.; Eyre, D.R.

J. Biol. Chem. 270, 18865-18870, 1995

A:Title: Structural analysis of cross-linking domains in cartilage type XI collagen. I

A:Reference number: A56978; MUID:95370194; PMID:7642541

A:Accession: B56979

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-6 <WJA>

A>Note: the residue designated "X" is modified lysine in collagen 1(II); some cross-link

Query Match 27.5%; Score 14; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4  
||  
Db 4 GH 5

## RESULT 14

S71299

ICL2 protein - Paramacium tetraurelia (fragment)

C:Species: Paramacium tetraurelia

C:Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999

C:Accession: S71299

R:Maddipati, L.; Klotz, C.; le Caer, J.P.; Beissson, J.

Eur. J. Biochem. 238, 121-128, 1996

A:Title: Characterization of centrin genes in Paramacium.

A:Reference number: S71298; MUID:96248429; PMID:8665928

A:Accession: S71299

A:Molecule type: protein

A:Residues: 1-7 <MAD>  
A:Experimental source: strain d4-2  
C:Genetics:  
A:Genetic code: SGCS

Query Match 27.5%; Score 14; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
DB 3 PP 4

RESULT: 15  
P:0283  
IG heavy chain CDR3 region (clone 4-94B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Aug-1996  
C:Accession: P0283  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Calton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: P0222; XUID:911C337; PMID:1899102  
A:Accession: P0283  
A:Molecule type: DNA  
A:Residues: 1-7 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 27.5%; Score 14; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
DB 6 PP 7

Search completed: November 5, 2003, 17:22:56  
Job time : 14.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein protein search, using sw model

Run on: November 5, 2003, 17:15:14 / Search time 9.5 Seconds  
(without alignments)  
39.601 Million cell updates/sec

Title: US-09 914-088-5  
Perfect score: 51  
Sequence: 1 GGSHFPPT 8

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0  
Maximum DB seq length: 8  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.4

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	33.3	8	1 LMT2_L0CM1	P22396 locusta mig
2	15	29.4	5	1 PAP2_PAPMA	P81864 pardachirus
3	14	27.5	3	1 GRW2_HUMAN	P01157 homo sapien
4	14	27.5	4	1 DCM2_BSECH	P13316 pseudomonas
5	14	27.5	7	1 PARS_HIRVE	P42364 hirudo med
6	14	27.5	7	1 TPEY_PACDA	P41455 pachymedusa
7	14	27.5	7	1 UF04_MOUSE	P13642 mus musculu
8	14	27.5	7	1 UN06_PIRUS	P13675 pinus pinas
9	14	27.5	8	1 AKH1_LBGAU	P13418 libellula a
10	14	27.5	8	1 ALL5_CALNG	P13841 calliphora
11	14	27.5	8	1 BRK2_PEPAM	P42392 periplaneta
12	14	27.5	8	1 UF06_MOUSE	P13644 mus musculu
13	13	25.5	6	1 FARP_MOUSE	P41966 moniezia ex
14	13	25.5	8	1 ALL6_CARMA	P41819 carcinus ma
15	13	25.5	8	1 ALL9_CARMA	P41812 carcinus ma
16	13	25.5	8	1 HTE1_PEPAM	P42548 periplaneta
17	13	25.5	8	1 HTE1_TENXC	P25419 tenebrio mo
18	13	25.5	8	1 RPCH_PANBO	P08939 pandanus bo
19	12	23.5	5	1 PRCT_PEPAM	P01373 periplaneta
20	12	23.5	6	1 TM0F_SARBU	P41495 sarcophaga
21	12	23.5	7	1 LANC_CARJ1	P36960 carinobacter
22	12	23.5	8	1 ACI1_THUAL	P18691 thunnus alb
23	12	23.5	8	1 AKH1_TABAT	P14595 tabanus atr
24	12	23.5	8	1 HTE2_PEPAM	P42549 periplaneta
25	12	23.5	8	1 LCK5_LEUMA	P19997 leucophaea
26	12	23.5	8	1 LPK1_LEUMA	P13049 leucophaea
27	12	23.5	8	1 NPB1_BOVIN	P15507 bos taurus
28	12	23.5	8	1 VGLG_HSV2B	P41783 herpes simp
29	12	23.5	8	1 WPI1_PEPAT	P41125 perkinsus a
30	11	21.6	5	1 RE12_PEPAT	P42073 periplaneta
31	11	21.6	6	1 ETO1_PEPAT	P42076 periplaneta
32	11	21.6	8	1 ALL1_CYDPO	P42152 cydia pomon
33	11	21.6	8	1 FARP_CALVE	P41854 calliphora

#### RESULT 1

LMT2\_L0CM1 LMT2\_L0CM1 STANDARD: PRT; 8 AA.  
AC P22396;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-AUG-1991 (Rel. 19, Last annotation update)  
DE Locustamytotropin 2 (LOC-MT-2).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC Tissue:Corpora cardiaca;  
RA Schoofs L., Holman G.X., Hayes T.K., Nachman R.J., de Loof A.;  
RT "Isolation, identification and synthesis of locustamytotropin II, an  
RT additional neuropeptide of Locusta migratoria. Member of the  
RT cephalomyotropic peptide family";  
RL Insect Biochem. 20:479-484(1990).  
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR InterPro: IPR001484; Pyrokinin.  
DR PROSITE: PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES. 8 AXIDATION.  
SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;

Query Match 33.3%; Score 17; DB 1; Length 8;  
Best Local Similarity 60.0%; Pred. No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GHFP 7

DB 2 GEFTP 6

#### RESULT 2

PAP2\_PAPMA PAP2\_PAPMA STANDARD: PRT; 5 AA.  
AC P81864;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Pardaxin II (PXII) (Fragment).  
OS Pardachirus marmoratus (Red sea moles sole).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Soleioidae; Soleidae; Pardachirus.  
OX NCBI\_TaxID=31097;  
RN [1]  
RP SEQUENCE.  
RC Tissue=Skin; Sarcotomus;

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RX MEDLINE=67057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT POLYPEPTIDES from the secretion of the Red sea murex sole (Paridachirus
RT "armatus").";
RD J. Biol. Chem. 261:16704-16713(1986).
CC -1- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON_TER 5
SQ SEQUENCE 5 AA; 614 MW; 7769090908100000 CRC64;

Query Match 29.4%; Score 15; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGFFP 6
Db |||
: GGFFP 5

RESULT 3
GRWM HUMAN
ID GRWM HUMAN STANDARD; PRT; 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 0; Created)
DT 21-JUL-1986 (Rel. 01; Last sequence update)
DT 21-JUL-1986 (Rel. 01; Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
FX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycy-l-histidyl-lysine.";
RL Exp. 33:324-325(1977)
CC -1- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR GO: GO:0001558; Proliferation of cell growth; HAS.
SQ SEQUENCE 3 AA; 340 MW; 6318100000000000000 CRC64.

Query Match 27.5%; Score 14; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4
Db |||
1 GH 2

RESULT 4
DCML PSECH
ID DCML PSECH STANDARD; PRT; 4 AA.
AC P19976;
DT 01-FEB-1991 (Rel. 17; Created)
DT 01-FEB-1991 (Rel. 17; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.9.2) (CO
DE dehydrogenase subunit L) (CO-OL L) (fragment).
GN CCTL.
OS Pseudomonas carboxydhydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE

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RX MEDLINE=90055678; PubMed=2878128;
RA Kraut M., Hugiendick I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -1- CATALYTIC ACTIVITY: CO + H2O + acceptor = CO(2) + reduced
CC acceptor.
CC -1- COFACTOR: Molybdenum (molybdopterin).
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR; PLC140; PL0140.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4
SQ SEQUENCE 4 AA; 441 MW; 7761876F00000000 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4
Db |||
2 GH 3

RESULT 5
FARS HIRME
ID FARS HIRME STANDARD; PRT; 7 AA.
AC P42564;
DT 01-NOV-1995 (Rel. 32; Created)
DT 01-NOV-1995 (Rel. 32; Last sequence update)
DT 01-NOV-1995 (Rel. 32; Last annotation update)
DE FMRFamide-like neuropeptide GGRYMRP-amide.
OS Hirudo medicinalis (Medicinal leech)
CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
CC Arynchobellida; Hirudiniformes; Hirudinidae; Hirudo.
CX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 858 MW; 64D4069553387810 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHF 5
Db |||
: GGRY 4

RESULT 6
TPFY PACDA
ID TPFY PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41; Created)
DT 28-FEB-2003 (Rel. 41; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE Tryptophyllin-1 (pdt-1)
OS Pachymedusa daemicolor (Giant mexican leaf frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
CC Phyllomedusinae; Pachymedusa.
CX NCBI_TaxID=75989;
RN [1]
RP SEQUENCE

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RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-1, AND AMIDATION OF
RC PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Cir D.F., Shaw C.;
RT "Pachymedusa dactylosa tryptophyllin-1 (PdT-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA.";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=VALDI.
DR GC: GO:0005576; Cerebral cellular; NAS.
DR GO: GO:0045986; P: negative regulation of smooth muscle contraction; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD_RES 3 3 HYDROXYLATION.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 2 PP 3

RESULT 7
UN06_MOUSE
ID UN06_MOUSE STANDARD; PRT; 7 AA.
AC P18642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P16) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Linkin J.F.;
RT "Separation and sequencing of familial and novel muscle proteins
RT using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 766 MW; 68640AB7776327C3 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 3 PP 4

RESULT 8
UN06_PINS
ID UN06_PINS STANDARD; PRT; 7 AA.
AC P1675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N14) (Fragment).
KW Pinus pinaster (Maritime pine).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 923 MW; 69D76724486B5740 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GHFP 6
Db 3 GNLFP 6

RESULT 9
AKH_LIBAU
ID AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaepodera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly."
RC Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR: S10596; S10596.
DR InterPro: IPR02047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 HFPT 8
Db 3 NFPS 7

RESULT 10
ALL5_CALVO
ID ALL5_CALVO STANDARD; PRT; 8 AA.
AC P41841;

```

DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).  
OS Callatostatin vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
CC Neoptera; Endopterygota; Hexapoda; Brachycera; Muscomorpha; Onsteroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93211980; PubMed=8466157;  
RA Duve H., Johansen A.H., Scott A.G., Yu C.G., Yagi K.N., Tobe S.S.,  
RA Thorpe A.;  
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria  
with sequence homology to cockroach allatostatins";  
RJ Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).  
RN [2]  
RP CHARACTERIZATION, AND HYDROXYLATION.  
RC TISSUE=Head;  
RX MEDLINE=94342269; PubMed=8061725;  
RA Duve H., Johansen A.H., Scott A.G., East P., Thorpe A.;  
RT "[Hyp3]Met-callatostatin. Identification and biological properties of  
a novel neuropeptide from the blowfly Calliphora vomitoria";  
RJ J. Biol. Chem. 269:21059-21066(1994).  
RN [3]  
RP FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY  
A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE  
INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO  
BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO  
FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.  
CC -1- TISSUE SPECIFICITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
DR PIR; E47393; E47393.  
KW Neuropeptide; Amidation; Hydroxylation.  
FT MOD\_RES 3 3 HYDROXYLATION (208).  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA: 883 MW; 7D9879CA8H47768 CRC64;  
  
Query Match 27.5%; Score 14; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 PP 7  
DB 2 PP 3  
  
RESULT 11  
ID PK2 PERAM STANDARD; PRT; 6 AA.  
AC P82692;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Pyrokinin-2 (Pea-PK-2) (EXPRJ-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattellidae; Periplaneta.  
OX NCBI\_TaxID=6975;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RX TISSUE=Corpora cardiaca;  
RC MEDLINE=97353921; PubMed=9210163;  
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Garde G.;  
RT "Isolation and structural elucidation of two pyrokinins from the  
retrocerebral complex of the American cockroach";  
RJ Peptides 18:473-478(1997).  
RN [2]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=20189894; PubMed=10723070;  
RA Predel R., Eckert M.;  
RT "Tissue-specific distribution of EXPRJ-amides in the nervous system of

RT the American cockroach.";  
RJ J. Comp. Neurol. 419:352-363(2000).  
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
(MYOTROPIC ACTIVITY).  
CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.  
CC -1- MASS SPECTROMETRY: MW=883; METHOD=MALDI.  
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR InterPro; IPR001494; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; FALSE\_NEG.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA: 884 MW; C834176DD9D7775 CRC64;  
  
Query Match 27.5%; Score 14; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 PP 7  
DB 2 PP 3  
  
RESULT 12  
ID UF06 MOUSE STANDARD; PRT; 8 AA.  
AC P38644;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCB:TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Fibroblast; PubMed=7523108;  
RX MEDLINE=95009907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins  
using preparative two-dimensional gel electrophoresis";  
RJ Electrophoresis 15:735-745(1994).  
CC -1- MISCELLANEOUS: CN THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN IS: 5.2, ITS MW IS: 50 kDa.  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA: 817 MW; A35D0878676B0581 CRC64;  
  
Query Match 27.5%; Score 14; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGCH 4  
DB 5 GGAY 8  
  
RESULT 13  
ID FARP MONEX STANDARD; PRT; 6 AA.  
AC P41966;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE FMRamide-like neuropeptide GNFRF-amide.  
OS Moniezia expansa (Sheep tapeworm).  
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;  
CC Cyclophyllidae; Anoplocephalidae; Moniezia.  
OX NCBI\_TaxID=28841;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93312289; PubMed=8232511;  
RA Maule A.C., Shaw C., Salton D.W., Thim L.;  
RT "GNFRFamide: a novel FMRamide-immunoreactive peptide isolated from

RT the sheep tapeworm, *Moniezia expansa*;  
 RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).  
 CC -1- SIMILARITY: BELONGS TO THE FARP (PYRIMIDINE RELATED PEPTIDE)  
 CC FAMILY.  
 DR PIR: A43129; A43129.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 6 6 6 AMIDATION.  
 SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481F00 CRC64;

Query Match 25.5%; Score 13; DB 1; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GHF 5  
 |||  
 Db 1 GNP 3

RESULT 14  
 ALL9 CARMA STANDARD; PRT; 8 AA.  
 ID A:16 CARMA  
 AC P81819;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinostatatin 16.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubrachyura; Portunoidea; Portunidae; Carcinus.  
 OX NCB:TaxID=6759;  
 RN |||  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Jates P.P.,  
 RA Thorpe A.;  
 RT Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab *Carcinus maenas*.;  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC Neuropeptide; Amidation; Multigene family.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 8 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 813 MW; 7C28E645A8476878 CRC64;

Query Match 25.5%; Score 13; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GHF 5  
 |||  
 Db 1 GNPY 4

RESULT 15  
 ALL9 CARMA STANDARD; PRT; 8 AA.  
 ID A:16 CARMA  
 AC P81812;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinostatatin 9.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubrachyura; Portunoidea; Portunidae; Carcinus.  
 OX NCB:TaxID=6759;  
 RN |||  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Jates P.P.,

RA Thorpe A.;  
 RT Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab *Carcinus maenas*.;  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC Neuropeptide; Amidation; Multigene family.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 8 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 781 MW; 7C2879C0CB476878 CRC64;

Query Match 25.5%; Score 13; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GHF 5  
 |||  
 Db 1 GNPY 4

Search completed: November 5, 2003, 17:21:09  
 Job time : 10.5 secs

GenCore version 5.1.6  
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OM protein protein search, using sw model

Run on: November 5, 2003, 17:18:09 : Search time 27.5 seconds  
(without alignments)  
75,070 Million cell updates/sec

Title: US-09-914-088-5  
Perfect score: 51  
Sequence: 1 GGGHFRPT 9

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 452

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23:  
1: sp.archaea:  
2: sp.bacteria:  
3: sp.fungi:  
4: sp.human:  
5: sp.invertebrate:  
6: sp.mammal:  
7: sp.mhc:  
8: sp.organelle:  
9: sp.phage:  
10: sp.plant:  
11: sp.podent:  
12: sp.virus:  
13: sp.vertebrate:  
14: sp.unclassified:  
15: sp.rvirus:  
16: sp.bacteriap:  
17: sp.archaeap:

Pred. No. is the number of results predicted by the model to have a score greater than or equal to the score of the best being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	33.3	8	13 Q91098	Q91098 manorina me
2	17	33.3	9	13 Q90498	Q90498 erythrura g
3	16	31.4	8	6 Q02831	Q02831 erythrolagus
4	15	29.4	8	6 Q9X571	Q9X571 canis famil
5	14	27.5	7	8 P92214	P92214 amblyopium
6	14	27.5	7	8 P92393	P92393 hordeum vul
7	14	27.5	7	8 P92433	P92433 ichthyopium
8	14	27.5	7	8 P92427	P92427 tetradiclyon
9	14	27.5	7	8 P92432	P92432 aegilops ta
10	14	27.5	7	8 P92221	P92221 bromus iner
11	14	27.5	7	8 P92425	P92425 pseudoroeg
12	14	27.5	7	8 P92181	P92181 hordeum bra
13	14	27.5	7	8 P92387	P92387 renardia p
14	14	27.5	7	8 P92210	P92210 aetopyron c
15	14	27.5	7	8 P92440	P92440 thnopyru
16	14	27.5	7	8 P92218	P92218 astralopy:

17	14	27.5	7	8 P92390	P92390 heteranthe
18	14	27.5	7	8 P92372	P92372 haynaldia v
19	14	27.5	7	8 P92442	P92442 taeniatheru
20	14	27.5	7	8 P92226	P92226 crithopsis
21	14	27.5	7	8 P92385	P92385 hordeum mar
22	14	27.5	7	8 P92421	P92421 psathyrosta
23	14	27.5	7	10 P82445	P82445 nicotiana t
24	14	27.5	8	4 Q16468	Q16468 homo sapien
25	14	27.5	8	10 Q8CTG5	Q8CTG5 lycopersico
26	14	27.5	8	12 Q9J205	Q9J205 hepatitis c
27	13	25.5	8	12 Q90345	Q90345 hepatitis g
28	12	23.5	7	8 Q98866	Q98866 spinacia ol
29	12	23.5	7	11 Q63490	Q63490 rattus norv
30	12	23.5	7	11 Q55184	Q55184 rattus norv
31	12	23.5	9	2 Q9RSL7	Q9RSL7 clostridium
32	12	23.5	8	4 Q15901	Q15901 homo sapien
33	12	23.5	8	4 Q9Y4J3	Q9Y4J3 homo sapien
34	12	23.5	8	5 Q02032	Q02032 lytechinus
35	12	23.5	8	5 P82688	P82688 periplaneta
36	12	23.5	8	8 Q9TXE5	Q9TXE5 leptospermu
37	12	23.5	8	9 Q8SBJ0	Q8SBJ0 bacterioph
38	12	23.5	8	9 Q8H9K1	Q8H9K1 bacterioph
39	12	23.5	8	11 Q9QV15	Q9QV15 rattus sp.
40	12	23.5	8	11 Q99P40	Q99P40 mus musculu
41	12	23.5	8	12 Q64971	Q64971 alfalfa mos
42	11	21.6	7	8 Q8MFY6	Q8MFY6 taraxacum (
43	11	21.6	7	11 Q8K3H6	Q8K3H6 rattus norv
44	11	21.6	8	2 Q45615	Q45615 bacillus su
45	11	21.6	8	5 Q9TWH6	Q9TWH6 perinereis

## ALIGNMENTS

RESULT 1					
Q91098	PRELIMINARY;	PRT;	8 AA.		
AC Q91098;					
DT 01-NOV-1996 (TReMBLrel. 01, Created)					
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)					
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)					
DE Myoglobin (Fragment).					
OS Manorina melanoccephala (Noisy miner).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Archosauria; Aves; Neognathae; Passeriformes; Meliphagidae; Manorina.					
OX NCBI_TaxID=44314;					
RN 11					
RP SEQUENCE FROM N.A.					
RC STRAIN=D02;					
RX MEDLINE=98208049; PubMed=9548272;					
RA Heslewood M.N., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;					
RT "Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae					
RT assessed by temperature gradient gel electrophoresis.";					
RL Electrophoresis 19:142-151(1998).					
DR EMBL; U04977; AAC60364.1; ..					
FT NON_TER	1	1			
FT NON_TER	8	8			
SQ SEQUENCE	8 AA;	893 NW;	C6C1F2C865B046DE CRC64;		
Query Match	33.3%	Score 17;	DB 13;	Length 8;	
Best Local Similarity	75.0%	Pred. No. 8.3e+05;			
Matches	3;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
QY	2	GGHF	5		
Db	5	GVHF	8		
RESULT 2					
Q90498	PRELIMINARY;	PRT;	8 AA.		
ID Q90498					
AC Q90498;					
DT 01-NOV-1996 (TReMBLrel. 01, Created)					



DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 D7 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Myoglobin (Fragment)  
 OS Erythrura gouldiae (Gouldian finch)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Passeriformes; Passeridae; Passeridae;  
 CC Erythrura  
 CX NCBI\_TaxID=44316;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EGG1;  
 RX MEDLINE=98208049; PubMed=9548272;  
 RA Heslewood M.M., Elphinstone M.S., Tidemann S., Paverstock P.R.,  
 RT "Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae  
 assessed by temperature gradient gel electrophoresis";  
 RL Electrophoresis 19:142-151(1998)  
 DR EMBL: U40496; AAC60363.1;  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 890 MW; C6C7F2C965B046DE CRC64;

Query Match 33.3%; Score 17; DB 13; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHF 5  
 DB 5 GVHF 8

## RESULT 3

OC2831  
 ID OC2831 PRELIMINARY; FRT; 8 AA.  
 AC OC2831  
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DE 01 DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Pro alpha 1 type II collagen protein (Fragment)  
 OS Oryctolagus cuniculus (Rabbit)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus  
 CX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=96377339; PubMed=8783161;  
 RA Metzaranta M., Kujala U.M., Peltomäki M., Oksanen J., Alho H.,  
 RA Vuorio E.  
 RT "Evidence for insufficient chondrocytic differentiation of articular cartilage repair  
 at full thickness defects of articular cartilage"  
 RL Matrix Biol 15:439-47(1996)  
 DR EMBL: S83371; AAC44331.1;  
 KW Collagen  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 1028 MW; H859C2728A77371 CRC64;

Query Match 31.4%; Score 16; DB 5; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 HFP 6  
 DB 1 HWP 3

## RESULT 4

Q9XSV1  
 ID Q9XSV1 PRELIMINARY; FRT; 8 AA.  
 AC Q9XSV1  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DE 01 NOV-1999 (TrEMBLrel. 12, Last annotation update)  
 DE Retinoblastoma protein (Fragment)  
 GN RBP1

OS Canis familiaris (Dog)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis  
 CX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=97049323; PubMed=8894053;  
 RX Venter P.J., Broillette J.A., Yuzbasiyan-Gurkan V., Brewer G.J.,  
 RT "Gene-specific universal mammalian sequence-tagged sites: application  
 to the canine genome";  
 RL Biochem. Genet. 34:321-341(1996)  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Venter P.J., Cao Y., Alexander L., Yuzbasiyan-Gurkan V.,  
 RT "Dinucleotide repeat polymorphism in the canine retinoblastoma (RB1)  
 gene";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF155737; AAD38807.1;  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 895 MW; 1425BB18676721E3 CRC64;

Query Match 29.4%; Score 15; DB 6; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HFP 6  
 DB 2 HLP 4

## RESULT 5

P92214  
 ID P92214 PRELIMINARY; FRT; 7 AA.  
 AC P92214  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein l1 (Fragment)  
 GN RPS11  
 OS Amblyoprium muticum  
 CC Chloroplast  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;  
 CC Triticeae; Amblyoprium  
 CX NCBI\_TaxID=4595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H8572; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.,  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997)  
 DR EMBL: Z77756; CAB01346.1;  
 KW Chloroplast  
 FT NON\_TER 1 1  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 DB 1 PP 2

## RESULT 6

P92393  
 ID P92393 PRELIMINARY; FRT; 7 AA.  
 AC P92393  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)

DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Hordeum vulgare (Barley).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 CX NCBI\_TaxID=4513;  
 RV [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H3139; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77764; CAB01370.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

## RESULT 7

P92403  
 ID P92403 PRELIMINARY; PRT; 7 AA.  
 AC P92403;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created);  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Triticum elongatum (Tall wheatgrass) (Aegilops elongatum).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Triticum.  
 CX NCBI\_TaxID=4588;  
 RV [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6692; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77743; CAB01307.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

## RESULT 8

P92427  
 ID P92427 PRELIMINARY; PRT; 7 AA.  
 AC P92427;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein (Fragment).  
 GN RPS11.  
 OS Peridictyon sanctum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Peridictyon.  
 CX NCBI\_TaxID=37683;  
 RV [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5575; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77749; CAB01325.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

## RESULT 9

P92430  
 ID P92430 PRELIMINARY; PRT; 7 AA.  
 AC P92430;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Aegilops tauschii (Aegilops squarrosa).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Aegilops.  
 CX NCBI\_TaxID=37682;  
 RV [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6668; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77758; CAB01352.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

## RESULT 10

P92221  
 ID P92221 PRELIMINARY; PRT; 7 AA.

P92237;  
 AC 01-MAY-1997 (TREMBlrel. 03, Created);  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update);  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update);  
 DE Ribosomal protein 11 (Fragment);  
 GN RPS11;  
 CS Bromus inermis (Smooth brome grass);  
 OG Chloroplast;  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Bromaeae; Bromus;  
 OX NCBI\_TaxID=15371;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OSA414; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77759; CAB01355.1; -;  
 KW Chloroplast;  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

RESULT 11  
 P92426  
 ID P92426 PRELIMINARY; PRT; 7 AA.  
 AC P92426;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created);  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update);  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update);  
 DE Ribosomal protein 11 (Fragment);  
 GN RPS11;  
 CS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum);  
 OG Chloroplast;  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Pseudoroegneria;  
 OX NCBI\_TaxID=4604;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H9082; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77744; CAB01310.1; -;  
 KW Chloroplast;  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

RESULT 12  
 P92387;  
 ID P92387 PRELIMINARY; PRT; 7 AA.  
 AC P92387;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created);  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update);  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update);  
 DE Ribosomal protein 11 (Fragment);  
 GN RPS11;  
 CS Hordeum brachyantherum;  
 OG Chloroplast;  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Hordeum;  
 OX NCBI\_TaxID=52712;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5556; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77748; CAB01322.1; -;  
 KW Chloroplast;  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

P92387;  
 ID P92387 PRELIMINARY; PRT; 7 AA.  
 AC P92387;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created);  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update);  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update);  
 DE Ribosomal protein 11 (Fragment);  
 GN RPS11;  
 CS Hordeum brachyantherum;  
 OG Chloroplast;  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Hordeum;  
 OX NCBI\_TaxID=52712;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5556; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77761; CAB01361.1; -;  
 KW Chloroplast;  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
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 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
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QY 6 PP 7  
 ||  
 Db 1 PP 2

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 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update);  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update);  
 DE Ribosomal protein 11 (Fragment);  
 GN RPS11;  
 CS Henrardia persica;  
 OG Chloroplast;  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Henrardia;  
 OX NCBI\_TaxID=37679;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5556; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77748; CAB01322.1; -;  
 KW Chloroplast;  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 1 PP 2

RESULT 14  
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 ID P92387 PRELIMINARY; PRT; 7 AA.  
 AC P92387;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created);  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update);  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update);  
 DE Ribosomal protein 11 (Fragment);  
 GN RPS11;  
 CS Henrardia persica;  
 OG Chloroplast;  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Henrardia;  
 OX NCBI\_TaxID=37679;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5556; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77748; CAB01322.1; -;  
 KW Chloroplast;  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 Query Match 27.5%; Score 14; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
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 Db 1 PP 2

Search completed: November 5, 2003, 17:22:18  
Job time : 28.5 secs

P92210  
ID P92210 PRELIMINARY; PRT: 7 AA.  
AC P92210;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein l1 (Fragment).  
GN RPS11.  
GN Agropyron cristatum.  
OS Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;  
OC Triticeae; Agropyron.  
OX NCBI\_TaxID=4593;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=H4349; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rps11  
sequence data."; Mol. Phylogenet. Evol. 7:217-230(1997).  
RL EMBL; 277771; CAB01391.1; -;  
KW Chl. plastid.  
FT NCN TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;  
Query Match 27.5%; Score 14; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
DB 1 PP 2

RESULT 15  
P92440  
ID P92440 PRELIMINARY; PRT: 7 AA.  
AC P92440;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein l1 (Fragment).  
GN RPS11.  
GN Thinopyrum bessarabicum.  
OS Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;  
OC Triticeae; Thinopyrum.  
OX NCBI\_TaxID=4601;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=H6725; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rps11  
sequence data."; Mol. Phylogenet. Evol. 7:217-230(1997).  
RL EMBL; 277769; CAB01385.1; -;  
KW Chl. plastid.  
FT NCN TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;  
Query Match 27.5%; Score 14; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
DB 1 PP 2

GenCore version 5.1.6  
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OX protein : protein search, using sw model

Run on: November 5, 2003, 17:14:39 ; Search time 33.5 Seconds  
(without alignments)  
37.905 Million cell updates

Title: US-09-914-088-5

Perfect score: 51

Sequence: : GGGHFPPT 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:

Minimum seg length: 0

Maximum DB seq length: 3	Maximum DB seq length: 3
Maximum DB seq length: 3	Maximum DB seq length: 3

POST-GRADUATE STUDENT - \$500

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listing first 45 summaries

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- 4: /SID1/cgcdata/geneseq/geneseqp-e/b1/AA1983.DAT:
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- 15: /SID1/cgcdata/geneseq/geneseqp-e/b1/AA1994.DAT:
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- 18: /SID1/cgcdata/geneseq/geneseqp-e/b1/AA1997.DAT:
- 19: /SID1/cgcdata/geneseq/geneseqp-e/b1/AA1998.DAT:
- 20: /SID1/cgcdata/geneseq/geneseqp-e/b1/AA1999.DAT:
- 21: /SID1/cgcdata/geneseq/geneseqp-e/b1/AA2000.DAT:
- 22: /SID1/cgcdata/geneseq/geneseqp-e/b1/AA2001.DAT:
- 23: /SID1/cgcdata/geneseq/geneseqp-e/b1/AA2002.DAT:
- 24: /SID1/cgcdata/geneseq/geneseqp-e/b1/AA2003.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARY

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2	51	100.0	8	22	AA016636	C-epsl: PS	
3	51	100.0	8	23	AB25232.1	Human 19E	
4	40	98.4	6	21	AA325934	PS multi-copy	
5	40	98.4	6	22	AA016559	C-epsl: PS	
6	40	98.4	6	23	AB25233.1	Human 19E	
7	28	94.9	8	17	AA084930	PS centromer	
8	29	94.9	8	21	AA321874	Cyclic psc	
9	29	94.9	8	21	AA321876	Centromer	

## ALIGNMENTS

## RESULT 1

RESOURCES  
AAB25911

ID	AA325911 standard; Peptide; 8 AA.
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4	4
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7	7
8	8
9	9
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13	13
14	14
15	15
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AC AA325911;

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DT 05 JAN 2003 (f:iss: entry)

XXXXXX

DE Ige C-epsilon-2 domain sur

[illegible]

Epitope; myotome; human;  
epitope; disc; human;

allergic disease; immunopre-

KW immunosuppressive; vaccine  
KW allergy; atopy

XX  
allergy; a copy.

50 HCO series

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PN WO20050460-A1.

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31-AUG-2000.

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PF 22-FEB-2000; 20COWO-EP0145

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PR 25-FEB-:993; 99GB-000440

PR 23-NOV-1999; 99GB-0027698.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (PEPT ) PEPTIDE THERAPEUTICS LTD.

XX Dyson M, Friede M, Greenwood J, Hewitt E, Mason A, Mason S,  
PI Randall R, Turnell WG, Van Meckelen WP, Vinals De Bassols YC;  
XX WPI; 2000-57207/53.

XX Peptides useful for treating, preventing and ameliorating allergic  
PT diseases, comprising an isolated surface exposed group of a specific  
PT domain from immunoglobulin E.

XX Claim 6; Page 5; 129pp; English.

XX The present invention describes a peptide (I) comprising an isolated  
CC surface exposed group/epitope (E) of C-epsilon-2 domain (D) of  
CC immunoglobulin E (IgE), or its mimotope. Also described are: (i) an  
CC immunogen (II) for treating allergy comprising (i); (2) a vaccine (III)  
CC for treating allergies comprising (i); (3) a ligand (IV) capable of  
CC recognising E; (4) a pharmaceutical composition (PC) comprising (IV);  
CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
CC (Iia) comprising (Ia); and (7) producing (III) by producing (II). (I)  
CC can have antiallergic and immunosuppressive activities, and can be used  
CC as a vaccine and histamine release inhibitor. (I), (II) and (III) are  
CC useful in medicine and in the manufacture of medicaments for treating  
CC and preventing allergies. (IV) is useful for identifying mimotopes of E,  
CC in medicine and also in manufacturing medicaments for treating  
CC allergies. (I) is useful in diagnostics and in the affinity purification  
CC of circulating anti-IgE antibodies from blood. (II), (III) and PC are  
CC useful for treating a patient susceptible to or suffering from allergies.  
CC (IV) is also useful in diagnosing atopy. AAB25907 to AAB26039 represent  
CC peptide sequences which are used in the exemplification of the present  
CC invention.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 21; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGHFPPT 8  
DB 1 GGGHFPPT 8

RESULT 2

AAU16616  
ID AAU16616 standard; Peptide; 8 AA.

XX AAU16616;  
XX 07 NOV-2001 (first entry)  
XX Peptide P5 derived from Cepsilon2 region of human IgE.  
XX Human; linkage technology; conjugated compound; carrier vehicle;  
XX epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
XX IgE mediated disease; antibody response.

XX Homo sapiens.

XX WO200145745-A2.

XX 28-JUN-2001.

XX 21-DEC-2000; 2000WO-GB04915.

XX 21-DEC-1999; 99GB-0030233.

XX 22-FEB-2000; 2000GB-0004096.

XX 22-AUG-2000; 2000GB-0023707.

XX 22-AUG-2000; 2000GB-0023708.

XX (ACAM-) ACAMIS RES LTD.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX Flinn N, Johnson T;  
XX WPI; 2001-521967/57.

XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
PT mediated diseases.

XX Example 4; Page 21; 48pp; English.

XX The present invention relates to linkage methodology for use in the  
CC conjugation of compounds (e.g. peptides) to carrier vehicles  
CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
CC biological and immunological constructs. The invention provides a  
CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
CC protein) for use in a pharmaceutical composition or a vaccine. The  
CC invention describes peptides derived from or mimotopes of the  
CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
CC (IgE) which are used to produce conjugated compounds. The compounds or  
CC compositions of the invention are useful in the manufacture of a  
CC medicament for the treatment of IgE mediated diseases. The invention  
CC allows for controlled conjugation of a peptide epitope (antigen) to a  
CC protein so as to form an immunogenic conjugate which may be able to  
CC raise a protective antibody response in an animal or human patient.  
CC AAU16632-AAU16913 represent peptides derived from or mimotopes of  
CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGHFPPT 8  
DB 1 GGGHFPPT 8

RESULT 3

ABU00221  
ID ABU00221 standard; Peptide; 8 AA.

XX ABU00221;  
XX 02-SEP-2002 (first entry)

XX Human IgE immunogenic peptide SEQ ID NO: 5.

XX Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
XX vaccine; anti-allergic.

XX Homo sapiens.

XX WO200216409-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-EPC9576.

XX 22-AUG-2000; 2000GB 0020717.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX Friede M, Mason S, Turnell WG, Vinals Bassols YC;  
XX WPI; 2002-489648/52.

XX Conjugate for use in vaccine for treatment of allergy, comprises  
PT disulfide bridge cyclized peptide and immunogenic carrier.

XX Claim 4; Page 9; 45pp; English.

PS The present invention relates to conjugates suitable for use in vaccines,

XX where the conjugate comprises a disulphide bridge cyclised peptide and an

CC immunogenic carrier. The vaccines can be used in the treatment of

CC allergies. The present invention is a peptide immunogen derived from human

CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.

XX Sequence 8 AA;

SQ Query Match 100.0%; Score 51; DB 23; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGHFFPT 8

DB 1 GGHFFPT 8

RESULT 4

ID AAB25934 standard; Peptide; 6 AA.

XX AAB25934;

AC AAB25934;

XX 05-JAN-2001 (first entry)

DT P5 mimotope peptide P5sh: SEQ ID NO:28.

DE Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;

XX allergic disease; immunophylaxis; immunotherapy; anti-allergic;

KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;

KW allergy; atopy.

XX Homo sapiens.

OS WO200050460-A1.

XX 31-AUG-2000.

PD 22-FEB-2000; 2000WO-EP04455.

PF 25-FEB-1999; 99GB-0004405.

XX 29-MAY-1999; 99GB-0007151.

ER 07-MAY-1999; 99GB-0010537.

PR 07-MAY-1999; 99GB-0010538.

PR 07-MAY-1999; 99GB-0010539.

PR 07-AUG-1999; 99GB-0018594.

PR 07-AUG-1999; 99GB-0018603.

PR 07-SEP-1999; 99GB-0021046.

PR 07-SEP-1999; 99GB-0021047.

PR 29-OCT-1999; 99GB-0025619.

PR 23-NOV-1999; 99GB-0027698.

XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.

FA (PEPT) PEPTIDE THERAPEUTICS LTD.

XX Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;

PI Randall R, Turnell WG, Van Mechelen MP, Vinals D, Bassols YC;

XX WPI; 2000-572073/53.

DR Peptides useful for treating, preventing and ameliorating allergic

XX diseases, comprising an isolated surface exposed group of a specific

PT domain from immunoglobulin E -

XX Disclosure; Page 9; 129pp; English.

PS The present invention describes a peptide (I) comprising an isolated

XX surface exposed group/epitope (E1) of C-epsilon-2 domain (D) of

CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an

CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)

CC for treating allergies comprising (II); (3) a ligand (IV) capable of

CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);

CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen

CC (Iia) comprising (Ia); and (7) producing (III) by producing (II). (I)

CC can have anti-allergic and immunosuppressive activities, and can be used

CC as a vaccine and histamine release inhibitor. (I), (II) and (III) are

CC useful in medicine and in the manufacture of medicaments for treating

CC and preventing allergies. (IV) is useful for identifying mimotopes of P,

CC in medicine and also in manufacturing medicaments for treating

CC allergies. (I) is useful in diagnostics and in the affinity purification

CC of circulating anti-IgE antibodies from blood. (I), (II) and (III) are

CC useful for treating a patient susceptible to or suffering from allergies.

CC (IV) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent

CC peptide sequences which are used in the exemplification of the present

CC invention.

XX Sequence 6 AA;

SQ Query Match 78.4%; Score 40; DB 21; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGHFFP 7

DB 1 GGHFFP 6

RESULT 5

ID AAU16659 standard; Peptide; 6 AA.

XX AAU16659;

AC AAU16659;

XX 07-NOV-2001 (first entry)

DT Peptide P5sh derived as mimotope of Cepsilon2 region of human IgE.

DE Human; linkage technology; conjugated compound; carrier vehicle;

XX epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;

KW IgE mediated disease; antibody response.

KW Homo sapiens.

OS Synthetic.

OS WO200145745-A2.

XX 28-JUN-2001.

PD 21-DEC-2000; 2000WO-GH04935.

PF 21-DEC-1999; 99GB-0030233.

PR 22-FEB-2000; 2000GB-0004096.

PR 22-AUG-2000; 2000GB-0020707.

PR 22-AUG-2000; 2000GB-0020708.

XX (ACAM) ACAMBIS RES LTD.

FA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Flinn N, Johnson T;

PI WPI; 2001-521967/57.

DR A linkage comprising an immunogenic conjugate useful treatment of IgE

PT mediated diseases -

XX Example 4; Page 21; 48pp; English.

PS The present invention relates to linkage methodology for use in the

XX conjugation of compounds (e.g. peptides) to carrier vehicles

CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce

CC biological and immunological constructs. The invention provides a

CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a

CC protein) for use in a pharmaceutical composition or a vaccine. The

CC invention describes peptides derived from or mimotopes of the

CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE-mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU:6632 AAU:6913 represent peptides derived from or mimotopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 SC Sequence 6 AA;

Query Match 78.4%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGHFPP 7  
 DB 1 GGHFPP 6

RESULT 6  
 AB000233  
 ID AB000233 standard; Peptide; 6 AA.

XX AR000233;  
 XX  
 DT 02-SEP-2002 (first entry)  
 XX  
 DE Human IgE immunogenic peptide SEQ ID NO: 17.

XX Immunogen; human; IgE; immunoglobulin E allergy; this is a linker;  
 XX vaccine; antiallergic.

XX Homo sapiens.

XX W0200216409.A2.

XX 28-FEB-2002.

XX 17 AUG-2001; 2001WO-EP09576.

XX 22 AUG-2000; 2000GB-0020717.

XX (SMK) SWITHKLINE BEECHAM BIOLOGICALS.

XX (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX Friede M, Mason S, Turnell WG, Vinalis B, et al.

XX WPI, 2002 429648/52.

XX Conjugate for use in vaccine for treatment of allergy, comprises  
 PT disulfide bridge cyclized peptide and immunogenic carrier.

XX Claim 4; Page 9; 45pp; English.

XX The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulphide bridge cyclised peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a peptide immunogen derived from human  
 CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
 XX

SC Sequence 6 AA;

Query Match 78.4%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGHFPP 7  
 DB 1 GGHFPP 6

RESULT 7  
 AAR98050  
 ID AAR98050 standard; peptide; 8 AA.  
 XX  
 AC AAR98050;  
 XX  
 DT 01-AUG-1996 (first entry)  
 XX  
 DE Pseudosteralin F, a cyclic octapeptide.  
 XX  
 KW tyrosinase inhibitor; melanin; skin cosmetic.  
 XX  
 OS Pseudostellaria heterophylla.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "not an N-terminal; this amino acid  
 FT condenses with the C-terminal to form  
 FT a cyclic peptide"  
 FT Modified-site 8  
 FT /note= "not a C-terminal; see above"

PN JP07324095-A.

XX 12-DEC-1995.

XX 30-MAY-1994; 94JP-0116499.

XX 30-MAY-1994; 94JP-0116499.

XX (ITOG/) ITOGAWA H.

PA (HONS) YAKULT HONSHA KK.

XX WPI, 1996-065475/C7.

XX New cyclic peptide(s) designated pseudosteralin A-G - are tyrosinase  
 PT inhibitors and melanin formation inhibitors useful in skin cosmetics  
 XX  
 PS Claim 6; Page 2; 13pp; Japanese.

XX The cyclic peptide is one component of the peptides designated  
 CC pseudosterals A-G which have been extracted from Taishijin root.  
 CC These peptides are tyrosinase inhibitors and melanin formation  
 CC inhibitors which are useful in skin cosmetics. Pseudosterals A,  
 CC B, C, D, E, F and G demonstrated tyrosinase inhibiting IC50 values of  
 CC 131, 187, 63, 100, 175, 50 and 75 microm resp., compared with a  
 CC value of 1.2 mM for arbutin.

XX Sequence 8 AA;

Query Match 54.9%; Score 28; DB 17; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHFPP 7  
 DB 1 GGVJPP 6

RESULT 8  
 AAB11894  
 ID AAB11894 standard; peptide; 8 AA.

XX AAB11894;

XX 14-NOV-2000 (first entry)

XX Cyclic pseudostellarin F.

XX Split intern; peptide cyclisation; trans splicing; peptide library;  
 KW peptide screening; cyclic ester intermediate; Ssp DnaE C-intein;  
 KW plasmid pARCP-p; plasmid pARCB0-p; pseudostellarin F; cyclic.

XX



OS Unidentified.  
XX Key Location/Qualifiers  
FH Modified site 1..8  
FT /note= "The C-terminus condenses with the N terminus to  
FT form a cyclic peptide"  
XX  
PN W0200036093-A2.  
XX  
XX 22-JUN-2000.  
XX  
XX 18-DEC-1999; 99WO-US30162.  
XX  
XX 18-DEC-1998; 98US-0112723.  
XX 07 OCT-1999; 99US-0158077.  
XX  
XX (PENN ) PENN STATE RES FOUND.  
XX  
XX Benkovic SJ, Scott CP, Abel-Santos EV;  
XX  
XX WPI; 2000-43:582/37.  
XX  
XX Non-naturally occurring nucleic acid molecule encodes a target peptide  
PT produced in a host system in a cyclized form or as a splicing  
PT intermediate of the cyclized form .  
XX  
XX Examples; Page 44; 92pp; English.  
XX  
XX The invention relates to methods of producing cyclic peptides which  
XX utilise the trans splicing ability of split inteins to catalyse  
XX cyclisation of a peptide from a precursor peptide. The precursor peptide  
XX has a target peptide interspersed between two portions of a split intein.  
XX The interaction of the two portions of the split intein creates a  
XX catalytically active intein, and also forces the target peptide into a  
XX loop configuration that stabilises the ester isomer of the amino acid at  
XX the junction between one of the intein portions and the target peptide.  
XX A heteroatom from the other intein portion then reacts with the ester to  
XX form a cyclic ester intermediate. The active intein catalyses the  
XX formation of an aminosuccinimide that liberates a cyclised form of the  
XX target peptide, which spontaneously rearranges to form the  
XX thermodynamically favoured backbone cyclic peptide product. The invention  
XX also discloses nucleic acids encoding the precursor peptide (i.e. the  
XX target peptide flanked by the two portions of the split intein),  
XX expression vectors and host cells comprising the nucleic acid, the  
XX cyclised peptide product or a splicing intermediate thereof (e.g., a  
XX thioester or a lariat intermediate), methods of generating peptide  
XX libraries, and methods of screening peptides. The nucleic acid molecules  
XX of the invention are used for making cyclic peptides and peptide  
XX splicing intermediates. The methods can be used for screening the cyclic  
XX peptides, for identifying molecules that bind to the target peptides and  
XX to detect the presence of a predetermined characteristic in a peptide  
XX e.g., the ability to specifically bind a target molecule. The present  
XX sequence represents cyclic pseudostellarin F which was generated  
XX in the exemplifications of the invention.  
SQ Sequence 8 AA;  
  
Query Match 54.9%; Score 28; DB 21; Length 8;  
Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GGHPFP 7  
|||  
Db 2 GGYLPP 7  
  
RESULT 9  
AAB11896  
id AAB11896 standard; Protein; 8 AA.  
XX  
XX AAB11896;  
XX  
XX 14-NOV-2000 (first entry)

XX Pseudostellarin F (linear).  
DE Split intein; peptide cyclisation; trans splicing; peptide library;  
KW peptide screening; cyclic ester intermediate; Ssp DnaE C-intein;  
KW plasmid PARCP-p; plasmid PARCBD-p; pseudostellarin F.  
XX  
XX Unidentified.  
OS  
XX W0200036093-A2.  
XX  
XX 22-JUN-2000.  
XX  
XX 18-DEC-1999; 99WO-US30162.  
XX  
XX 18-DEC-1998; 98US-0112723.  
XX 07-OCT-1999; 99US-0158077.  
XX  
XX (PENN-) PENN STATE RES FOUND.  
XX  
XX Benkovic SJ, Scott CP, Abel-Santos EV;  
XX  
XX WPI; 2000-43:582/37.  
XX N-PSDB; AAA61909.  
XX  
XX Non-naturally occurring nucleic acid molecule encodes a target peptide  
PT produced in a host system in a cyclized form or as a splicing  
PT intermediate of the cyclized form .  
XX  
XX Examples; Fig 3e; 92pp; English.  
XX  
XX The invention relates to methods of producing cyclic peptides which  
XX utilise the trans splicing ability of split inteins to catalyse  
XX cyclisation of a peptide from a precursor peptide. The precursor peptide  
XX has a target peptide interspersed between two portions of a split intein.  
XX The interaction of the two portions of the split intein creates a  
XX catalytically active intein, and also forces the target peptide into a  
XX loop configuration that stabilises the ester isomer of the amino acid at  
XX the junction between one of the intein portions and the target peptide.  
XX A heteroatom from the other intein portion then reacts with the ester to  
XX form a cyclic ester intermediate. The active intein catalyses the  
XX formation of an aminosuccinimide that liberates a cyclised form of the  
XX target peptide, which spontaneously rearranges to form the  
XX thermodynamically favoured backbone cyclic peptide product. The  
XX invention also discloses nucleic acids encoding the precursor peptide  
XX (i.e. the target peptide flanked by the two portions of the split  
XX intein), expression vectors and host cells comprising the nucleic acid,  
XX the cyclised peptide product or a splicing intermediate thereof (e.g., a  
XX thioester or a lariat intermediate), methods of generating peptide  
XX libraries, and methods of screening peptides. The nucleic acid molecules  
XX of the invention are used for making cyclic peptides and peptide  
XX splicing intermediates. The methods can be used for screening the cyclic  
XX peptides, for identifying molecules that bind to the target peptides and  
XX to detect the presence of a predetermined characteristic in a peptide  
XX e.g., the ability to specifically bind a target molecule. The present  
XX sequence represents pseudostellarin F in its linear form. Plasmids  
XX PARCP-p and PARCBD p encode pseudostellarin F. Expression of these  
XX plasmids generates cyclic pseudostellarin F (AAB11894).  
SQ Sequence 8 AA;  
  
Query Match 54.9%; Score 28; DB 21; Length 8;  
Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GGHPFP 7  
|||  
Db 2 GGYLPP 7  
  
RESULT 10  
AAB15296  
id AAB15296 standard; Protein; 7 AA.



PT and preventing rheumatoid arthritis  
PS Claim 1; Page 25; 38pp; English.

XX The peptide is an example of a synthetic peptide contg. a thiol-  
CC active cysteine residue and at least two positively charged amino  
CC acid residues situated at the the N and/or C terminal sides of the  
CC thiol-active cysteine. The peptide is pref. amidated at the C-  
CC terminus. The peptides may be used in conjunction with an antibody  
CC complex comprising a domain specific for an antigenic determinant of  
CC a complex of human IgA and alpha-1-antitrypsin, for use in therapy of  
CC rheumatoid arthritis. Admin. is oral or parenteral.  
CC See also AAR36613-74.

XX Sequence 7 AA;

Query Match 51.0%; Score 26; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGH 4  
|  
|  
|  
|  
DB 3 GGGH 6

RESULT 13  
ABG77672  
ID ABG77672 standard; Peptide; 7 AA.

AC ABG77672;

XX 05-NOV-2002 (first entry)

XX Targetting peptide selective for human organ, tissue or cell type #205.

XX Human; cytostatic; antiinflammatory; antidiabetic; cardiovascular;  
KW immunomodulator; antibacterial; antiviral; gene therapy; cancer;  
XX arthritis; diabetes; inflammatory disease; atherosclerosis;  
XX autoimmune disease; bacterial infection; viral infection;  
KW cardiovascular disease; degenerative disease.

XX Homo sapiens.

XX WC20C20723-A2.

XX 14-MAR 2002.

XX 07-SEP-2001; 2001WC-US28044.

XX 08-SEP-2003; 2003US-231266P.

XX 17-JAN-2001; 2001US-0765101.

XX TEXA; UNIV TEXAS SYSTEM.

PI Arap W, Pasqualini R;

XX WPI; 2002-599247/64.

XX New targeting peptides identified by phage display, useful for treating  
PT a disease state, e.g. cancer, diabetes, inflammatory disease,  
PT atherosclerosis, autoimmune disease, bacterial or viral infection or  
PT cardiovascular disease.

PS Claim 16; Fig 2B; 269pp; English.

XX The invention describes an isolated peptide of 100 amino acids or less  
CC in size. The peptide is useful for treating a disease state, e.g. cancer,  
CC arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune  
CC disease, bacterial infection, viral infection, cardiovascular disease  
CC or degenerative disease. This sequence represents a human targeting  
CC peptide selective for human organs, tissues or cell types.

XX Sequence 7 AA;

Query Match 51.0%; Score 26; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGH 5  
|  
|  
|  
|  
DB 1 GGGH 4

RESULT 14  
AAR36669  
ID AAR36669 standard; peptide; 8 AA.

XX AAR36669;

XX 07-SEP-1993 (first entry)

XX Group 4 synthetic peptide 117.

XX Thiol-active cysteine; antibody; complex; rheumatoid arthritis;  
KW therapy; IgA-alpha-antitrypsin.

XX Synthetic.

XX Key Location/Qualifiers  
FT Modified-site 8 /note= "amidated"

XX GB226:665-A.

XX 26-MAY-1993.

XX 25-NOV-1992; 92GB-0024684.

XX 25-NOV-1991; 91GB-0025024.

XX (BRITE-) BRITISH TECHNOLOGY GROUP LTD.

PI Kirby J, Lewin IV, Nayyar S, Stanworth DR;

XX WPI; 1993-169522/21.

XX New synthetic peptide(s) - cause dissociation or prevent  
PT formation of IgA-alpha-antitrypsin complex, useful for treating  
PT and preventing rheumatoid arthritis

XX Claim 1; Page 27; 38pp; English.

XX The peptide is an example of a synthetic peptide contg. a thiol-  
CC active cysteine residue and at least two positively charged amino  
CC acid residues situated at the the N and/or C terminal sides of the  
CC thiol-active cysteine. The peptide is pref. amidated at the C-  
CC terminus. The peptides may be used in conjunction with an antibody  
CC complex comprising a domain specific for an antigenic determinant of  
CC a complex of human IgA and alpha-1-antitrypsin, for use in therapy of  
CC rheumatoid arthritis. Admin. is oral or parenteral.  
CC See also AAR36613-74 and AAR37353-74.

XX Sequence 8 AA;

Query Match 51.0%; Score 26; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGH 4  
|  
|  
|  
|  
DB 2 GGGH 5

RESULT 15  
AAY65873  
ID AAY65873 standard; Peptide; 8 AA.

XX AAY65873;  
 AC  
 XX 10-FEB-2000 (first entry)  
 DT  
 XX R-myc mutant peptide 2.  
 DE  
 XX Human; frameshift mutant; T cell response; tumour treatment; cancer;  
 KW mutatin.  
 KW  
 XX Homo sapiens.  
 OS  
 XX Synthetic.  
 OS  
 XX W09958552.A2.  
 PN  
 XX 18 NOV 1999.  
 PD  
 XX 03-MAY-1999; 59WO-N000143.  
 EF  
 XX 08-MAY-1998; 98NC-0002097.  
 PR  
 XX (NH2) NCRSK HYDRO AS.  
 PA  
 XX Gaudernack G, Eriksen JA, Moller M, Gjelsten MK, Sauterdal I;  
 P  
 XX WPI; 2000-039064/03.  
 DP  
 XX  
 XX New peptides derived from genes with frameshift mutations, used to  
 PT develop products for the treatment and prophylaxis of cancers .  
 PT  
 XX  
 XX Claim 13; Page 29; 166pp; English.  
 ES  
 XX  
 XX Peptides AAY6584 Y6642 are fragments of mutant proteins arising from a  
 CC frameshift mutation in a gene from a cancer cell. The peptides are  
 CC characterised in that they:  
 CC (i) are at least 8 amino acids long and a fragment of a mutant protein  
 CC arising from a frameshift mutation in a gene of a cancer cell;  
 CC (ii) consist of at least one amino acid of the mutant part of a protein  
 CC sequence encoded by the gene;  
 CC (iii) comprise 0-10 amino acid from the carboxyl terminus of the normal  
 CC part of the protein sequence preceding the amino terminus of the mutant  
 CC sequence and may further extend to the carboxyl terminus of the mutant  
 CC part of the protein as determined by a new stop codon generated by the  
 CC frameshift mutation; and  
 CC (iv) induce, either in their full length or after processing by an  
 CC antigen presenting cell (APC), T cell responses.  
 CC The genes that the peptides are derived from are also defined as  
 CC susceptible to frameshift mutation by having a 3' non-coding base  
 CC repeat sequence of at least 5 residues. The 3' non-coding base repeat  
 CC sequence of at least 4 dinucleoside base units in peptides are  
 CC created by the addition or deletion of 1 or 2 dinucleoside base residues  
 CC from the repeat sequence. The novel peptides can elicit T cell responses  
 CC and toxicity against tumours and cancer cells carrying genes with  
 CC frameshift mutations. The novel peptides and DNA sequences can be used  
 CC for the preparation of a composition for the treatment or prophylaxis of  
 CC cancer.  
 CC  
 XX  
 XX Sequence A AA:  
 SC  
 Query Match 51.0%; Score 26; DB 21; Length 47  
 Best local similarity 100.0%; Pos. No. 100.0%;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 1 GGGH 4  
 III  
 Rn 1 GGGH 4

Search completed: November 5, 2003, 17:20:36  
 Job time: 133.5 secs

GenCore version 5.1.6  
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OM protein - protein: search, using sw model

Run on: November 5, 2003, 17:22:25 ; Search time 22 seconds  
(without alignments)  
62.454 Million cell updates/sec

Title: US-09-914-088-5

Perfect score: 51

Sequence: 1 GGGHFPPT 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 42162

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA:

- 1: /cgn2\_6/ptodata/2/pubaa/US07\_PUBCOMB.pcp.
- 2: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pcp.
- 3: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pcp.
- 4: /cgn2\_6/ptodata/2/pubaa/US06\_PUBCOMB.pcp.
- 5: /cgn2\_6/ptodata/2/pubaa/US07\_NEW\_PUB.pcp.
- 6: /cgn2\_6/ptodata/2/pubaa/PCTUS\_PUBCOMB.pcp.
- 7: /cgn2\_6/ptodata/2/pubaa/US08\_NEW\_PUB.pcp.
- 8: /cgn2\_6/ptodata/2/pubaa/US08\_PUBCOMB.pcp.
- 9: /cgn2\_6/ptodata/2/pubaa/US09A\_PUBCOMB.pcp.
- 10: /cgn2\_6/ptodata/2/pubaa/US09B\_PUBCOMB.pcp.
- 11: /cgn2\_6/ptodata/2/pubaa/US09C\_PUBCOMB.pcp.
- 12: /cgn2\_6/ptodata/2/pubaa/US09\_NEW\_PUB.pcp.
- 13: /cgn2\_6/ptodata/2/pubaa/US10A\_PUBCOMB.pcp.
- 14: /cgn2\_6/ptodata/2/pubaa/US10B\_PUBCOMB.pcp.
- 15: /cgn2\_6/ptodata/2/pubaa/US10C\_PUBCOMB.pcp.
- 16: /cgn2\_6/ptodata/2/pubaa/US10\_NEW\_PUB.pcp.
- 17: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pcp.
- 18: /cgn2\_6/ptodata/2/pubaa/US06\_PUBCOMB.pcp.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	51	100.0	8	12	US-10-082-014-276
2	51	100.0	8	12	US-10-372-076-130
3	26	51.0	4	15	US-10-058-636-7
4	26	51.0	7	12	US-10-080-263C-12
5	25	49.0	6	11	US-09-774-633-225
6	25	49.0	6	11	US-09-969-710-321
7	25	49.0	8	15	US-10-012-035A-32
8	24	47.1	5	12	US-10-301-499A-36
9	23	45.1	7	11	US-09-229-751A-25
10	23	45.1	7	11	US-09-229-751A-31
11	23	45.1	8	15	US-10-043-344-75
12	22	43.1	7	11	US-09-791-151A-20
13	22	43.1	7	12	US-10-223-033-19
14	22	43.1	8	15	US-10-043-344-146
15	22	43.1	8	15	US-10-226-007-1336

16	22	43.1	8	15	US-10-226-007-1336	Sequence 1336, Ap
17	22	43.1	8	15	US-10-226-007-1349	Sequence 1349, Ap
18	21	41.2	6	9	US-09-062-113-1	Sequence 1, Appli
19	21	41.2	6	11	US-09-994-595-89	Sequence 89, Appli
20	21	41.2	6	12	US-10-232-858-1	Sequence 1, Appli
21	21	41.2	6	15	US-10-209-323-6	Sequence 6, Appli
22	21	41.2	7	9	US-09-205-658-296	Sequence 296, App
23	21	41.2	7	9	US-09-782-650-1	Sequence 1, Appli
24	21	41.2	7	9	US-09-731-242A-24	Sequence 24, Appli
25	21	41.2	7	9	US-09-845-667-12	Sequence 12, Appli
26	21	41.2	7	11	US-09-910-582B-2	Sequence 2, Appli
27	21	41.2	7	11	US-09-281-495-9	Sequence 9, Appli
28	21	41.2	7	11	US-09-940-727B-60	Sequence 60, Appli
29	21	41.2	7	11	US-09-940-727B-63	Sequence 63, Appli
30	21	41.2	7	11	US-09-940-727B-66	Sequence 66, Appli
31	21	41.2	7	11	US-09-940-727B-78	Sequence 78, Appli
32	21	41.2	7	12	US-09-963-693-296	Sequence 296, App
33	21	41.2	8	12	US-10-073-333A-17	Sequence 17, Appli
34	21	41.2	8	14	US-10-011-436-10	Sequence 10, Appli
35	21	41.2	8	15	US-10-140-164-18	Sequence 18, Appli
36	21	41.2	8	15	US-10-140-164-47	Sequence 47, Appli
37	20	39.2	3	10	US-09-898-376-2	Sequence 2, Appli
38	20	39.2	3	10	US-09-986-897-2	Sequence 2, Appli
39	20	39.2	3	11	US-09-852-910-167	Sequence 167, App
40	20	39.2	4	12	US-09-800-187-64	Sequence 64, Appli
41	20	39.2	4	12	US-09-800-187-65	Sequence 65, Appli
42	20	39.2	4	12	US-09-800-187-66	Sequence 66, Appli
43	20	39.2	4	12	US-09-800-187-67	Sequence 67, Appli
44	20	39.2	4	12	US-09-800-187-68	Sequence 68, Appli
45	20	39.2	4	12	US-09-800-187-68	Sequence 68, Appli

## ALIGNMENTS

### RESULT 1

US-10-082-014-276  
; Sequence 276, Application US/10082014  
; Publication No. US2003018588A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL  
; FILE REFERENCE: ICC-130.0 4564/85124  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR FILING DATE: 2001-C8-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 276  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-276

Query Match 100.0%; Score 51; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qv 1 GGGHFPPT 8  
| | | | | | | |  
Db 1 GGGHFPPT 8

### RESULT 2

US-10-372-076-130  
; Sequence 130, Application US/10372076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Mark  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS

```

; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-076-130

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Query Match          100.0%; Score 51.0%; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 GGCHFPPT 8
    |||||
DB 1 GGCHFPPT 8

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RESULT 3
US-10-058-636-7
; Sequence 7, Application US/10058636
; Publication No. US20030049270A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: National Research Council of Canada
; TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
; TITLE OF INVENTION: Campylobacter jejuni and its uses
; FILE REFERENCE: 014137-013210US
; CURRENT APPLICATION NUMBER: US/10/058,636
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/212,940
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/038,891
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/272,960
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Linker between
; OTHER INFORMATION: two fusion protein domains
US-10-058-636-7

```

```

Query Match          51.0%; Score 26; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 GGCH 4
    |||
DB 1 GGCH 4

```

```

RESULT 4
US-10-080-263C-32
; Sequence 32, Application US/10080263C
; Publication No. US20030143670A1
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A.
; APPLICANT: Huang, Ling-Yan
; APPLICANT: Wilson, Amy
; TITLE OF INVENTION: DNA ENCODING SW, SEQ4 SECFEETOR
; FILE REFERENCE: 1795/59370-A/CPW/ADM/ANX

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; CURRENT APPLICATION NUMBER: US/10/090,263C
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-263C-32

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```

Query Match          51.0%; Score 26; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 GGCH 5
    ||||
DB 2 GGCH 5

```

```

RESULT 5
US-09-774-639-225
; Sequence 225, Application US/09774639
; Publication No. US2003003555A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 225
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-225

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Query Match          49.0%; Score 25; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 FPPT 8
    |||
DB 3 FPPT 6

```

```

RESULT 6
US-09-969-730-321
; Sequence 321, Application US/09969730
; Publication No. US20030054443A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P2
; CURRENT APPLICATION NUMBER: US/09/969,730
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364

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1 PRIOR FILING DATE: 1997-08-19
2 PRIOR APPLICATION NUMBER: 60/056,370
3 PRIOR FILING DATE: 1997-08-19
4 PRIOR APPLICATION NUMBER: 60/056,367
5 PRIOR FILING DATE: 1997-08-19
6 PRIOR APPLICATION NUMBER: 60/056,365
7 PRIOR FILING DATE: 1997-08-19
8 PRIOR APPLICATION NUMBER: 60/056,733
9 PRIOR FILING DATE: 1997-08-19
10 PRIOR APPLICATION NUMBER: 60/056,557
11 PRIOR FILING DATE: 1997-08-19
12 PRIOR APPLICATION NUMBER: 60/056,543
13 PRIOR FILING DATE: 1997-08-19
14 PRIOR APPLICATION NUMBER: 60/055,970
15 PRIOR FILING DATE: 1997-08-18
16 PRIOR APPLICATION NUMBER: 60/055,986
17 PRIOR FILING DATE: 1997-08-18
18 PRIOR APPLICATION NUMBER: 60/055,311
19 PRIOR FILING DATE: 1997-08-05
20 PRIOR APPLICATION NUMBER: 60/054,808
21 PRIOR FILING DATE: 1997-08-05
22 PRIOR APPLICATION NUMBER: 60/054,803
23 PRIOR FILING DATE: 1997-08-05
24 PRIOR APPLICATION NUMBER: 60/054,804
25 PRIOR FILING DATE: 1997-08-05
26 PRIOR APPLICATION NUMBER: 60/054,809
27 PRIOR FILING DATE: 1997-08-05
28 PRIOR APPLICATION NUMBER: 60/054,806
29 PRIOR FILING DATE: 1997-08-05
30 PRIOR APPLICATION NUMBER: 60/055,312
31 PRIOR FILING DATE: 1997-08-05
32 PRIOR APPLICATION NUMBER: 60/054,798
33 PRIOR FILING DATE: 1997-08-05
34 PRIOR APPLICATION NUMBER: 60/055,309
35 PRIOR FILING DATE: 1997-08-05
36 PRIOR APPLICATION NUMBER: 60/055,312
37 PRIOR FILING DATE: 1997-08-05
38 PRIOR APPLICATION NUMBER: 60/054,807
39 PRIOR FILING DATE: 1997-08-05
40 PRIOR APPLICATION NUMBER: 60/055,386
41 NUMBER OF SEQ ID NOS: 373
42 SOFTWARE: Patent In Ver. 2.0
43 SEQ ID NO 32:
44   1 2 3 4 5 6
45   | | | | |
46   TYPE: PRT
47 ORGANISM: Homo sapiens
48 US 09 969 730-321

Query Match 49.0%; Score 25; DB 11; Length 41
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 5 GHFP 9
Db 3 GHFP 6

RESULT 7
US-10-012-035A-12
; Sequence 32, Application US/10012035A
; Publication No. US20030004103A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel
; TITLE OF INVENTION: MODULATORS OF ACTIVITY OF
; TITLE OF INVENTION: G-PROTEIN-COUPLED RECEPTOR KINASES
; FILE REFERENCE: BEN-SASSON-2C
; CURRENT APPLICATION NUMBER: US/10/012-035A
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 09/735,274
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US98/20314
; PRIOR FILING DATE: 1998-05-20

1 PRIOR APPLICATION NUMBER: US 08/861,338
2 PRIOR FILING DATE: 1997-05-21
3 NUMBER OF SEQ ID NOS: 41
4 SOFTWARE: Fast-SEQ for Windows Version 4.0
5 SEQ ID NO 32
6 LENGTH: 8
7 TYPE: PRT
8 ORGANISM: Artificial Sequence
9 FEATURE:
10 OTHER INFORMATION: Myr:styl:styl at position 1
11 US-10-012-035A-32

Query Match 49.0%; Score 25; DB 15; Length 8;
Best Local Similarity 90.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 GHFP 6
Db 1 GHSP 5

RESULT 8
US-10-301-499A-36
; Sequence 36, Application US/10301499A
; Publication No. US20030148932A1
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Mamachandran
; APPLICANT: Berzov, Alan
; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND METHODS OF USING THE SAME
; FILE REFERENCE: 4040/1K999-US1
; CURRENT APPLICATION NUMBER: US/10/301,499A
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/331,935
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 36
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: synthetic peptide
; US 10-301-499A-36

Query Match 47.1%; Score 24; DB 12; Length 5;
Best Local Similarity 75.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 3 GHFP 6
Db 2 GHVP 5

RESULT 9
US-09-229-751A-25
; Sequence 25, Application US/09229751A
; Publication No. US20030044838A1
; GENERAL INFORMATION:
; APPLICANT: Turbough, Charles K
; TITLE OF INVENTION: PEPTIDE LIGANDS THAT BIND TO SURFACES
; OF BACTERIAL CELLS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glenna Hendricks
; STREET: P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: USA
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/229,751A  
FILING DATE: 14-Jan-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hendricks, Glenna M  
REGISTRATION NUMBER: 32,535  
REFERENCE/DOCKET NUMBER: turn  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 425-8405  
TELEFAX: (703) 425-8406  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Query Match 45.1%; Score 23; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HFPPT 8  
|||  
Db 2 HFLPT 6

RESULT 10  
US-09-229-751A-25  
Sequence 11, Application US/09229751A  
Publication No. US20030644838A1  
GENERAL INFORMATION:  
APPLICANT: Turnbough, Charles K  
TITLE OF INVENTION: PEPTIDE LIGANDS THAT BIND TO SURFACES  
OF BACTERIAL CELLS  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Glenna Hendricks  
STREET: P.O. Box 2509  
CITY: Fairfax  
STATE: VA  
COUNTRY: USA  
ZIP: 22031

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/229,751A  
FILING DATE: 14-Jan-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hendricks, Glenna M  
REGISTRATION NUMBER: 32,535  
REFERENCE/DOCKET NUMBER: turn  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 425-8405  
TELEFAX: (703) 425-8406

INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-229-751A-31

Query Match 45.1%; Score 23; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HFPPT 8  
|||  
Db 2 HFLPT 6

RESULT 11  
US-10-043-344-75  
Sequence 75, Application US/10043344  
Publication No. US200308086A1  
GENERAL INFORMATION:  
APPLICANT: Loomore, Sheena M.  
APPLICANT: Harkness, Robin E.  
APPLICANT: Schryvers, Anthony B.  
APPLICANT: Cheng, Pele  
APPLICANT: Gray-Owen, Scott  
APPLICANT: Mordin, Andrew D.  
APPLICANT: Klein, Michel H.  
TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES  
FILE REFERENCE: 1038-1221 M15  
CURRENT APPLICATION NUMBER: US/10/043,344  
CURRENT FILING DATE: 2002-07-01  
PRIOR APPLICATION NUMBER: 08/649,518  
PRIOR FILING DATE: 1996-05-17  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 75  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Haemophilus influenzae  
US-10-043-344-75

Query Match 45.1%; Score 23; DB 15; Length 8;  
Best Local Similarity 80.0%; Pred. No. 5.9e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGHF 5  
|||  
Db 3 GGGSF 7

RESULT 12  
US-09-791-153A-20  
Sequence 20, Application US/09791153A  
Publication No. US20030103978A1  
GENERAL INFORMATION:  
APPLICANT: Deshpande, Rajendra  
APPLICANT: Hitz, Anna  
APPLICANT: Boyle, William  
APPLICANT: Sullivan, John  
TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOCALCIN BINDING PROTEIN  
FILE REFERENCE: A-633A  
CURRENT APPLICATION NUMBER: US/09/791,153A  
CURRENT FILING DATE: 2001-07-17  
PRIOR APPLICATION NUMBER: 09/511,139  
PRIOR FILING DATE: 2000-02-23  
NUMBER OF SEQ ID NOS: 154  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 20  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-791-153A-20

Query Match 43.1%; Score 22; DB 11; length 7;



Best Local Similarity 80.0%; Pred. No. 5.8e-05; Mismatches 0; Indels 1; Gaps 0;

QY 1 GGGF 5  
|||

Db 1 GGGF 5

RESULT 13

US-10-220-033-18  
; Sequence 18, Application US/10220033  
; Publication No. US20030186906A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene  
; TITLE OF INVENTION: and a molecule binding to an expression product of that  
; TITLE OF INVENTION: gene  
; FILE REFERENCE: P68119US0  
; CURRENT APPLICATION NUMBER: US/10/220,033  
; CURRENT FILING DATE: 2003-03-17  
; PRIOR APPLICATION NUMBER: PCT/EP01/02694  
; PRIOR FILING DATE: 2001-03-10  
; PRIOR APPLICATION NUMBER: EP00105190.3  
; PRIOR FILING DATE: 2000-03-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide  
; OTHER INFORMATION: obtained by screening randomly synthesized  
; OTHER INFORMATION: peptides  
US-10-220-033-18

Query Match 43.1%; Score 22; DB 12; Length 7;  
Best Local Similarity 75.0%; Pred. No. 5.8e-05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPPP 7  
|||

Db 3 HPPP 6

RESULT 14

US-10-043-344-146  
; Sequence 146, Application US/10043344  
; Publication No. US2003008086A1  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M.  
; APPLICANT: Harkness, Robin E.  
; APPLICANT: Schryvers, Anthony B.  
; APPLICANT: Cheng, Pele  
; APPLICANT: Gray-Owen, Scott  
; APPLICANT: Mardin, Andrew D.  
; APPLICANT: Klein, Michel H.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES  
; FILE REFERENCE: 1038-1221 MIS  
; CURRENT APPLICATION NUMBER: US/10/043,344  
; CURRENT FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 08/649,519  
; PRIOR FILING DATE: 1996-05-17  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 146  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Haemophilus influenzae  
US-10-043-344-146

Query Match 43.1%; Score 22; DB 15; Length 8;

Best Local Similarity 66.7%; Pred. No. 5.8e+05; Mismatches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGHFP 7  
|||

Db 3 GGFPG 8

RESULT 15

US-10-226-007-1323  
; Sequence 1323, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,983  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1323  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 7  
US-10-226-007-1323

Query Match 43.1%; Score 22; DB 15; Length 8;  
Best Local Similarity 75.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPPP 7  
|||

Db 1 HPPP 4

Search completed: November 5, 2003, 17:30:36  
Job time : 23 secs

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: November 5, 2003, 17:19:19 Search time 14 seconds  
(without alignments)  
24.178 Million cell updates/sec

Title: US-09 914-088-5  
Perfect score: 51  
Sequence: 1 GGHFPT 8

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 147

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA:  
1: /cgn2\_6/prodata/1/aa/5A\_COMB.pep:  
2: /cgn2\_6/prodata/1/aa/5B\_COMB.pep:  
3: /cgn2\_6/prodata/1/aa/5A\_COMB.pep:  
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5: /cgn2\_6/prodata/1/aa/ACTUS\_COMB.pep:  
6: /cgn2\_6/prodata/1/aa/backlit.esl.pep:

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:

Result No.	Score	Query Match	Length	DB ID	Description
1	27	52.9	7	5196510-10	Patent No. 5196510
2	26	51.0	4	3 US-08-660-697A-5	Sequence 5, Appl
3	26	51.0	4	4 US-09-464-358-4	Sequence 4, Appl
4	26	51.0	6	2 US-08-244-496-41	Sequence 41, Appl
5	26	51.0	7	2 US-08-244-496-42	Sequence 42, Appl
6	26	51.0	8	2 US-08-244-496-58	Sequence 58, Appl
7	25	49.0	7	1 US-07-968-781A-65	Sequence 65, Appl
8	25	49.0	8	3 US-08-444-818-394	Sequence 334, Appl
9	23	45.1	4	1 US-08-159-342A-41	Sequence 43, Appl
10	23	45.1	6	3 US-02-570-761-2	Sequence 2, Appl
11	23	45.1	8	1 US-08-159-342A-31	Sequence 31, Appl
12	23	45.1	8	1 US-08-159-342A-35	Sequence 35, Appl
13	23	45.1	8	1 US-08-487-892A-75	Sequence 75, Appl
14	23	45.1	8	2 US-08-478-435-75	Sequence 75, Appl
15	23	45.1	8	2 US-08-337-483-75	Sequence 75, Appl
16	23	45.1	8	2 US-08-478-373-75	Sequence 75, Appl
17	23	45.1	8	3 US-08-474-671-75	Sequence 75, Appl
18	23	45.1	8	3 US-08-483-577A-75	Sequence 75, Appl
19	23	45.1	8	3 US-08-444-819-395	Sequence 395, Appl
20	23	45.1	8	3 US-08-897-435-75	Sequence 75, Appl
21	23	45.1	8	4 US-08-637-654-75	Sequence 75, Appl
22	23	45.1	8	4 US-08-649-518-75	Sequence 75, Appl
23	22	43.1	7	1 US-07-969-307A-14	Sequence 14, Appl
24	22	43.1	8	1 US-07-969-307A-17	Sequence 17, Appl
25	22	43.1	8	1 US-08-197-793-4	Sequence 4, Appl
26	22	43.1	8	1 US-08-502-989-3	Sequence 3, Appl
27	22	43.1	8	1 US-08-467-890A-146	Sequence 146, Appl

28	22	43.1	8	2 US-08-636-176-4	Sequence 4, Appl
29	22	43.1	8	2 US-08-478-435-146	Sequence 146, Appl
30	22	43.1	8	2 US-08-337-483-146	Sequence 146, Appl
31	22	43.1	8	2 US-08-478-373-146	Sequence 146, Appl
32	22	43.1	8	3 US-08-474-671-146	Sequence 146, Appl
33	22	43.1	8	3 US-08-483-577A-146	Sequence 146, Appl
34	22	43.1	8	3 US-08-946-329A-16	Sequence 16, Appl
35	22	43.1	8	3 US-08-567-357A-16	Sequence 16, Appl
36	22	43.1	8	3 US-08-729-743A-16	Sequence 16, Appl
37	22	43.1	8	3 US-08-997-438-146	Sequence 146, Appl
38	22	43.1	8	3 US-08-349-498-16	Sequence 16, Appl
39	22	43.1	8	4 US-08-637-654-146	Sequence 146, Appl
40	22	43.1	8	4 US-08-649-518-146	Sequence 146, Appl
41	22	43.1	8	5 PCT-US94-05355-3	Sequence 3, Appl
42	22	43.1	8	5 PCT-US95-01618-4	Sequence 4, Appl
43	22	43.1	8	5 PCT-US95-15463-16	Sequence 16, Appl
44	22	43.1	8	5 PCT-US95-15923-16	Sequence 16, Appl
45	21	41.2	4	2 US-08-667-001-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
5196510-10  
; Patent No. 5196510  
; APPLICANT: RODWELL, JOHN D.; MCKEARN, THOMAS J.; ALVAREZ,  
; VERNON, L.; RADCLIFFE, ROBERT D.  
; TITLE OF INVENTION: MOLECULAR RECOGNITION UNITS  
; NUMBER OF SEQUENCES: 43  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/519,702  
; FILING DATE: 07-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 291,730  
; FILING DATE: 29-DEC-1988  
; SEQ ID NO: 10:  
; LENGTH: 7  
5196510-10

Query Match 52.9%, Score 27; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 3 GHFP 6  
|||  
DB 1 GHFP 4

RESULT 2  
US-08-660-697A-5  
; Sequence 5, Application US/08660697A  
; Patent No. 6327711  
; GENERAL INFORMATION:  
; APPLICANT: Sharma, Shubh D.  
; TITLE OF INVENTION: STRUCTURALLY DETERMINED  
; METALLO-CONSTRUCTS AND APPLICATIONS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby P.C.  
; STREET: 805 Third Ave.  
; CITY: New York  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb  
; MEDIUM TYPE: Storage  
; COMPUTER: IBM PC/XT/AT, IBM PS/2 or  
; COMPATIBLES  
; OPERATING SYSTEM: PC-DOS or MS-DOS  
; SOFTWARE: Wordperfect 6.1 for Windows  
; CURRENT APPLICATION DATA:

? APPLICATION NUMBER: US/08/660,697A  
 ? FILING DATE: 05-JUN-1996  
 ? CLASSIFICATION: 424  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: 08/476,652  
 ? FILING DATE: 07-JUN-1995  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: ADEA C. GOGORIS  
 ? REGISTRATION NUMBER: 29,714  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: (212) 527-7700  
 ? TELEFAX: (212) 753-6237  
 ? INFORMATION FOR SEQ ID NO: 5:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 4 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: Peptide  
 ? HYPOTHETICAL: NO  
 ? ANTI-SENSE: NO  
 ?  
 ? US-08-660-697A-5

Query Match 51.0%, Score 26; DP 3; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGH 4  
 DB 1 GGGH 4

## RESULT 3

US-09-464-358-4  
 ? Sequence 41, Application US/09464358  
 ? Patent No. 5837686

? GENERAL INFORMATION:  
 ? APPLICANT: Pharmed Incorporated  
 ? APPLICANT: Sharma Ph.D., Snubh D.  
 ? TITLE OF INVENTION: Structurally Determined Cyclic Peptide Constructs and  
 ? FILE REFERENCE: Cyclic Peptide Divisional  
 ? CURRENT APPLICATION NUMBER: US/09/464,358  
 ? CURRENT FILING DATE: 1999-12-15  
 ? PRIOR APPLICATION NUMBER: 08/660,697  
 ? PRIOR FILING DATE: 1996-06-05  
 ? PRIOR APPLICATION NUMBER: 08/476,652  
 ? PRIOR FILING DATE: 1995-06-07  
 ? NUMBER OF SEQ ID NOS: 5  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO: 4  
 ? LENGTH: 4  
 ? TYPE: PPT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURES:  
 ? OTHER INFORMATION: Description of Artificial Sequence: Protein  
 ? US-09-464-358-4

Query Match 51.0%, Score 26; DP 4; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGH 4  
 DB 1 GGGH 4

## RESULT 4

US-08-244-496-4  
 ? Sequence 41, Application US/08244496  
 ? Patent No. 5837686

? GENERAL INFORMATION:  
 ? APPLICANT:

? TITLE OF INVENTION: PEPTIDES AND ANTIBODIES FOR TREATMENT OF  
 ? FILING DATE: RHEUMATOID ARTHRITIS  
 ? NUMBER OF SEQUENCES: 85  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
 ? CURRENT APPLICATION DATA: US/08/244,496  
 ? APPLICATION NUMBER: US/08/244,496  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: GB 9125024.1  
 ? FILING DATE: 25-NOV-1991  
 ? INFORMATION FOR SEQ ID NO: 41:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 6 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: peptide  
 ? FEATURE:  
 ? NAME/KEY: Modified-site  
 ? LOCATION: 6  
 ? OTHER INFORMATION: /product= "OTHER"  
 ? OTHER INFORMATION: /note= "AMIDATED"  
 ? US-08-244-496-41

Query Match 51.0%, Score 26; DP 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGH 4  
 DB 2 GGGH 5

## RESULT 5

US-08-244-496-42  
 ? Sequence 42, Application US/08244496  
 ? Patent No. 5837686  
 ? GENERAL INFORMATION:  
 ? APPLICANT:

? TITLE OF INVENTION: PEPTIDES AND ANTIBODIES FOR TREATMENT OF  
 ? FILING DATE: RHEUMATOID ARTHRITIS  
 ? NUMBER OF SEQUENCES: 85  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
 ? CURRENT APPLICATION DATA: US/08/244,496  
 ? APPLICATION NUMBER: US/08/244,496  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: GB 9125024.1  
 ? FILING DATE: 25-NOV-1991  
 ? INFORMATION FOR SEQ ID NO: 42:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 7 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: peptide  
 ? FEATURE:  
 ? NAME/KEY: Modified-site  
 ? LOCATION: 7  
 ? OTHER INFORMATION: /product= "OTHER"  
 ? OTHER INFORMATION: /note= "AMIDATED"  
 ? US-08-244-496-42

Query Match 51.0%, Score 26; DP 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1  GGCH 4
      1  1111
Db      3  GGCH 6

RESULT 6
US-08-244 496-58
: Sequence 58, Application US/08244456
: Patent No. 5837686
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: PEPTIDES AND ANTIBODIES FOR RHEUMATOID ARTHRITIS
: NUMBER OF SEQUENCES: 85
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.10 (beta)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/244,456
: PRIOR APPLICATION NUMBER: GR 912524.1
: FILING DATE: 25 NOV-1991
: INFORMATION FOR SEQ ID NO: 58:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: NAME/KEY: Modified-site
: LOCATION: 8
: OTHER INFORMATION: /product: "OTHER"
: OTHER INFORMATION: /note: "AMITATED"
US 08-244-496-58

Query Match 51.0%; Score 26; FR 21, 100% E. N.
Best Local Similarity 100.0%; Pred. No. 2, 100-100;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGCH 4
      1  1111
Db      2  GGCH 6

RESULT 7
US-07-968 781A-65
: Sequence 65, Application US/07968781A
: Patent No. 5430137
: GENERAL INFORMATION:
: APPLICANT: Gaertner, Frank H.
: APPLICANT: Sick, August J.
: APPLICANT: Thompson, Mark
: APPLICANT: Schneft, H. Ernest
: APPLICANT: Schwab, George E.
: APPLICANT: Narva, Kenneth E.
: TITLE OF INVENTION: Probes for the Identification of B-cell
: NUMBER OF SEQUENCES: 89
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David R. Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A
: CITY: Gainesville
: STATE: FL
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.10

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/968, 781A
: FILING DATE: 1992-03-0
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Saliwanchik, David R.
: REGISTRATION NUMBER: 31,794
: REFERENCE/DOCKET NUMBER: MA44.FWCC1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 904-375-8100
: TELEFAX: 904-372-5800
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7 amino acids
: TYPE: AMINO ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-968-781A-65

Query Match 49.0%; Score 25; FR 1, Length 7;
Best Local Similarity 80.0%; Pred. No. 2, 50-05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4  HFFPT 8
      1  1111
Db      3  HFFPT 7

RESULT 8
US-08 444-618-334
: Sequence 334, Application US/084444818
: Patent No. 6150097
: GENERAL INFORMATION:
: APPLICANT: Chien, David Y.
: APPLICANT: Ruster, William J.
: TITLE OF INVENTION: NARVY Diagnostics and Vaccines
: NUMBER OF SEQUENCES: 777
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Chicon Corporation
: STREET: 4560 Horton Street
: CITY: Emeryville
: STATE: CA
: COUNTRY: USA
: CLIENT: 08-08-200
: COMMENTS: PATENTABLE PEX.
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.10
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/444,618
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/403,530
: FILING DATE: 14 MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Barbin, Alisa A.
: REGISTRATION NUMBER: 31,895
: REFERENCE/DOCKET NUMBER: 0110.002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (508)359-3876
: TELEFAX: (508)359-3885
: INFORMATION FOR SEQ ID NO: 334:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08 444-618-334

```

Query Match 49.0% Score 25; DB 3; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 HFFP 7  
 ||||  
 DB 5 HFFP 8

RESULT 9  
 US-08-159-340A-43  
 ; Sequence 43, Application US/08159340A  
 ; Patent No. 5565352  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hochstrasser, Mark  
 ; APPLICANT: Papa, Peroz  
 ; TITLE OF INVENTION: DEUBIQUITINATING ENZYME: COMPOSITIONS  
 ; TITLE OF INVENTION: AND METHODS  
 ; NUMBER OF SEQUENCES: 44  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P.O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: USA  
 ; ZIP: 77210  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/159,340A  
 ; FILING DATE: 24 NOV-1993  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Highlander, Steven L.  
 ; REGISTRATION NUMBER: 37,642  
 ; REFERENCE/DOCKET NUMBER: APCD:112/HYL  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (512) 418-3000  
 ; TELEFAX: (512) 474-7577  
 ; INFORMATION FOR SEQ ID NO: 43:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-159-340A-43

Query Match 45.1% Score 23; DB 3; Length 4;  
 Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGHF 5  
 ||||  
 DB 1 GGHY 4

RESULT 10  
 US-08-570-761-2  
 ; Sequence 2, Application US/08570761  
 ; Patent No. 6009190  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Meade, Thomas J.  
 ; APPLICANT: Takeuchi, Toshihiro  
 ; APPLICANT: Gray, Harry B.  
 ; APPLICANT: Simon, Melvin  
 ; APPLICANT: Louis, Angeleique Y.  
 ; TITLE OF INVENTION: COBALT SCHIFF BASE COMPOUNDS  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Fiehr, Hobbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/570,761  
 ; FILING DATE: 12-DEC-1995  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Silva, Robin M.  
 ; REGISTRATION NUMBER: 38,304  
 ; REFERENCE/DOCKET NUMBER: A-62630/RFT/RMS  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 ; US-08-570-761-2

Query Match 45.1% Score 23; DB 3; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHFP 6  
 ||||  
 DB 1 GGGFP 5

RESULT 11  
 US-08-159-340A-31  
 ; Sequence 31, Application US/08159340A  
 ; Patent No. 5565352  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hochstrasser, Mark  
 ; APPLICANT: Papa, Peroz  
 ; TITLE OF INVENTION: DEUBIQUITINATING ENZYME: COMPOSITIONS  
 ; TITLE OF INVENTION: AND METHODS  
 ; NUMBER OF SEQUENCES: 44  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P.O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: USA  
 ; ZIP: 77210  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/159,340A  
 ; FILING DATE: 24-NOV-1993  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Highlander, Steven L.  
 ; REGISTRATION NUMBER: 37,642  
 ; REFERENCE/DOCKET NUMBER: APCD:112/HYL  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-159-340A-31

Query Match 45.1%; Score 23; DB 1; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGHF 5  
|||  
Db 1 GGHY 4

RESULT 12  
US-08-159-340A-35  
Sequence 35, Application US/0815934CA  
Patent No. 5565352  
GENERAL INFORMATION:  
APPLICANT: Hochstrasser, Mark  
TITLE OF INVENTION: Papa, Peroz  
TITLE OF INVENTION: DEBICQUINATING ENZYME COMPOSITIONS  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Dutke  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/159.34CA  
FILING DATE: 24 NOV-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARCU112/HYL  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-159-340A-35

Query Match 45.1%; Score 23; DB 1; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGHF 5  
|||  
Db 1 GGHY 4

RESULT 13  
US-08-487-890A-75  
Sequence 75, Application US/0848789CA

Patent No. 5768149  
GENERAL INFORMATION:  
APPLICANT: Loomore, Sheena  
APPLICANT: Harkness, Robin  
APPLICANT: Schryvers, Anthony  
APPLICANT: Chong, Pele  
APPLICANT: Gray-Owen, Scott  
APPLICANT: Yang, Yan-Ping  
APPLICANT: Mardin, Andrew  
APPLICANT: Klein, Michel  
TITLE OF INVENTION: Transferrin Receptor Genes  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,890A  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/175,116  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/148,968  
FILING DATE: 08-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-466 MIS.jb  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-487-890A-75

Query Match 45.1%; Score 23; DB 1; Length 8;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGHF 5  
|||  
Db 3 GGSF 7

RESULT 14  
US-08-478-435-75  
Sequence 75, Application US/08478435  
Patent No. 5922123  
GENERAL INFORMATION:  
APPLICANT: Loomore, Sheena  
APPLICANT: Harkness, Robin  
APPLICANT: Schryvers, Anthony  
APPLICANT: Chong, Pele  
APPLICANT: Gray-Owen, Scott  
APPLICANT: Yang, Yan-Ping  
APPLICANT: Mardin, Andrew  
APPLICANT: Klein, Michel  
TITLE OF INVENTION: Transferrin Receptor Genes  
NUMBER OF SEQUENCES: 147

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08 NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/174,116
FILING DATE: 29-DEC 1993
APPLICATION DATA: US 08/144,978
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:JD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-435-75

```

```

Query Match: 45.1%; Score 23; DB 2; Length 8;
Best Local Similarity: 80.0%; Pred. No. 2.5e+05;
Matches: 4; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

```

```

QY 1 GCGHF 5
DB 3 GCGSF 7

```

```

RESULT 18
US-08-478-483-75
Sequence 75, Application US/08337483
Patent No. 5925662
GENERAL INFORMATION:
APPLICANT: Cosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schuyvers, Anthony
APPLICANT: Cheng, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Mardin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Gene
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:JD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-337-483-75

```

```

Query Match: 45.1%; Score 23; DB 2; Length 8;
Best Local Similarity: 80.0%; Pred. No. 2.5e+05;
Matches: 4; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

```

```

QY 1 GCGHF 5
DB 3 GCGSF 7

```

```

Search completed: November 5, 2003, 17:23:36
Job time: 15 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: November 5, 2003, 17:44:56 : Search time 21 Seconds  
(without alignments):  
27.477 Million cell updates/sec

Title: US-09-914-088-6

Perfect score: 32

Sequence: 1 PGTIN1 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 116

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	50.0	6	A61049	halo-toxin - Pseudomonas syringae pv. mori
2	14	43.8	5	A61049	halo-toxin - Pseudomonas syringae pv. mori
3	13	40.6	4	A44624	50kD related neuro
4	13	40.6	4	A44624	14 heavy chain CRD
5	13	40.6	5	PT0274	T-cell receptor be
6	13	40.6	5	PT0274	surface protein te
7	13	40.6	6	PT0274	T-cell receptor be
8	13	40.6	6	A35039	hypothetical colla
9	11	34.4	4	PT0566	T-cell receptor be
10	11	34.4	5	F22565	R phycoerythrin ga
11	11	34.4	5	S51077	alpha-amylase - ri
12	11	34.4	5	S51077	T-cell receptor be
13	11	34.4	5	PT0525	T-cell receptor be
14	11	34.4	5	PT0721	T-cell receptor be
15	11	34.4	6	165545	MHC H2-B antigen -
16	11	34.4	6	PT0531	T-cell receptor be
17	11	34.4	6	PT0531	T-cell receptor be
18	11	34.4	6	PT0568	T-cell receptor be
19	11	34.4	6	PT0568	T-cell receptor be
20	11	34.4	6	PT0721	T-cell receptor be
21	10	31.2	4	T30563	hypothetical prote
22	10	31.2	4	PT0274	14 heavy chain CRD
23	10	31.2	5	S62963	serinal plasma pro
24	10	31.2	5	G44817	27.5 kDa structura
25	10	31.2	5	I44817	27.5 kDa structural p
26	10	31.2	5	E44817	27.5 kDa structural p
27	10	31.2	5	C44817	27.5 kDa structural p
28	10	31.2	5	A44817	27.5 kDa structural p
29	9	28.1	4	A37843	protein Pseudomyx

30	9	28.1	5	2	I40702	primase - Citrobac
31	9	28.1	5	2	PQ0008	angiotensin-conver
32	8	25.0	5	2	A60521	glycogen phosphory
33	8	25.0	5	2	E60274	major protein anti
34	8	25.0	5	2	PT0278	Ig heavy chain CRD
35	8	25.0	5	2	PT0295	Ig heavy chain CRD
36	8	25.0	6	2	S11024	hydrogensulfite re
37	8	25.0	6	2	A19780	transferrin - bovi
38	8	25.0	6	2	B26206	alpha-1,4-glucan-p
39	8	25.0	6	2	A20196	fatty-acid synthas
40	7	21.9	3	3	RHDT0	thyloliberin - Bom
41	7	21.9	3	3	RHPGT	thyloliberin - pig
42	7	21.9	3	3	RHSHT	thyloliberin - she
43	7	21.9	3	3	A92971	thyloliberin - eas
44	7	21.9	3	3	A33802	thyrotropin-releas
45	7	21.9	3	3	A43391	TRH-like tripeptid

ALIGNMENTS

RESULT 1

A61049  
halo-toxin - Pseudomonas syringae pv. mori  
C:Species: Pseudomonas syringae pv. mori  
A:Note: host mulberry tree  
C:Date: 10-Mar-1994 #sequence\_revision: 10-Mar-1994 #text\_change 21-Jan-1997  
C:Accession: A61049  
R:Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, I.  
Chem. Lett. 00, 679-680, 1989  
A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas s;  
A:Reference number: A61049  
A:Accession: A61049  
A:Molecule type: protein  
A:Residues: 1-6 <KAJ>  
A:Note: sequence confirmed by synthesis  
C:Comment: This toxin is one of the etiological agents of halo bright disease in mulb-  
C:Keywords: toxin

Query Match 50.0%; Score 16; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : 1 PGT 4  
DB : 1 PGT 6

RESULT 2

S53595  
hypothetical protein upstream of transcription factor, CCAAT-binding) - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 15-Jul-1995 #sequence\_revision: 01-Sep-1995 #text\_change 07-May-1999  
C:Accession: S53595  
R:Calhoun, C.F.; Bouman, P.R.C.; Snippe, L.; Ab, G.  
Nucleic Acids Res. 22, 5540-5547, 1994  
A:Title: Translation start site multiplicity of the CCAAT/enhancer binding protein al;  
A:Reference number: S53595; MJID:95140613; PMID:7838705  
A:Accession: S53595  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-5 <CAJ>  
A:Cross-references: EXBL:X66844

Query Match 43.8%; Score 14; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY : 1 PGT 4  
DB : 2 PGT 5



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RESULT 3
A34626
R:CH-related neurotrophin - ferruginous spindles
C:Species: Rhus ferrugineus (ferruginous spindle)
C:Date: 30-Jul-1990 #sequence_revision 30-Jul-1990 #text_change 30-Dec-1993
C:Accession: A34626
R:Kutokki, Y.; Kanda, T.; Kubota, T.; Fujisawa, Y.; Ikeda, T.; Minamitake, Y.;
R:Kocher, Biophys. Res. Commun. 167, 273-279, 1990
A:Title: A molluscan neurotrophin related to the crustacean homologue, RPNH.
A:Reference number: A34626; MUID:90174762; PMID:2311394
A:Accession: A34626
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <KUR>
C:Keywords: neurotrophin

Query Match 40.6%; Score 13; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2
DB 2 PG 3

RESULT 4
P70240
C: heavy chain CRD3 region (clone 2 100R) human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16 Aug-1996
C:Accession: P70240
R:Yarada, Y.; Wasserman, R.; Reichard, B.A.; Shane, S.; Catlin, A.C.; Rovera, G.
C:Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: P70222; MUID:91108337; PMID:1899102
A:Accession: P70240
A:Molecule type: DNA
A:Residues: 1-4 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 40.6%; Score 13; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2
DB 2 PG 3

RESULT 5
P70714
T-cell receptor beta chain V-D-J region (165-3A) mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 10 May-1997
C:Accession: P70714
R:Feeney, A.J.
C:Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: P70509; MUID:91277601; PMID:1711558
A:Accession: P70714
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FEF>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell; receptor

Query Match 40.6%; Score 13; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2
DB 2 PG 3

RESULT 6
P70715
T-cell receptor beta chain V-D-J region (165-3A) mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: P70715
R:Feeney, A.J.
C:Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: P70509; MUID:91277601; PMID:1711558
A:Accession: P70715
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-6 <FEF>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell; receptor

Query Match 40.6%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2
DB 4 PG 5

RESULT 7
P70715
T-cell receptor beta chain V-D-J region (165-3A) mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: P70715
R:Feeney, A.J.
C:Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: P70509; MUID:91277601; PMID:1711558
A:Accession: P70715
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-6 <FEF>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell; receptor

Query Match 40.6%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2
DB 4 PG 5

RESULT 8
A35039
Hypothetical collagen alpha 2(I) intron 2 protein 1 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: A35039
R:Bennett, V.D.; Adams, S.L.
J. Biol. Chem. 265, 2223-2230, 1990
A:Title: Identification of a cartilage-specific promoter within intron 2 of the chick
A:Reference number: A35039; MUID:90130479; PMID:1688851
A:Accession: A35039
A:Molecule type: mRNA
A:Residues: 1-6 <BEN>
A:Cross-references: GN:M33382; NID:9211043
A:Note: This ORF is not translated in GenBank entry CHKA21CG
C:Comment: This sequence is the translation of a cartilage specific alternative trans
C:Keywords: alternative splicing; cartilage

Query Match 40.6%; Score 13; DB 4; Length 6;

```

```

DB 4 PG 5

RESULT 6
S69237
surface protein tetraabrachion heavy chain - Staphylothermus marinus (fragment)
C:Species: Staphylothermus marinus
C:Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C:Accession: S69237
R:Peterson, J.; Nitsch, M.; Kuehnmoorgen, B.; Goibik, R.; Lupas, A.; Kellermann, J.; Eng
J. Mol. Biol. 245, 385-401, 1995
A:Title: Tetraabrachion: a filamentous archaeobacterial surface protein assembly of uni
A:Reference number: S69237; MUID:95113068; PMID:7837271
A:Accession: S69237
A:Molecule type: protein
A:Residues: 1-5 <PET>
A:Experimental source: strain Fl, DSM 3639
C:Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 40.6%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTI 4
DB 1 GTL 3

RESULT 7
P70715
T-cell receptor beta chain V-D-J region (165-3A) mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: P70715
R:Feeney, A.J.
C:Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: P70509; MUID:91277601; PMID:1711558
A:Accession: P70715
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-6 <FEF>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell; receptor

Query Match 40.6%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2
DB 4 PG 5

RESULT 8
A35039
Hypothetical collagen alpha 2(I) intron 2 protein 1 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: A35039
R:Bennett, V.D.; Adams, S.L.
J. Biol. Chem. 265, 2223-2230, 1990
A:Title: Identification of a cartilage-specific promoter within intron 2 of the chick
A:Reference number: A35039; MUID:90130479; PMID:1688851
A:Accession: A35039
A:Molecule type: mRNA
A:Residues: 1-6 <BEN>
A:Cross-references: GN:M33382; NID:9211043
A:Note: This ORF is not translated in GenBank entry CHKA21CG
C:Comment: This sequence is the translation of a cartilage specific alternative trans
C:Keywords: alternative splicing; cartilage

Query Match 40.6%; Score 13; DB 4; Length 6;

```

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PG 2  
||  
Db 5 PG 6

RESULT 9  
PT0566  
T-cell receptor beta chain V-D-J region (141-168) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30 May 1997  
C:Accession: PT0566  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0566  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-4 <PEE>  
A:Experimental source: day 19 fetal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 34.4%; Score 11; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3  
||  
Db 3 GT 4

RESULT 10  
F22565  
R-phycocerythrin gamma A chain - red alga (Gastrodiclonium coulteri) (fragment)  
C:Species: Gastrodiclonium coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: F22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A:Title: Characterization of the bilin attachment sites in R-phycocerythrin.  
A:Reference number: A22565; MUID:95182601; PMID:19486644  
A:Accession: F22565  
A:Molecule type: protein  
A:Residues: 1-5 <KAG>

Query Match 34.4%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3  
||  
Db 1 GT 2

RESULT 11  
S51077  
alpha-amylase - rice  
C:Species: Oryza sativa (rice)  
C:Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 01-Sep-1995  
C:Accession: S51077  
R:Terashima, M.; Kubo, A.; Suzawa, M.; Itoh, Y.; Katoh, S.  
Eur. J. Biochem. 226, 249-254, 1994  
A:Title: The roles of the N-linked carbohydrate chain of rice alpha-amylase in thermostability.  
A:Reference number: S51077; MUID:95045597; PMID:7957236  
A:Accession: S51077  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <TER>

Query Match 34.4%; Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3  
||  
Db 3 GT 4

RESULT 12  
CS3284  
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: CS3284  
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 881-888, 1991  
A:Title: Evolutionarily conserved organization and sequences of germline diversity and A:Reference number: A53284; MUID:91342695; PMID:1678859  
A:Accession: CS3284  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-5 <HAR>  
A:Cross-references: GB:S60737; NID:g233916; PIDN:AAB19519.1; PID:g233919  
A:Note: sequence extracted from NCBI backbone (NCBI:60737, NCBIP:60740)  
C:Keywords: T-cell receptor

Query Match 34.4%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3  
||  
Db 1 GT 2

RESULT 13  
PT0525  
T-cell receptor beta chain V-D-J region (100-4J) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0525  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0525  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-5 <FHE>  
A:Experimental source: adult thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 34.4%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3  
||  
Db 4 GT 5

RESULT 14  
PT0701  
T-cell receptor beta chain V-D-J region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0658; PT0701  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0658  
A:Status: translation not shown

A: Molecule type: mRNA  
 A: Residues: 1-5 <FE2>  
 A: Experimental source: day 4 postnatal thymus, strain BALB/c, 121-3E  
 A: Accession: P10701  
 A: Status: translation not shown  
 A: Molecule type: DNA  
 A: Residues: 1-5 <FE2>  
 A: Experimental source: newborn thymus, strain BALB/c, 161-2E  
 C: Keywords: T-cell receptor

Query Match 34.4%; Score 11; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3  
 ||  
 DB 4 GT 5

RESULT 15  
 I65546  
 MHC H2-L antigen - mouse (fragment)  
 C: Species: Mus musculus (house mouse)  
 C: Date: 02 Aug-1996 #sequence\_revision 02-Aug-1996 #text change 65-Nov-1999  
 C: Accession: I65546  
 R: Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.  
 Cell 44, 261-272, 1986  
 A: Title: Detailed analysis of the mouse H 2Kb promoter: Enhancer-like sequences and their  
 A: Reference number: 152778; PMID:86105202; PMID:1510743  
 A: Accession: I65546  
 A: Status: preliminary; translated from GH/EMBL/DBP  
 A: Molecule type: DNA  
 A: Residues: 1-6 <RES>  
 A: Cross-references: GB:M12483; NID:193565; P1EN:AAA19641.1; P1D:G554214

Query Match 34.4%; Score 11; DB 2; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PCTL 4  
 |||  
 DB 3 PCTL 6

Search completed: November 5, 2003, 1:14:40  
 Job time: 22 sec

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:16:16 / Search time 10 seconds  
(without alignments)  
28.216 Million c.e.: updates/sec

Title: US-09-914-088-6  
Perfect score: 32  
Sequence: : PGIN: 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 2.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28.1	9	5	E104_LITRU	P42103 Litoria rub
2	25.0	8	6	TM0F_SARBU	P41495 sarcophaga
3	25.0	6	1	UN06_CLOPA	P13011 clostridium
4	21.9	3	1	THYL_PIG	P11151 sus scrofa
5	21.9	4	1	DCVL_PSETH	P19916 pseudomonas
6	21.9	4	1	EC01_HUMAN	P27731 homo sapien
7	21.9	4	1	OCPI_OCTV	P26649 octopus min
8	21.9	4	1	RM01_YEAST	P45515 saccharomyc
9	21.9	4	1	TUFT_HUMAN	P01858 homo sapien
10	21.9	5	1	BPP7_POTIN	P20425 bothriops in
11	21.9	5	1	E1C3_LITRU	P82039 litoria rub
12	21.9	5	1	PAP2_PAPMA	P41864 pardachirus
13	21.9	5	1	PRCT_PERAM	P01373 periplaneta
14	21.9	5	1	SUGA_ACHDO	P19931 acheta dome
15	21.9	6	1	CIP1_MYTED	P13736 mytilus edu
16	21.9	6	1	E1C1_LITRU	P82036 litoria rub
17	21.9	6	1	OM1_LITRU	P42985 leptonotars
18	21.9	6	1	OM1_LITRU	P42985 leptonotars
19	21.9	6	1	TRP1_PSEPU	P36414 pseudomonas
20	21.9	6	1	VP19_HSV1K	P2321C herpes simp
21	18.8	3	1	GRW1_HUMAN	P01157 homo sapien
22	18.8	4	1	ACHU_ANTEL	P58767 anthopleura
23	18.8	4	1	FLRN_ANTEL	P58767 anthopleura
24	18.8	4	1	OCPI_OCTV	P26649 octopus min
25	18.8	5	1	AL14_CARMA	P41817 carcinus ma
26	18.8	5	1	RE32_LITRU	P82073 litoria rub
27	18.8	5	1	TP1S_CANFA	P34714 canis fami
28	18.8	5	1	TRM3_ECOL	P13973 escherichia
29	18.8	5	1	UF01_MOUSE	P38639 mus musculu
30	18.8	5	1	UXA4_CHLTR	P38005 chlamydia t
31	18.8	6	1	ASP2_LACSN	P92655 lactobacilli
32	18.8	6	1	PARP_MONEX	P41966 moniezia ex
33	18.8	6	1	LOK1_LOCOM	P41491 locusta mig

RESULT 1  
E104\_LITRU STANDARD; PRT; 5 AA.  
ID E104\_LITRU  
AC P82100;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electric 4.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella".  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD\_RES 5  
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;  
Query Match 28.1%; Score 9; DB 1; Length 5;  
Best Local Similarity 33.3%; Pred. No. 1.3e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 TIN 5  
DB 3 TVH 5

RESULT 2  
TM0F\_SARBU STANDARD; PRT; 6 AA.  
ID TM0F\_SARBU  
AC P41495;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Trypsin-modulating oostatic factor (TMOF).  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyogota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Ovary;  
RX MEDLINE=94211930; PubMed=8159807;  
RA Bylermans D., Bcrowsky D., Hunt D.F., Shabanowitz J., Grauwels L.,  
de Locf A.;  
RT "Sequencing and characterization of trypsin modulating oostatic

P13071 citrobacter  
P58261 daucus caro  
P82072 litoria rub  
P24272 vibrio fisc  
P58706 anthopleura  
P41853 artiopesthi  
P82070 litoria rub  
P82071 litoria rub  
P80628 zea mays im  
P25154 oycetolagus  
P42562 hirudo medi  
P42561 hirudo medi

RT factor (TMPI) from the ovaries of the grey fleshfly, *Neobellieria*  
 RI (*Sarcophaga*) *bullata*.";  
 RL Regul. Rept. 50:61-72(1994).  
 CC -1- FUNCTION: HAS AN OOSPASTIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS  
 CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN  
 CC CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE  
 CC DEVELOPMENT.  
 CC -2- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR  
 CC EPITHELIUM AFTER A BLOOD MEAL.  
 KW Hormone.  
 SQ SEQUENCE 6 AA; 695 MW; 61E72461E7642200 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 6;  
 Best Local Similarity 20.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PUTIN 5  
 Db 2 PYNLH 6

## RESULT 3

INFE\_CLOPA STANDARD; PRT; 6 AA.  
 ID UK06\_CLOPA  
 AC PR1351;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Unknown protein CP 6 from 2D-page (fragment).  
 OS Clostridium pasteurianum.  
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CC Clostridium.  
 CC NCBI TaxID=501;  
 RN 1;  
 RP SEQUENCE.  
 RC STRAIN=WS;  
 RX MEDLINE=98291870; Pubmed=9629919;  
 RA Fergusson R., Skjeldal L.;  
 RT "Two dimensional gel electrophoresis separation and N terminal  
 RT sequence analysis of proteins from Clostridium pasteurianum WS.";  
 RL Electrophoresis 19:802-806(1998).  
 CC 1 MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P: CP THIS UNKNOWN  
 CC PROTEIN IS: 5.0, ITS MW IS: 75.9 KDa  
 FT NCM TER 6  
 SQ SEQUENCE 6 AA; 657 MW; 606P1D7A5A4D76 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 1.0e+04;  
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TINI 6  
 Db 3 TAVL 6

## RESULT 4

THYL\_PIG STANDARD; PRT; 3 AA.  
 ID THYL\_PIG  
 AC P01167;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Thyroliberin (thyrotropin releasing hormone) (THRL) (Protein).  
 OS Sus scrofa (Pig),  
 OS Sus scrofa (Pig),  
 OS Ovis aries (Sheep),  
 OS Bombina orientalis (Oriental fire-bellied toad), and  
 OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus  
 CC NCBI TaxID=9923; 9940, 8346, 8316;  
 RN 1;  
 RP SEQUENCE.  
 RC SPECIES=Pig; TISSUE:Hypothalamus;

RX MEDLINE=70136150; Pubmed=4984938;  
 RA Nair R.M.G., Barrett C.F., Bowers C.Y., Schally A.V.;  
 RT "Structure of porcine thyrotropin releasing hormone.";  
 RL Biochemistry 9:1103-1106(1970).  
 RN 2;  
 RP SYNTHESIS.  
 RC SPECIES=Pig;  
 RX MEDLINE=70039904; Pubmed=4982117;  
 RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;  
 RT "The identity of chemical and hormonal properties of the thyrotropin  
 RT releasing hormone and pyroglutanyl-histidyl-proline amide.";  
 RL Biochem. Biophys. Res. Commun. 37:735-710(1969).  
 RN 3;  
 RP SEQUENCE.  
 RC SPECIES=Sheep; TISSUE:Hypothalamus;  
 RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R.,  
 RA Ward D.N.;  
 RT "The elucidation of the primary structure of the hypothalamic thyroid  
 RT stimulating hormone releasing factor of ovine origin by means of mass  
 RT spectrometry.";  
 RL Orig. Mass Spectrom. 5:221-228(1971).  
 RN 4;  
 RP SYNTHESIS.  
 RC SPECIES=Sheep;  
 RX MEDLINE=70163386; Pubmed=4985794;  
 RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,  
 RA Guillemin R.;  
 RT "Characterization of ovine hypothalamic hypophysiotropic  
 RT TSH-releasing factor.";  
 RL Nature 226:321-325(1970).  
 RN 5;  
 RP SEQUENCE.  
 RC SPECIES=B. orientalis; TISSUE=Skin;  
 RX MEDLINE=76138399; Pubmed=815011;  
 RA Yasuhara T., Nakajima T.;  
 RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";  
 RL Chem. Pharm. Bull. 23:330-3303(1975).  
 RN 6;  
 RP SEQUENCE.  
 RC SPECIES=N. viridescens;  
 RX MEDLINE=75035605; Pubmed=4214528;  
 RA Grimm-Joergensen Y., McKelvy J.F.;  
 RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus  
 RT viridescens) brain in vitro. Isolation and characterization of  
 RT thyrotropin releasing factor.";  
 RL J. Neurochem. 23:471-478(1974).  
 CC -1- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH  
 CC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/  
 CC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.  
 CC DR PIR; A90919; RHDTTO.  
 CC DR PIR; A92971; A92971.  
 CC DR PIR; A93750; RHSH.  
 KW Amidation; Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD\_RES 3 3 AMIDATION  
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B3000000000000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 P 1  
 Db 3 P 3

## RESULT 5

DCML\_PSECH STANDARD; PRT; 4 AA.  
 ID DCML\_PSECH  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO  
 DE dehydrogenase subunit L) (CO-BH 5) (Fragment).  
 GN CUTL.

OS Pseudomonas carboxydohydrogena.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae.  
 OX NCBI\_TaxID=290;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90055678; PubMed=2818128;  
 RA Kraut M., Hugendieck I., Herwig S., Meyer C.;  
 PT "Homology and distribution of CO dehydrogenase structural genes in  
 PT carboxydophilic bacteria.";   
 RL Arch. Microbiol. 152:335-341(1999).  
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
 CC dioxide.  
 CC -!- CATALYTIC ACTIVITY: CO + H<sub>2</sub>O + acceptor = CO(2) + reduced  
 CC acceptor.  
 CC -!- COFACTOR: Molybdenum (molybdopterin).  
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND  
 CC SMALL.  
 DR PIR; P01140; P01140.  
 KW Oxidoreductase; Molybdenum.  
 FT NON TER 4  
 FT MOD RES 4  
 SQ SEQUENCE 4 AA; 441 MW; 77615876FC0000C CRC64;

Query Match 21.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1

DB 4 P 4

RESULT 6

EOS1\_HUMAN  
 ID EOS1\_HUMAN STANDARD; PRT; 4 AA.  
 AC P02731;  
 DT 21-JUL-1996 (Rel. 01, Created)  
 DT 21-JUL-1996 (Rel. 01, Last sequence update)  
 DT 21-JUL-1996 (Rel. 01, Last annotation update)  
 DE Eosinophilic peptides.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catartida; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76078412; PubMed=1060393;  
 RA Goetzl E.J., Austen K.F.;  
 PT "Purification and synthesis of eosinophilic peptides of  
 PT human lung tissue: identification as eosinophilic chemotactic factor of  
 RT anaphylaxis";   
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).  
 CC -!- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG  
 CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS  
 CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING  
 CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE  
 CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.  
 DR GO; GO:0030105; P:anaphylaxis; IDA.  
 DR GO; GO:0006935; P:chemotaxis; IDA.  
 FT VARIANT 1  
 FT VARS A (IN OTHER PEPTIDES).  
 FT /FTID=VAR\_005201.  
 SQ SEQUENCE 4 AA; 390 MW; 6B05B962AC0000C CRC64;

Query Match 21.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Q1 3

DB 2 GS 1

RESULT 7  
 OCP3\_OCTM:  
 ID OCP3\_OCTM1 STANDARD; PRT; 4 AA.  
 AC P58439;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cardioactive peptides Ocp-3/Ocp-4.  
 OS Octopus minor (Octopus).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Nectopoda;  
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
 OX NCBI\_TaxID=89766;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
 RC TISSUE=Brain;  
 RX MEDLINE=20336815; PubMed=10976044;  
 RA Iwakoshi E., Hisada M., Minakata H.;  
 PT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
 RT Octopus minor.";   
 RL Peptides 21:623-630(2000).  
 CC -!- FUNCTION: Cardioactive; has both positive chronotropic and  
 CC inotropic effects on the heart. Ocp-4 is a 1000 time less  
 CC active than Ocp-3.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.  
 CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.  
 KW Hormone; D-amino acid.  
 FT MOD RES 2  
 FT D-SERINE (IN OCP-4).  
 SQ SEQUENCE 4 AA; 463 MW; 6AB35B81000000C CRC64;

Query Match 21.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GT 3

DB 1 GS 2

RESULT 8

RM01\_YEAST  
 ID RM01\_YEAST STANDARD; PRT; 4 AA.  
 AC P36515;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).  
 GN MRPL1  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=91285106; PubMed=2060026;  
 RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,  
 RA Kitakawa M.;  
 PT "Extended N-terminal sequencing of proteins of the large ribosomal  
 RT subunit from yeast mitochondria";   
 RL FEBS Lett. 284:51-56(1991).  
 DR PIR; S17255; S17255.  
 DR SGD; L0002881; MRPL1.  
 KW Ribosomal protein; Mitochondrion.  
 FT NON TER 4  
 FT MOD RES 4  
 SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000C CRC64;

Query Match 21.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1

CC - FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.

DR P.R. G37196; G37196;  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 5 AA; 629 MW; 776DC37326B0C000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1  
 |  
 Db 5 P 5

## RESULT 11

E103 LITRU STANDARD; PRT; 5 AA.  
 AC P82099;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update);  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Electrin 3.  
 OS Eukarya; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 PE Peleodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE-SKIN secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RL Aust. J. Chem. 52:639-645(1999).

CC - TISSUE-SKIN LOCATION: Secreted.  
 CC - TISSUE SPECIFICITY: Skin.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD RES 5 5 AMIDATION  
 SQ SEQUENCE 5 AA; 630 MW; 569761F2C9A0C000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1  
 |  
 Db 4 P 4

## RESULT 12

PAP2 PARMA STANDARD; PRT; 5 AA.  
 AC P82864;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Pardaxin II (PXII) (Fragment).

OS Pardachirus ramaratus (Red sea roses sole).  
 OC Eukarya; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 OC Soleidae; Soleidae; Pardachirus.  
 OX NCBI\_TaxID=31087;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE-SKIN secretion;  
 RA MEDLINE#7057359; PubMed#3782138;  
 RX Lazarevic P., Primot N., Loew E.M.;

Db 4 P 4

## RESULT 9

TUFT\_HUMAN STANDARD; PRT; 4 AA.  
 AC P01958;  
 DT 21-JUL-1986 (Rel. 31, Created)  
 DT 21-JUL-1986 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Phagocytosis-stimulating peptide (tuftsin).  
 OS Homo sapiens (Human).  
 CC Eukarya; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE#72187087; PubMed#4112769;  
 RA Nishioka K., Constantopoulos A., Saroh P.S., Najjar V.A.;  
 RT "The characteristics, isolation and synthesis of the phagocytosis  
 RT stimulating peptide tuftsin."  
 RL Biochem. Biophys. Res. Commun. 47:172-179(1972).  
 RN [2]  
 RP IMMUNOGLOBULIN CLASS.

RX MEDLINE#68091045; PubMed#4169272;  
 RA Fidalgo B.V., Najjar V.A.;  
 RT "The physiological role of the lymphoid system. VI. The stimulatory  
 RT effect of leucophagic gamma globulin (leucokinin) on the phagocytic  
 RT activity of human polymorphonuclear leucocyte."  
 RL Biochemistry 6:3386-3392(1967).

CC - MISCELLANEOUS: AN IGG CALLED LEUCOKININ BINGS REVERSIBLY TO THE  
 CC CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE  
 CC MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.  
 CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC  
 CC ACTIVITY OF NEUTROPHILS.

DR PIR; A02147; A02147.  
 DR XMM; 191150;  
 DR GO; GO:0007823; Phagocytosis; NAS.  
 DR GO; GO:0006909; Phagocytosis; NAS.  
 SQ SEQUENCE 4 AA; 501 MW; 74196321C0C0C000 CRC64.

Query Match 21.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1  
 |  
 Db 3 P 3

## RESULT 10

BP77 BOTIN STANDARD; PRT; 5 AA.  
 AC P30425;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide S5,2 (SA) (Angiotensin converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Quimada jararaca).  
 CC Eukarya; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;  
 CC Viperidae; Crotalinae; Bothrops.  
 CX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE#90351557; PubMed#2386617;  
 RA Gupta A.C.O., Vieira C.A., Giglio J.R.;

RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptide from Bothrops insularis snake venom."  
 RX J. Protein Chem. 9:221-227(1990)

RT "Purification and pore-forming activity of two hydrophobic  
 RT polypeptides from the secretion of the Red sea moses sole (Paralichthys  
 RT tarmatatus).";  
 RT C. Biol. Chem. 261:16704-16713(1986).  
 CC !- FUNCTION: Exhibits unusual, shark repellent and surfactant  
 CC properties. Forms voltage-dependent, ion-permeable channels  
 CC in membranes. At high concentration causes cell membrane lysis.  
 CC !- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.  
 CC !- SUBCELLULAR LOCATION: Secreted.  
 CC !- SIMILARITY: BELONGS TO THE PARADAXIN FAMILY.  
 KW Toxin.  
 FT NON TER 5 5  
 SQ SEQUENCE 5 AA: 614 MW; 7769C9C8100000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1  
 DB 5 P 5

RESULT 11  
 PRCT\_PERAM STANDARD; PRT; 5 AA.  
 AC P01373;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Proctolin.  
 OS Periplaneta americana (American cockroach).  
 CS Limulus polyphemus (Atlantic horseshoe crab), and  
 CS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;  
 CC Blattidae; Periplaneta.  
 CC NCBI\_TaxID=6978, 6850, 6759;  
 RN [1].  
 RP SEQUENCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=76074708; PubMed=576;  
 RA Starbuck A.N., Brown B.E.;  
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter  
 RT in insects.";  
 RL Life Sci. 19:1253-1256(1975).  
 RN [2].  
 RP BIOLOGICAL SOURCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=8:225865; PubMed=6113690;  
 RA O'Shea M., Adams M.E.;  
 RT "Pentapeptide (proctolin) associated with an identified neuron.";  
 RL Science 213:567-569(1981).  
 RN [3].  
 RP SEQUENCE.  
 RC SPECIES=L.polyphemus;  
 RX MEDLINE=90284800; PubMed=2356151;  
 RA Groomer J.R., Tillinghast E.K., Townley M.A., Vertovs A.,  
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,  
 RA Shabanowitz J.;  
 RT "Identification of proctolin in the central nervous system of the  
 RT horseshoe crab, Limulus polyphemus.";  
 RL Peptides 11:205-211(1990).  
 RN [4].  
 RP SEQUENCE.  
 RC SPECIES=C.maenas;  
 RX MEDLINE=86232789; PubMed=2872661;  
 RA Stangier J., Dirksen H., Keller R.;  
 RT "Identification and immunocytochemical localization of proctolin in  
 RT pericardial organs of the shore crab, Carcinus maenas.";  
 RL Peptides 7:167-72(1986).  
 CC !- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.  
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.

CC !- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN  
 CC THE CRAB PERICARDIAL ORGANS.  
 DR PIR; A01644; HORCHA.  
 DR PIR; A60411; A60411.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA: 649 MW; 71B7671B44600000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1  
 DB 4 P 4

RESULT 14  
 SUGA\_ACHDO STANDARD; PRT; 5 AA.  
 AC P1991;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Suboesophageal ganglion pentapeptide.  
 OS Acheta domestica (House cricket).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
 CC Acheta.  
 CC NCBI\_TaxID=6997;  
 RN [1].  
 RP SEQUENCE.  
 RA Wicker C., Wicker C.;  
 RT "Isolation and structure of a peptide isolated from the  
 RT suboesophageal ganglion of Acheta domestica (orthoptera).";  
 RL Comp. Biochem. Physiol. 89C:185-187(1987).  
 CC !- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL  
 CC GANGLIA.  
 DR PIR; JS0319; JS0319.  
 SQ SEQUENCE 5 AA: 476 MW; 69D76DDDD8000000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1  
 DB 4 P 4

RESULT 15  
 CIFI\_MYTED STANDARD; PRT; 6 AA.  
 AC P13736;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Contraction-inhibiting peptide I (MIP I).  
 OS Mytilus edulis (Blue mussel).  
 CC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 CC Mytiloidea; Mytilidae; Mytilus.  
 CC NCBI\_TaxID=6550;  
 RN [1].  
 RP SEQUENCE.  
 RC TISSUE=Pedal ganglion;  
 RX MEDLINE=88240357; PubMed=3377776;  
 RA Hirata T., Kubota I., Iwasaki N., Takabatake I., Ikeda T., Munesaka Y.;  
 RA "Structures and actions of Mytilus inhibitory peptides.";  
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
 CC !- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN  
 CC MUSCLES.  
 CC !- SIMILARITY: TO MIP II.  
 DR PIR; A27696; A27696.  
 KW Hormone, Amidation.



PT MOD PES 6 6 AMINATION.  
SQ SEQUENCE 6 AA: 637 MW: 7209068775881900 ORC\*4;  
Query Match 21.94; Score 7; DB 1; Length 6;  
Res. Local Similarity 50.04; Pred. No. 1.1e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
CY 2 GT 1  
Et 1; GS 2

Search completed: November 5, 2003, 17:47:23  
Job time : 11 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:44:11 : Search time 33 seconds  
(without alignment)  
46,919 Million cell updates/sec

Title: US-09-914-088-6

Perfect score: 32

Sequence: 1 PGTINI 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mmc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_todent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_vivitus.*
16: sp_bacteriap.*
17: sp_archaeap.*

```

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	28.1	4	11 Q08433	Q08433 rattus sp.
2	7	21.9	5	13 P83309	P83309 gallus gall
3	6	18.8	5	10 Q99007	Q99007 hordeum vul
4	5	15.6	5	2 P83073	P83073 bacillus ce
5	5	15.6	6	10 P82181	P82181 spinacia ol
6	5	15.6	6	10 P82541	P82541 spinacia ol
7	5	15.6	6	10 P82152	P82152 spinacia ol

## ALIGNMENTS

RESULT 1

Q08433

ID Q08433

AC Q08433

PRELIMINARY;

PRT: 4 AA.

DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Bilirubin UDP-glucuronosyltransferase (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Gunn;  
 RX MEDLINE=91282758; PubMed=1840486;  
 RA Sato H., Aono S., Kashiwamata S., Koiwai O.;  
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the  
 RT hyperbilirubinemic Gunn rat.";  
 RL Biochem. Biophys. Res. Commun. 177:1161-1164 (1991).  
 DR EMBL; S38636; AAB19259.1; -;  
 KW Transferase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 28.1%; Score 9; DB 11; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 NI 6  
 DB 1 NV 2

## RESULT 2

P83308

ID P83308

AC P83308

DE 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE FMRamide-like neuropeptide (LPRF-amide).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Brain;  
 RX PubMed=6137771;  
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;  
 RT "A novel active pentapeptide from chicken brain identified by  
 RT antibodies to FMRamide.";  
 RL Nature 305:329-330 (1983).

CC -1- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)

CC FAMILY.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 21.9%; Score 7; DB 13; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 P 1  
 DB 2 P 2

## RESULT 3

Q99007

ID Q99007

AC Q99007

DE 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

PRELIMINARY;

PRT: 5 AA.



```

RESULT 7
P21182
ID P82182 PRELIMINARY; PRI: 6 AA.
AC P82182;
DT 01-JUN-2000 (TREMUREL. 14, Created)
E1 01-JUN-2000 (TREMUREL. 14, Last sequence update)
E2 01-MAR-2002 (TREMUREL. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
CS Spinacia oleracea (Spinach).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
CC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.
OX NCBI_TaxID:3562;
RN 11;
RP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=Leaf;
EX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RL the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC 1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC 1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC 1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC 1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC 1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR001790; Ribosomal_L10.
DR Pfam: PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA: 63213415E05DB300 CRC64;

Query Match 15.6%; Score 5; DB 10; Length 6;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 3
DB 5 5

Search completed: November 5, 2003, 17:43:09
Job time : 33 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: November 5, 2003, 17:45:26 : Search time 40 seconds  
(without alignment)  
23,809 Million cell updates/sec

Title: US 09-914-088-6

Perfect score: 32

Sequence: 1 PGTIN1 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1:07863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 50962

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A: Geneseq 19Jun03.\*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
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13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
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18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	6	21	IGF C epsilon-2 do
2	32	100.0	6	22	Peptide p6 derived
3	32	100.0	6	23	Human IGE immunoge
4	22	68.8	6	23	Campothecin pepti
5	22	68.8	6	23	Campothecin pepti
6	20	62.5	6	15	IGF-1 analogue N-t
7	20	62.5	6	23	Human CD66 family
8	19	59.4	6	21	Ad5 HSV5 loop frag
9	18	56.2	3	21	T cell antigen rec

10	18	56.2	4	24	AA533660	Human BCA3 SH2-dom
11	18	56.2	5	19	AA214493	Human neuroendocri
12	18	56.2	5	23	ABG93533	Human P-glycoprote
13	18	56.2	6	14	AA382334	Alzheimer paired h
14	18	56.2	6	14	AA337553	Phosphorylated tau
15	18	56.2	6	19	AA445755	Apoptotic protease
16	18	56.2	6	20	AA235110	V beta 6 clone fou
17	18	56.2	6	21	AA95785	LPXIX motif of er
18	18	56.2	6	22	AAU05491	Synthetic hexapept
19	18	56.2	6	23	AAE20559	Soybean diverged d
20	17	53.1	5	18	AAW31287	Bovine beta casein
21	17	53.1	5	23	ABP67559	Human CD66 family
22	17	53.1	6	16	AA70280	Soluble laminin (L
23	17	53.1	6	17	AA95608	Diabetogenic hexap
24	17	53.1	6	20	AA14090	Affinity ligand fo
25	17	53.1	6	21	AA83404	WT43 immunogenic p
26	17	53.1	6	22	AAE59293	Peptide encoded by
27	17	53.1	6	23	ABP67549	Human CD66 family
28	17	53.1	6	24	ABU57841	Soluble laminin ce
29	16	50.0	4	19	AAW79576	Peptide 1, from LK
30	16	50.0	4	23	ABP67571	Human CD66 family
31	16	50.0	4	23	ABP67582	Human CD66 family
32	16	50.0	5	10	AA95653	Sequence of varian
33	16	50.0	5	19	AAW31288	Bovine beta casein
34	16	50.0	5	19	AAW87388	Peptide determined
35	16	50.0	5	23	ABP67560	Human CD66 family
36	16	50.0	5	23	ABP67561	Human CD66 family
37	16	50.0	6	10	AA93345	Portion of myc var
38	16	50.0	6	14	AA44419	rBPI-IgG fusion N-
39	16	50.0	6	18	AAW45377	Peptide antagonist
40	16	50.0	6	19	AAW87396	Peptide determined
41	16	50.0	6	19	AAW75368	Hexapeptide #8 bin
42	16	50.0	6	19	AAW75300	Hexapeptide #8 bin
43	16	50.0	6	21	AA49376	Beta-casomorphin d
44	16	50.0	6	22	AAE09360	rBPI(1-199) Ig fus
45	16	50.0	6	22	AA891590	Opioid peptide SEQ

## ALIGNMENTS

### RESULT 1

AA825912  
ID AAB25912 standard; Peptide: 6 AA.

XX AAB25912.

XX AC

XX DT 05 JAN-2001 (first entry)

XX DE IGE C-epsilon-2 domain surface exposed epitope peptide P6 SEQ ID NC.6.

XX XX

XX KW Epitope; mimotope; human; immunoglobulin E; IGE; C-epsilon-2 domain;

XX KM allergic disease; immunophylaxis; immunotherapy; anti-allergic;

XX KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;

XX KW allergy; atopy.

XX XX

OS Homo sapiens.

XX XX

XX PN WO200058460-A1.

XX XX

XX PD 31-AUG-2000.

XX XX

XX PF 22-FEB-2000; 2000WO-BP01455.

XX XX

XX PR 25-FEB-1999; 99GB-0004405.

XX PR 29-MAR-1999; 99GB-0007151.

XX PR 07-MAY-1999; 99GB-0010537.

XX PR 07-MAY-1999; 99GB-0010538.

XX PR 07-AUG-1999; 99GB-0018694.

XX PR 07-AUG-1999; 99GB-0018693.

XX PR 07-SEP-1999; 99GB-0021046.

XX PR 07-SEP-1999; 99GB-0021047.

XX PR 29-OCT-1999; 99GB-0025619.



XX Claim 4; Page 9; 45pp; English.

XX The present invention relates to conjugates suitable for use in vaccines,  
XX where the conjugate comprises a disulphide bridge cyclised peptide and an  
XX immunogenic carrier. The vaccines can be used in the treatment of  
XX allergies. The present sequence is a peptide immunogen derived from human  
XX immunoglobulin E (IgE) suitable to be cyclised and used in the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 32; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. NO. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGTINI 6  
DB 1 PGTINI 6

RESULT 4  
ABP53525  
ID ABP53525 standard; peptide; 6 AA.

AC ABP53525;

DT 12-DEC-2002 (first entry);

DE Carptothecin peptide conjugate II.21.

KW Carptothecin peptide conjugate; cytostatic; glycoconjugate; tumour;  
KW specifically cleavable peptidic linking unit; cancer.

OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminally modified with 20-O-"

FT Modified-site 6 /note= "C-terminally modified with camptothecin TFA"

PN EPI19305 AL.

XX 03-JUL 2002.

PF 27-DEC-2000; 2000EP-0128402.

PR 27 DEC-2000; 2000EP-0128402.

PA (FARB ) BAYER AG.

PI Lerchen H, Baumgarten J, Lockhoff O;

DR WPI; 2002 629644/68.

PT Cytostatic-glycoconjugates useful for treating cancer have specifically  
PT cleavable peptide linking units so as to deliver drug to tumor only  
PS Example; Page 17; 46pp; English.

XX The present invention describes a conjugate (I) and its salts. (I) has  
XX the formula C<sub>1</sub>-Li-Sp<sub>2</sub>-K; where: C<sub>1</sub> = cytotoxic radical or radical of  
XX a cytostatic derivative optionally also carrying a CH<sub>3</sub>, C<sub>2</sub>H<sub>5</sub> or NH<sub>2</sub> group;  
XX Li = linker comprising 5 to 8 amino acids each optionally carrying  
XX protecting groups; Sp<sub>1</sub> = absent, CO or CS; Sp<sub>2</sub> = optionally substituted  
XX arylene or alkylene; and K = unsubstituted or regioselectively modified  
XX carbohydrate radical. Also described: (1) a process for preparation of  
XX the conjugate; (2) a medicament comprising the conjugate; (3) has  
XX cytostatic activity. The conjugates are useful for treating cancer.  
XX The conjugate is cleaved by enzymes found especially in tumor tissue  
XX to release the cytotoxic drug. As the drug is not active until after  
XX cleavage it will not cause harm to non-tumor proliferating cells.  
XX therefore reducing the side-effects associated with the use of such

CC drugs. The present sequence represents a camptothecin peptide conjugate,  
CC which is used in an example from the present invention.

XX Sequence 6 AA;

Query Match 68.8%; Score 22; DB 23; Length 6;  
Best Local Similarity 50.0%; Pred. NO. 9.3e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PGTINI 6  
DB 1 PGGLNV 6

RESULT 5

ABG31530

ID ABG31530 standard; Peptide; 6 AA.

AC ABG31530;

XX 05-NOV-2002 (first entry);

XX Camptothecin peptide conjugate #19.

KW Camptothecin; integrin receptor antagonist; cytostatic agent;  
KW tumour cell; metallo matrix protease; MMP; carcinomatous disorder;  
KW integrin alpha\_vbeta\_3 receptor antagonist; tumour growth inhibitor;  
KW tumour; integrin; camptothecin-bis-trifluoroacetate.

OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 6 /label= OTHER

FT /note= "Bound to Camptothecin bis-trifluoroacetate  
at position 20-O"

PN EPI19305-AL.

XX 03-JUL-2002.

XX 27-DEC-2000; 2000EP-0128401.

XX 27-DEC-2000; 2000EP-0128401.

XX (FARB ) BAYER AG.

XX Lerchen H, Baumgarten J, Lockhoff O, Albers M, Schoop A;

XX WPI; 2002-576993/62.

XX New conjugates of integrin receptor antagonist and a cytostatic agent  
XX with specific cleavable linking unit useful in the treatment of cancer

XX Examples; Page 61; 127pp; English.

XX This invention relates to conjugates of integrin receptor antagonist and  
XX a cytostatic agent with cleavable linking unit that are selectively  
XX cleaved by tumour cell metallo matrix proteases (MMPs). The  
XX conjugates of the invention may have cytostatic activity and may be  
XX used as an integrin alpha\_vbeta\_3 receptor antagonist or a tumour  
XX growth inhibitor. The conjugates of the invention may be used in the  
XX production of a medicament for the treatment of carcinomatous disorders.  
XX Compounds of the invention containing the conjugates of the invention  
XX exhibit a selective and tumour-specific action as a result of linkage to  
XX alpha\_vbeta\_3 integrin antagonists via linking units which can be  
XX selectively cleaved by enzymes such as metallo matrix proteases, i.e.  
XX enzymes found in tumour tissue. The linking units can also maintain the  
XX serum stability of the conjugate of cytostatic and alpha\_vbeta\_3  
XX integrin antagonist, and at the same time, show the desired  
XX intracellular action within tumour cells as a result of its specific  
XX enzymatic and hydrolytic cleavability with release of the cytostatic.

CC The present sequence represents a carboxyhectin-bis-trifluoroacetate  
 CC conjugated peptide used in an example of the method of the invention.

XX  
 SQ Sequence 6 AA;

Query Match 68.8%; Score 22; DB 23; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PGTLN: 6  
 DB 1 PGGLNV 6

RESULT 6  
 AAR51446  
 ID AAR51446 standard; peptide; 6 AA.

XX AAR51446;  
 AC AAR51446;  
 XX  
 XX  
 XX Insulin-like growth factor; IGF-1; IGF 2; birds; chickens; egg;  
 KW in ovo; growth; promotion; increase; long R3 IGF-1; DR3 IGF-1;  
 XX  
 XX Homo sapiens.  
 CS  
 XX  
 XX WO9426445-A1.  
 XX  
 XX 31-MAR-1994.  
 XX  
 XX 02-SEP-1993; 93WO-US08279.  
 XX  
 XX 17 SEP-1994; 92US-0947035.  
 XX  
 XX (EMPR-) EMPREX INC.  
 PA (GROUP-) GROPEP PTY LTD.  
 PA (USDA ) US SEC OF AGRIC.  
 XX  
 XX Ballard RJ, Francis GL, McMurtry JP, Phelps PV;  
 PI Walton PE;  
 XX  
 XX WPI; 1994 118144/14.

XX  
 XX Increasing growth of birds with insulin like growth factor  
 PT delivered to the egg before hatching exp. for the resulting egg gain  
 PT in chickens.  
 XX  
 XX Claim 6; Page 37; 45pp; English.

PS  
 XX Growth of birds is increased by (a) adding to the bird, in ovo,  
 CC insulin-like growth factor (IGF-1 or -2 or their active analogues;  
 CC (b) incubating to hatch and (c) growing the birds for at least 3  
 CC weeks after hatch.  
 CC IGF-1 analogues used pref. (i) lack 1-8 N-terminal amino acids or  
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,  
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced  
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal  
 CC given in AAR51439-49.  
 CC IGF 2 analogues used pref. have Glu(2) or Glu(3) absent or replaced  
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent  
 CC to Glu can be replaced by Arg or Gly. The IGF 2 analogue pref.  
 CC comprises the N-terminal given in AAR51450-53  
 CC esp. long R3 IGF-1, given in AAR51454 is used. It is the full human  
 CC IGF 1 sequence with Arg replacing Glu(3) and a 15 amino acid  
 CC N-terminal extension.  
 CC (updated on 25-MAR-2003 to correct in field.)

XX Sequence 6 AA;

Query Match 62.5%; Score 20; DB 15; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGTL 4  
 DB 2 PGTL 5

RESULT 7  
 ABP67550  
 ID ABP67550 standard; Peptide; 6 AA.

XX AC ABP67550;  
 XX  
 XX 10-DEC-2002 (first entry)  
 XX  
 XX Human CD66 family modulating peptide SEQ ID NO 421.  
 XX  
 XX Human; CD66; CEACAM; cytostatic; antiinflammatory; immunomodulator;  
 KW antibacterial; virucide; gene therapy; vaccine; neutrophil;  
 KW immune system; autoimmune disease; cancer; infection; bacterial; virus;  
 KW inflammatory disease; transplantation; immunisation.

XX Homo sapiens.

XX WO200269601-A2.  
 XX  
 XX 06-SEP-2002.  
 XX  
 XX 27-FEB-2002; 2002WO-US05720.  
 XX  
 XX 28-FEB 2001; 2001US-272113P.

XX (SKUB/) SKUBITZ K M.  
 PA (SKUB/) SKUBITZ A P N.

XX Skubitz KV, Skubitz APN;  
 XX WPI; 2002.70698:/76.

XX New peptide from a surface exposed region of a CD66 family member,  
 PT useful for modulating the function of CD66 family members, e.g.  
 PT activation of neutrophils, for treating or diagnosing autoimmune  
 PT diseases or cancer, and as a vaccine.

XX Claim 2; Page 27; 96pp; English.

XX The invention relates to an isolated peptide (I) from a surface exposed  
 CC region of a CD66 family member (ABP6713C ABP67990). The peptide  
 CC modulates:  
 CC (a) activation of neutrophils;  
 CC (b) activation or inhibition of T-cells, B-cells, NK cells, LAK cells,  
 CC dendritic cells or other immune system cells;  
 CC (c) proliferation and/or differentiation of the above cells, including  
 CC epithelial cells;  
 CC (d) homotypic and/or heterotypic adhesion among CD66 family members;  
 CC and  
 CC (e) adhesion of CD66 family members to other ligands. The peptide is  
 CC useful in modulating the function of CD66 family members and/or their  
 CC ligands, such as activation of neutrophils and activation, inhibition,  
 CC proliferation and/or differentiation of the immune cells. The peptides  
 CC may also be used in treating or diagnosing autoimmune diseases, cancer,  
 CC infections (e.g. bacterial or viral) or inflammatory diseases, in  
 CC transplantation therapies and for immunisation.

XX Sequence 6 AA;

Query Match 62.5%; Score 20; DB 23; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PGTLN: 6



DB 1 PCTLNW 6

RESULT 8  
 AAY90183  
 ID AAY90183 standard; peptide; 6 AA.  
 XX  
 AC AAY90183;  
 DT 21 SEP-2000 (first entry);  
 XX  
 DE Ad5 HVR5 loop fragment.  
 XX  
 KW Ligand epitope; UPAR; urokinase-type plasminogen activator receptor;  
 KW adenovirus; hexon HVR5 loop; hexon HI loop; peripheral artery disease;  
 KW recombinant adenovirus vector; tumor; restenosis; gene therapy; asthma;  
 KW smooth muscle cell proliferation inhibitor; coronary artery disease;  
 KW obesity; neurodegenerative disease; infection; autoimmune disease; HIV;  
 KW thrombosis; diabetes; tropism-modified virus.  
 XX  
 CS Adenovirus sp.  
 XX  
 PN WC220012738-A1.  
 XX  
 PD 09-MAR-2000.  
 XX  
 PF 27 AUG-1999; 99MO-IB01524.  
 XX  
 PR 27-AUG 1998; 98US-0098028.  
 XX  
 PA (AVET) AVENTIS PHARMA SA.  
 PI Vigne E, Dedieu J, Latta M, Yeh P, Perricaudet M;  
 XX  
 DR MPI; 2000-256653/22.  
 XX  
 PT Urokinase-type plasminogen activator receptor (UPAR)-targeted  
 PT adenovirus vectors having modified hexon HVR5 and HI loops and modified  
 PT fiber proteins useful for targeted gene therapy to treat cancer or  
 PT restenosis.  
 XX  
 PS Example 1; Page 32; 128pp; English.  
 XX  
 CC This sequence is a fragment of the adenovirus Ad5 hexon containing the  
 CC HVR5 loop. The invention relates to an adenovirus from which at  
 CC least a part of the hexon HVR5 or HI loop is replaced with a binding  
 CC peptide, or targeting sequence, flanked by activating amino acid spacers,  
 CC to functionally display its binding specificity at the capsid surface.  
 CC The invention also relates to a recombinant adenovirus vector where a  
 CC binding peptide, or targeting sequence, is connected to the C-terminus of  
 CC the fiber by a connecting spacer, or linker, so as to functionally  
 CC display its binding specificity at the capsid surface. The adenovirus or  
 CC recombinant adenovirus vector can be used to preferentially express a  
 CC gene in a target cell, especially a cell that expresses a UPAR. The  
 CC targeted adenovirus vector preferably comprises a heterologous gene  
 CC encoding a gene for treatment of a tumor or restenosis. The targeted  
 CC adenovirus vector is useful for gene therapy treatment of a disease, and  
 CC for manufacturing a medicine used in gene therapy treatment of a disease.  
 CC The viruses can also be used to inhibit smooth muscle cell proliferation,  
 CC to treat peripheral artery diseases, coronary artery diseases, obesity,  
 CC neurodegenerative diseases, infections, autoimmune diseases, asthma, HIV,  
 CC thrombosis, and diabetes. The viruses are particularly targeted against a  
 CC urokinase-type plasminogen activator receptor (UPAR). The adenoviruses  
 CC are tropism-modified without adversely affecting productivity of the  
 CC vectors.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 59.4%; Score 19; DB 21; Length 6;  
 Best local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TINI 6  
 DB 3 TINI 6  
 RESULT 9  
 AAY66968  
 ID AAY66968 standard; peptide; 3 AA.  
 XX  
 AC AAY66968;  
 XX  
 DT 11-APR-2000 (first entry)  
 XX  
 DE T cell antigen receptor Vbeta chain CDR3 peptide.  
 XX  
 KW Rheumatoid arthritis; arthritis deformans; T-cell antigen receptor;  
 KW Vbeta chain; autoantigen; immunological tolerance.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO9963084-A1.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 28-MAY-1999; 99MO-JP02814.  
 XX  
 PR 29-MAY-1998; 98JP-0149855.  
 PR 14-OCT-1998; 98JP-0328761.  
 XX  
 PA (TORI) TORII PHARM CO LTD.  
 XX  
 PI Nishioka K, Yoshino S;  
 XX  
 DR MPI; 2000-086978/97.  
 XX  
 PT T-cell antigen receptor V-beta chain CDR3 region sequences accumulated  
 PT in synovial membranes of rheumatoid arthritis patients.  
 XX  
 PS Claim 4; Page 15; 136pp; Japanese.  
 XX  
 CC The invention relates to peptide sequences present in the synovial fluid  
 CC and membranes of rheumatoid arthritis patients, arising from the CDR  
 CC region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.  
 CC Compositions which contain autoantigenic peptides binding specifically  
 CC to T cells expressing receptors containing the peptide sequences, which  
 CC include antigen-specific immunological tolerance to rheumatoid arthritis  
 CC can be used for the treatment and prevention of rheumatoid arthritis.  
 CC The invention can be used for the diagnosis, treatment and prevention  
 CC of rheumatoid arthritis. Sequences AAY66959-977 represent peptides from  
 CC the CDR3 region of various Vbeta chains of T cell antigen receptor.  
 XX  
 SQ Sequence 3 AA;  
 Query Match 56.2%; Score 18; DB 21; Length 3;  
 Best local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PGT 3  
 DB 1 PGT 3  
 RESULT 10  
 AAE33660  
 ID AAE33660 standard; peptide; 4 AA.  
 XX  
 AC AAE33660;  
 XX  
 DT 16-APR-2003 (first entry)  
 XX  
 DE Human BCA3 SH2 domain binding site #5.  
 XX  
 KW Human; breast cancer-associated gene; BCA-related disorder; lymphoma;



```

XX 17-JUL-2002.
XX
XX
XX 11-JAN-2002; 2002EP-0075095.
XX
XX 14-JAN-2003; 2001L-0140681.
XX 19-OCT-2001; 2001CS-0982172.
XX
XX (KATZ/) KATZ E J.
XX
XX Katz EI;
XX
XX WPI; 2002 645691/70.
XX
XX Generating amino acid sequences representative of desired polypeptide,
XX by computationally generating proteolytic cleavage products, analyzing
XX and selecting the set of products, thus generating amino acid sequences
XX
XX Example 1; Page 13; 124pp; English.
XX
XX The invention relates to generating set of amino acid sequences (AAS)
XX representative of one desired polypeptide (1), involving computationally
XX generating a number of proteolytic cleavage products (PCP) from (1),
XX analysing the PCP according to one parameter defining a characteristic
XX of AAS and selecting a set of PCP according to a preset criteria for
XX each parameter, thus generating the set of AAS representative of (1).
XX Also included are (1) a computer readable storage media (11) comprising a
XX database of amino acid sequences corresponding to the polypeptide of
XX interest; (2) a system (111) for generating a database of amino acid
XX sequences corresponding to a polypeptide of interest, comprises a
XX processing unit which executes a software application configured
XX for generating the number of proteolytic cleavage products from one
XX polypeptide of interest, and analysing the number of proteolytic
XX cleavage products according to one parameter defining a characteristic
XX of amino acid sequence; (3) a kit for quantifying at least one
XX polypeptide of interest, comprises a number of peptides or antibodies
XX each capable of specifically recognising at least one peptide, where the
XX number of peptides is generated according to information derived from
XX computational analysis of the polypeptide of interest; and
XX (4) quantifying one polypeptide of interest in a biological
XX sample, involving contacting the biological sample with proteolytic
XX agent, so as to obtain a proteolysed biological sample, contacting the
XX proteolysed biological sample with at least one antibody and at least
XX one peptide of a number of peptides, and detecting presence, absence
XX and/or level of antibody binding to thus quantify one polypeptide of
XX interest in the biological sample. The method is useful for generating at
XX least one antibody specific to a polypeptide of interest. The
XX peptides or antibodies generated may be used to: (1) induce diabetes,
XX Parkinson's disease, Alzheimer's disease, human immunodeficiency virus
XX infection, malaria, cholera, influenza, rabies, diphtheria, cancer (e.g.
XX breast, colon, cervix, melanoma, lung, ovary, pancreas, prostate,
XX lymphomas and leukaemias). The present sequence is a predicted tryptic
XX peptide from human P-glycoprotein generated to form part of a kit for
XX identifying multi-drug (MDR) resistance associated proteins.
XX
XX Sequence 5 AA;
XX
XX Query Match 56.2%; Score 18; DB 23; Length 5;
XX Best Local Similarity 75.0%; Pred. No. 9.3e+05;
XX Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 3 TINI 6
XX |||
XX 1 TINV 4
XX
XX RESULT 13
XX AAR38234
XX ID AAR38234 standard; peptide; 6 AA.
XX
XX AAR38234;
XX
XX

```

```

DT 25-MAR-2003 (updated);
DT 08-OCT-1993 (first entry)
XX
XX Alzheimer paired helical filament tau protein epitope 200-205.
XX
XX Alzheimer tau protein; phosphorylation-dependent; PHF;
XX neuronal microtubule; mitogen activated protein kinase; MAP kinase.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 3..4
XX /label= Phosphorylation_motif
XX
XX MO9311231-A1.
XX
XX 10-JUN-1993.
XX
XX 07-DEC-1992; 92WO-EP02829.
XX
XX 06-DEC-1991; 91EP-0120974.
XX 16-NOV-1992; 92EP-0119551.
XX (PLAC ) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.
XX
XX Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow E;
XX Steiner B;
XX
XX WPI; 1993-197050/24.
XX
XX Tau protein epitope(s), specific antibodies and protein kinase(s)
XX - used in the prevention, diagnosis and treatment of Alzheimer's
XX disease
XX
XX Claim 5; Page 89; 148pp; English.
XX
XX This is one of 26 preferred epitopes which occur in a phosphorylated
XX state in tau protein from Alzheimer paired helical filaments. The
XX epitopes all include phosphorylatable serine residues in Ser-Pro
XX motifs, 1le-Gly-Ser motifs or Cys-Gly-Ser motifs and/or
XX phosphorylatable threonine residues in Thr-Pro motifs. The pattern
XX of tau protein phosphorylation differs between Alzheimer's and
XX non-Alzheimer's individuals. Knowledge of the phosphorylated
XX epitopes and antibodies which recognise them may be useful in
XX diagnosis, treatment and prevention of Alzheimer's Disease. The
XX protein kinases present in mammalian brain which phosphorylate the
XX different epitopes are also claimed but no sequences are given.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 6 AA;
XX
XX Query Match 56.2%; Score 18; DB 14; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 PGT 3
XX |||
XX 4 PGT 6
XX
XX Db
XX
XX RESULT 14
XX AAR37553
XX ID AAR37553 standard; peptide; 6 AA.
XX
XX AAR37553;
XX
XX 25-MAR-2003 (updated)
XX 07-OCT-1993 (first entry)
XX
XX Phosphorylated tau protein epitope.
XX
XX Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
XX treatment; formation; inhibition; inhibitor.

```

XX Homo sapiens.  
 CS  
 XX  
 EN EP544342.A1.  
 PE 09-JUN-1993.  
 XX  
 PF 06-DEC-1991; 9:EP-0120974.  
 XX  
 PE 06-DEC-1991; 9:EP-0120974.  
 XX  
 PA (PLAT) MAX PLANCK GES FÖRDERUNG WISSENSCHAFTEN.  
 XX  
 PI Biernat J, Drewes G, Lichtenberg-Kraag B, Wanker Kow EM, Steiner B;  
 XX  
 CR WPT; 1993 183841/23.  
 XX  
 PI Phosphorylated tau protein epitope associated with Alzheimer's  
 PT disease - is used as protein kinase inhibitor for treatment and  
 PT diagnosis  
 XX  
 PS Claim 4; Page 16; 34pp; English.  
 XX  
 CC The sequence is that of an epitope of tau protein which specifically  
 CC occurs in a phosphorylated state in tau protein from Alzheimer's  
 CC paired helical fragments. It may be used as part of a method for the  
 CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may  
 CC also be used in an in vitro model for the study of the generation of  
 CC the Alzheimer state of proteins and the testing of substances which  
 CC prevent the conversion of normal to Alzheimer tau protein. The  
 CC epitope occurs at residues 202-205 of human tau protein.  
 CC (Updated on 25-MAR-2003 to correct PM field.)  
 CS  
 XX  
 SQ Sequence 6 AA:  
 Query Match 56.2%; Score 18; DB 14; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PGT 3  
 DE 4 PGT 6  
 XX  
 RESULT 14  
 AA045755  
 ID AA045755 standard; peptide; 6 AA  
 XX  
 AC AA045755;  
 XX  
 DT 19 JUN-1998 (first entry)  
 XX  
 DE Apoptotic protease activating factor 2 tryptic peptide #4.  
 XX  
 XX Cytochrome c tryptic peptide; Apaf-2; Hela cell S-100; apoptosis;  
 XX apoptotic protease activating factor 2; cytosolic antitumour.  
 XX  
 CS Homo sapiens.  
 XX  
 EN W09802579 A1.  
 XX  
 PE 22-JAN-1999.  
 XX  
 PF 11 JUL-1997; 97WO-US12090.  
 XX  
 PF 12 JUL-1996; 96US-0012269.  
 XX  
 PA (JVEEM) DNIV EMORY.  
 XX  
 PI Liu X, Wang X.  
 XX  
 CR WPT; 1998 110623/10.  
 XX  
 XX  
 PT Cell-free assay to identify compositions that regulate apoptosis  
 PT from their effect on e.g. cytosolic cytochrome c levels in cellular  
 PT extracts, particularly to identify antitumour agents  
 XX  
 PS Example 8; Page 22; 42pp; English.  
 XX  
 CC This sequence represents an apoptotic protease activating factor-2  
 CC (Apaf-2) tryptic peptide which corresponds to residues 40-53 of  
 CC human cytochrome c. The invention relates to an in vitro model for  
 CC studying the regulation of apoptosis. Compositions are assayed in vitro  
 CC for regulation of apoptosis by (a) preparing a 100000 g supernatant  
 CC extract (A) from cells, not committed to apoptosis, from a multicellular  
 CC eukaryote; (b) adding test composition to (A); (c) preparing control  
 CC assays comprising (A) and a known inhibitor or known inducer of  
 CC apoptosis, or a compound known to have no effect on apoptosis; (d)  
 CC assessing either (i) activation of apoptosis from an increase in  
 CC cytosolic cytochrome c; CPP32 protease activity or ability to fragment  
 CC genomic DNA, relative to system without added test compounds or (ii)  
 CC inhibition of apoptosis by a reduction in these quantities in a  
 CC mixture containing a known inducer, relative to control without test  
 CC compound. The test is performed on mammalian cells, specifically HeLa  
 CC cells. Cytochrome c is determined by immunoassay and CPP32 by adding  
 CC radiolabelled poly(adenosine diphosphate-ribose) polymerase (PARP) or  
 CC labelled sterol regulatory binding protein (SRBP), and then detecting  
 CC fragments of these compounds by sodium dodecylsulphate-polyacrylamide gel  
 CC electrophoresis (SDS-PAGE). DNA fragmentation is determined by adding  
 CC intact mammalian cell nuclei, incubating, extracting genomic DNA and  
 CC analysing its size distribution. The extract contains enough dATP and/or  
 CC corresponding diphosphate (dNTP) to allow induction of an apoptotic  
 CC response. dATP and soluble cytochrome c are required for initiation of  
 CC apoptosis in the cell-free system. The method is especially used to  
 CC identify chemotherapeutic agents that can induce apoptosis in tumour  
 CC cells even when these express the Bcl-2 protein associated with  
 CC resistance to chemotherapy. Compounds identified this way may also (a)  
 CC improve the effect of apoptosis-inducing chemotherapeutic agents or (b)  
 CC antagonise decyadenosine triphosphate (dATP) in the cytosol of patients  
 CC with adenosine deaminase deficiency (severe combined immune  
 CC deficiency), as a potential treatment for this condition. Unlike known  
 CC methods, this process does not use cells in which the apoptotic pathway  
 CC has already been induced, i.e. it is not subject to interference from  
 CC other apoptosis-inducing factors or other conditions.  
 XX  
 SQ Sequence 6 AA:  
 Query Match 56.2%; Score 18; DB 19; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PGT 3  
 DB 3 PGT 5  
 XX  
 Search completed: November 5, 2003, 17:47:00  
 Job time : 41 secs

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OX protein - protein search, using sw model  
Run on: November 5, 2003, 17:48:12 : Search time 28 seconds  
(without alignment)  
36,803 Million cell updates/sec

Title: US-09-914-088-6

Perfect score: 32

Sequence: 1 PGTINI 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 17174292 residues

Total number of hits satisfying chosen parameters: 1688

Minimum DB seq length: 0

Maximum DB seq length: 6

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA:

- 1: /cgn2\_6/ptodata/2/pubaa/US07\_PUBCOMB.pep\*
- 2: /cgn2\_6/ptodata/2/pubaa/PCF\_NEW\_PUB.pep\*
- 3: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pep\*
- 4: /cgn2\_6/ptodata/2/pubaa/US06\_PUBCOMB.pep\*
- 5: /cgn2\_6/ptodata/2/pubaa/US07\_NEW\_PUB.pep\*
- 6: /cgn2\_6/ptodata/2/pubaa/PCFUS\_PUBCOMB.pep\*
- 7: /cgn2\_6/ptodata/2/pubaa/US08\_NEW\_PUB.pep\*
- 8: /cgn2\_6/ptodata/2/pubaa/US08\_PUBCOMB.pep\*
- 9: /cgn2\_6/ptodata/2/pubaa/US09\_PUBCOMB.pep\*
- 10: /cgn2\_6/ptodata/2/pubaa/US09\_PUBCOMB.pep\*
- 11: /cgn2\_6/ptodata/2/pubaa/US09\_PUBCOMB.pep\*
- 12: /cgn2\_6/ptodata/2/pubaa/US09\_NEW\_PUB.pep\*
- 13: /cgn2\_6/ptodata/2/pubaa/US10\_PUBCOMB.pep\*
- 14: /cgn2\_6/ptodata/2/pubaa/US10\_PUBCOMB.pep\*
- 15: /cgn2\_6/ptodata/2/pubaa/US10\_PUBCOMB.pep\*
- 16: /cgn2\_6/ptodata/2/pubaa/US10\_NEW\_PUB.pep\*
- 17: /cgn2\_6/ptodata/2/pubaa/US10\_NEW\_PUB.pep\*
- 18: /cgn2\_6/ptodata/2/pubaa/US10\_PUBCOMB.pep\*

Pred. No. is the number of results predicted by BLAST to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	6	12	US-10-082-014-277
2	32	100.0	6	12	US-10-372-076-131
3	19	59.4	6	12	US-09-791-524-57
4	18	56.2	4	11	US-09-812-464-12
5	18	56.2	5	10	US-09-962-172-55
6	18	56.2	6	8	US-09-891-525-4
7	18	56.2	6	12	US-10-256-126-3
8	18	56.2	5	15	US-10-196-530-4
9	16	50.0	5	15	US-10-206-699-248
10	16	50.0	6	10	US-09-817-193A-9
11	16	50.0	6	11	US-09-853-257-4
12	16	50.0	6	12	US-10-283-811-1
13	16	50.0	6	14	US-10-156-820-69
14	15	46.9	5	11	US-09-768-006-142
15	15	46.9	5	11	US-09-768-006-143

16	15	46.9	5	11	US-09-788-006-144	Sequence 144, App
17	15	46.9	5	15	US-10-006-869-451	Sequence 451, App
18	15	46.9	5	15	US-10-006-869-1031	Sequence 1031, App
19	15	46.9	5	15	US-10-286-699-182	Sequence 182, App
20	15	46.9	6	9	US-09-997-900-7	Sequence 7, Appl
21	15	46.9	6	9	US-09-484-704-10	Sequence 10, Appl
22	15	46.9	6	10	US-09-818-656A-15	Sequence 15, Appl
23	15	46.9	6	10	US-09-947-387-141	Sequence 141, App
24	15	46.9	6	11	US-09-507-362-122	Sequence 122, App
25	15	46.9	6	12	US-10-187-049-7	Sequence 7, Appl
26	15	46.9	6	12	US-10-357-467-11	Sequence 11, Appl
27	15	46.9	6	15	US-10-006-869-452	Sequence 452, App
28	15	46.9	6	15	US-10-006-869-454	Sequence 454, App
29	15	46.9	6	15	US-10-006-869-1032	Sequence 1032, App
30	15	46.9	6	15	US-10-006-869-1034	Sequence 1034, App
31	14	43.8	4	10	US-09-768-155-8	Sequence 8, Appl
32	14	43.8	5	9	US-09-817-661-33	Sequence 33, Appl
33	14	43.8	5	15	US-10-206-699-181	Sequence 181, App
34	14	43.8	6	9	US-09-741-148A-17	Sequence 17, Appl
35	14	43.8	6	10	US-09-865-018-22	Sequence 22, Appl
36	14	43.8	6	10	US-09-990-762-39	Sequence 39, Appl
37	14	43.8	6	11	US-09-974-879-421	Sequence 421, App
38	14	43.8	6	11	US-09-858-852A-39	Sequence 39, Appl
39	14	43.8	6	11	US-09-303-736-421	Sequence 421, App
40	14	43.8	6	12	US-10-262-435-10	Sequence 10, Appl
41	14	43.8	6	12	US-10-348-232-94	Sequence 94, Appl
42	14	43.8	6	12	US-10-020-354-102	Sequence 102, App
43	14	43.8	6	12	US-10-086-208-10	Sequence 10, Appl
44	14	43.8	6	14	US-10-011-436-12	Sequence 12, Appl
45	14	43.8	6	14	US-10-156-820-48	Sequence 48, Appl

## ALIGNMENTS

RESULT 1  
US-10-082-014-277  
; Sequence 277, Application US/0092014  
; Publication No. US2003018585A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL  
; FILE REFERENCE: ICC-130.0 4564/85124  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/930,915  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 277  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-277

Query Match 100.0% Score 32; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGTINI 6  
|||||  
Db 1 PGTINI 6

RESULT 2  
US-10-372-076-131  
; Sequence 131, Application US/10372076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS

FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/172,076  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/080,299  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 131  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Homo sapiens  
US 10-372 076-131

Query Match 100.0%; Score 32; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGTNI 6  
Db 1 PGTNI 6

RESULT 3  
US-09-791-524-57  
Sequence 57, Application US/09791524  
Publication No. US20030143209A1  
GENERAL INFORMATION:  
APPLICANT: Aventis Pharmaceuticals Products Inc.  
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes  
FILE REFERENCE: A339A  
CURRENT APPLICATION NUMBER: US/09/791,524  
CURRENT FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: 60/03828  
PRIOR FILING DATE: 1998-08-27  
NUMBER OF SEQ ID NOS: 150  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 57  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Adenovirus  
US 09-791 524-57

Query Match 59.4%; Score 19; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TINI 6  
Db 3 TINI 6

RESULT 4  
US-09 932-464 12  
Sequence 12, Application US/09832464  
Publication No. US20030096953A1  
GENERAL INFORMATION:  
APPLICANT: de Boer, Piet A.J.  
Hale, Cynthia A.  
TITLE OF INVENTION: COMPOSITIONS AND METHOD FOR SCREENING ANTIMICROBIALS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MESLEN & CARROLL  
STREET: 220 Montgomery Street, Suite 120  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/832,464  
FILING DATE: 11-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/184,826  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Peter G.  
REGISTRATION NUMBER: 12,837  
REFERENCE/DOCKET NUMBER: CASE-02249  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: No. US20030096953A1 Relevant  
TOPOLOGY: No. US20030096953A1 Relevant  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-832-464-12

Query Match 56.2%; Score 18; DB 11; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGT 3  
Db 1 PGT 3

RESULT 5  
US-09-982-172-53  
Sequence 53, Application US/09982172  
Patent No. US20020137119A1  
GENERAL INFORMATION:  
APPLICANT: Emli Israel Katz  
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING SUCH PEPTIDES  
TITLE OF INVENTION: UTILIZING EACH  
FILE REFERENCE: 01/22283  
CURRENT APPLICATION NUMBER: US/09/982,172  
CURRENT FILING DATE: 2001-10-15  
NUMBER OF SEQ ID NOS: 243  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 53  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-53

Query Match 56.2%; Score 18; DB 10; Length 5;  
Best Local Similarity 75.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TINI 6  
Db 1 TINI 4

RESULT 6  
US-08-921 525-4  
Sequence 4, Application US/08991525  
Publication No. US20020081643A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Xiaodong  
APPLICANT: LIA, Xuesong

TITLE OF INVENTION: Regulation of Apoptosis and In Vitro  
TITLE OF INVENTION: Model for Studies Thereof  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,525  
FILING DATE: 11-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/021,248  
FILING DATE: 12-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 45-96  
TELEPHONE: (303) 499-8089  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-08-891-525-4

Query Match 56.2%; Score 18; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Cy 1 PGT 3  
Db 3 PGT 5

RESULT 7  
US-10-256-326-3  
Sequence 3, Application US/10256326  
Publication No. US20030186326A1  
GENERAL INFORMATION:  
APPLICANT: PURDUE RESEARCH FOUNDATION  
TITLE OF INVENTION: MATERIALS AND METHODS FOR CONTROLLING ISOTOPE EFFECTS DURING  
FRACTIONATION OF ANALYTES  
FILE REFERENCE: 290.00230101  
CURRENT APPLICATION NUMBER: US/10/256,326  
CURRENT FILING DATE: 2002-09-27  
PRIOR APPLICATION NUMBER: US 60/325,335  
PRIOR FILING DATE: 2001-09-27  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 3  
LENGTH: 6  
TYPE: PR7  
ORGANISM: artificial  
FEATURE:  
OTHER INFORMATION: test peptide  
US-10-256-326-3

Query Match 56.2%; Score 18; DB 12; Length 6;

Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cy 1 PGT 3  
Db 3 PGT 5

RESULT 8  
US-10-198-590-4  
Sequence 4, Application US/10198590  
Publication No. US20030032045A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Xiaodong  
TITLE OF INVENTION: Regulation of Apoptosis and In Vitro  
MODEL for Studies Thereof  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/198,590  
FILING DATE: 18-JUL-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/891,525  
FILING DATE: 11-JUL-1997  
APPLICATION NUMBER: US 60/021,268  
FILING DATE: 12-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Voc-Warren, Heela  
REGISTRATION NUMBER: 45,495  
REFERENCE/DOCKET NUMBER: 45-96A  
TELEPHONE: (303) 499-8089  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-198-590-4

Query Match 56.2%; Score 18; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 PGT 3  
Db 3 PGT 5

RESULT 9  
US-10-236-699-228  
Sequence 228, Application US/10206699  
Publication No. US20030102510A1  
GENERAL INFORMATION:  
APPLICANT: Sundata-Oorthy, N.

```
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: YHRH 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/352,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 65/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,954
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 228
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-228

Query Match
Best Local Similarity 50.0%; Score 16; DB 15; Length 5;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTIN 5
Db 2 GTIN 5

RESULT 10
US-09-917-199A-9
; Sequence 9, Application US/69817199A
; Publication No. US20020142390A1
; GENERAL INFORMATION:
; APPLICANT: SHAG, Wei, et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLOC01187
; CURRENT APPLICATION NUMBER: US/09/817,199A
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-817-199A-9

Query Match
Best Local Similarity 50.0%; Score 16; DB 15; Length 6;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PGTI 4
Db 3 PGAV 6

RESULT 11
US-09-853-257-4
; Sequence 4, Application US/09853257
; Publication No. US20030021032A1
; GENERAL INFORMATION:
; APPLICANT: Bonnie L. Bassler
; APPLICANT: Brendan N. Lilley
; TITLE OF INVENTION: LUXO-SIGMAS4 INTERACTIONS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: P01V.002A
; CURRENT APPLICATION NUMBER: US/09/853,257
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/202,999
; PRIOR FILING DATE: 2000-05-10
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; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: portion of consensus sequence of sigma-54 domains
; NAME/KEY: VARIANT
; LOCATION: 11...16;
; OTHER INFORMATION: Xaa = Trp or Phe
US-09-853-257-4

Query Match
Best Local Similarity 50.0%; Score 16; DB 11; Length 6;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PGTI 4
Db 3 PGNV 6

RESULT 12
US-10-280-833-1
; Sequence 1, Application US/10280833
; Publication No. US20030195150A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Charles Eric
; APPLICANT: Dashper, Stuart Geoffrey
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Talbot, Gert Hoy
; APPLICANT: Malkoski, Marina
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: BOMP-CC1CON
; CURRENT APPLICATION NUMBER: US/10/280,833
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/554,997
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: PP 0514
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: bovine
US-10-280-833-1

Query Match
Best Local Similarity 50.0%; Score 16; DB 12; Length 6;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PGTI 4
Db 1 PGP: 4

RESULT 13
US-10-156-820-69
; Sequence 69, Application US/10156820
; Publication No. US2002015058A1
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/10/156,820
; CURRENT FILING DATE: 2002-06-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/0.005
; PRIOR FILING DATE: 1997-01-30
```



; PRIOR APPLICATION NUMBER: FR 97/11166  
 ; PRIOR FILING DATE: 1997-09-09  
 ; NUMBER OF SEQ ID NOS: 98  
 ; SOFTWARE: FastSeq for Windows Version 4.3  
 ; SEQ ID NO 69  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Phagotome  
 US-10-156-820-69

Query Match 50.0%; Score 16; DB 14; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 5.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTI 4  
 DB 3 PNTI 6

RESULT 14  
 US-09-788-006-142  
 ; Sequence 142, Application US/09788006  
 ; Publication No. US2003003603A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Floudas, Christopher A.  
 ; APPLICANT: Klepeis, John L.  
 ; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and  
 ; TITLE OF INVENTION: Polypeptide Tertiary Structures  
 ; FILE REFERENCE: PU-0007  
 ; CURRENT APPLICATION NUMBER: US/09/788,006  
 ; CURRENT FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ ID NOS: 170  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 142  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Hordeum vulgare  
 US-09-788-006-142

Query Match 46.9%; Score 15; DB 11; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTI 4  
 DB 3 GTI 5

RESULT 15  
 US-09-788-006-143  
 ; Sequence 143, Application US/09788006  
 ; Publication No. US2003003603A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Floudas, Christopher A.  
 ; APPLICANT: Klepeis, John L.  
 ; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and  
 ; TITLE OF INVENTION: Polypeptide Tertiary Structures  
 ; FILE REFERENCE: PU-0007  
 ; CURRENT APPLICATION NUMBER: US/09/788,006  
 ; CURRENT FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ ID NOS: 170  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 143  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Hordeum vulgare  
 US-09-788-006-143

Query Match 46.9%; Score 15; DB 11; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTI 4  
 DB 2 GTI 4

Search completed: November 5, 2003, 17:53:22  
 Job time : 29 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:46:11 ; Search time 22 Seconds  
(without alignments)  
11.539 Million cell updates/sec

Title: US-09-914-088-6

Perfect score: 32  
Sequence: 1 PGT:NI 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 37639

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 3%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA\*  
1: /cgn2\_6/ptodata/1/1aa/5A-COMB.pep\*  
2: /cgn2\_6/ptodata/1/1aa/5B-COMB.pep\*  
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5: /cgn2\_6/ptodata/1/1aa/PTUS-COMB.pep\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles.pep\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	62.5	6	1	US-07 947-035-10
2	20	62.5	6	1	US-08 321-585A-9
3	18	56.2	4	2	US-08 651-918A-12
4	18	56.2	4	3	US-09 184-826-12
5	18	56.2	5	1	US-07-989-962-1
6	19	56.2	5	1	US-07-989-962-4
7	18	56.2	5	1	US-08-213-402-3
8	18	56.2	5	1	US-08-213-402-4
9	18	56.2	5	1	US-08 459-888-4
10	18	56.2	5	1	US-08 459-888-4
11	19	56.2	5	2	US-08 460-452-3
12	18	56.2	5	2	US-08 460-452-4
13	18	56.2	5	2	US-08 459-557-3
14	18	56.2	5	2	US-08 459-557-4
15	18	56.2	5	2	US-08 459-209-3
16	18	56.2	5	2	US-08 459-209-4
17	18	56.2	5	3	US-09 274-642-21
18	18	56.2	5	4	US-09 282-089-3
19	18	56.2	5	4	US-09 282-089-4
20	18	56.2	6	1	US-07-989-962-1
21	18	56.2	6	1	US-07 989-962-13
22	18	56.2	6	1	US-07 989-962-19
23	18	56.2	6	1	US-08 213-402-3
24	18	56.2	6	1	US-08 213-402-12
25	18	56.2	6	1	US-08 213-402-19
26	18	56.2	6	1	US-08 459-644-18
27	18	56.2	6	1	US-08 459-644-18

28	18	56.2	6	1	US-08-459-888-19
29	18	56.2	6	2	US-08-460-452-5
30	18	56.2	6	2	US-08-460-452-18
31	18	56.2	6	2	US-08-460-452-19
32	18	56.2	6	2	US-08-459-557-5
33	18	56.2	6	2	US-08-459-557-18
34	18	56.2	6	2	US-08-459-557-19
35	18	56.2	6	2	US-08-637-759B-476
36	18	56.2	6	2	US-08-459-209-5
37	18	56.2	6	2	US-08-459-209-18
38	18	56.2	6	2	US-08-459-209-19
39	18	56.2	6	2	US-08-724-354D-23
40	18	56.2	6	3	US-08-871-355A-476
41	18	56.2	6	3	US-09-270-984A-23
42	18	56.2	6	3	US-09-274-642-22
43	18	56.2	6	4	US-09-201-945-476
44	18	56.2	6	4	US-09-282-089-5
45	18	56.2	6	4	US-09-282-089-18

## ALIGNMENTS

RESULT 1  
US-07-947-035-10  
: Sequence 10, Application US/07947035  
: Patent No. 5444045  
: GENERAL INFORMATION:  
: APPLICANT: Francis, Geoffrey L.  
: APPLICANT: Walton, Paul E.  
: APPLICANT: Ballard, Francis J.  
: APPLICANT: McMurty, John P.  
: APPLICANT: Phelps, Patricia V.  
: TITLE OF INVENTION: Method of Administering IGF-1, IGF-2,  
: TITLE OF INVENTION: and Analogs Thereof to Birds  
: NUMBER OF SEQUENCES: 18  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Kenneth D. Sibley  
: STREET: P.O. Drawer 34009  
: CITY: Charlotte  
: STATE: No. 5444045th Carolina  
: COUNTRY: US  
: ZIP: 28234  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent In Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/07/947,035  
: FILING DATE: 17-SEP-1992  
: CLASSIFICATION: 514  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Sibley, Kenneth D.  
: REGISTRATION NUMBER: 31,665  
: REFERENCE/DOCKET NUMBER: 5175-59  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (919) 881-3140  
: TELEFAX: (919) 881-3175  
: TELEX: 575102  
: INFORMATION FOR SEQ ID NO: 10:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 6 amino acids  
: TYPE: amino acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: Peptide  
: HYPOTHETICAL: NO  
US-07-947-035-10

Query Match 62.5% Score 20; DB 1; Length 6;  
Best Local Similarity 75.0% Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGTI 4  
Db 2 PGTI 5

RESULT 2  
US-08-321-585A-8  
Sequence 9, Application US/08321585A  
Patent No. 5679771  
GENERAL INFORMATION:  
APPLICANT: Ballard, Francis  
APPLICANT: Read, Leanna  
TITLE OF INVENTION: METHOD FOR TREATING INTESTINAL DISEASES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Xerchart, Gould, Smith, Edell, Welker & Schmidt  
STREET: 3100 No. 5679771 West Center, 90 S. 7th Street  
CITY: Minneapolis  
STATE: MN  
COUNTRY: U.S.A.  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/321,585A  
FILING DATE: 11-OCT-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/954,983  
FILING DATE: 28-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Hillson, Randall A.  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 6159-245USWO  
TELEPHONE: 612/332-5300  
TELEFAX: 612/332/9081  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-08-321-585A-8

Query Match 62.5%; Score 20; DB 1; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.4e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGT: 4  
Db 2 PGTI 5

RESULT 3  
US-08-651-818A-12  
Sequence 12, Application US/08651818A  
Patent No. 5948889  
GENERAL INFORMATION:  
APPLICANT: de Boer, Piet A.J.  
APPLICANT: Hale, Cynthia A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING  
TELECOMMUNICATION INFORMATION:

NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/651,818A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Peter G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: CASE-02249  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-651-818A-12

Query Match 56.2%; Score 18; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGT 3  
Db 1 PGT 3

RESULT 4  
US-09-184-826-12  
Sequence 12, Application US/99184826  
Patent No. 6248543  
GENERAL INFORMATION:  
APPLICANT: de Boer, Piet A.J.  
APPLICANT: Hale, Cynthia A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING  
TELECOMMUNICATION INFORMATION:  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/184,826  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Peter G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: CASE-02249  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-09 184-826-12

Query Match 56.2%; Score 18; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGT 3  
DB 1 PGT 3

RESULT 5  
US-07-989-962-3  
Sequence 3, Application US/07989962  
Patent No. 5324820  
GENERAL INFORMATION:  
APPLICANT: Baxter, Robert  
TITLE OF INVENTION: ACID-LABILE SUBUNIT  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/989,962  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/646,779  
FILING DATE:  
APPLICATION NUMBER: PCT/AU89/00299  
NAME: 14-JUL-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P03350/89  
NAME: 23-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P19314/88  
NAME: 15-JUL-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 521p1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/266-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-07 989-962-3

Query Match 56.2%; Score 18; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PGT 3  
DB 3 PGT 5

RESULT 6  
US-07-989-962-4  
Sequence 4, Application US/07989962  
Patent No. 5324820  
GENERAL INFORMATION:  
APPLICANT: Baxter, Robert  
TITLE OF INVENTION: ACID-LABILE SUBUNIT  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/989,962  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/646,779  
FILING DATE:  
APPLICATION NUMBER: PCT/AU89/00299  
NAME: 14-JUL-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P03350/89  
NAME: 23-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P19314/88  
NAME: 15-JUL-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 521p1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/266-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-07-989-962-4

Query Match 56.2%; Score 18; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGT 3  
DB 3 PGT 5

RESULT 7  
US-08-213-402-3  
Sequence 3, Application US/08213402  
Patent No. 5561046  
GENERAL INFORMATION:  
APPLICANT: Baxter, Robert



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; APPLICATION NUMBER: 08/213422
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/989962
; FILING DATE: 11-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/646779
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 52:PICID3
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-459-888-3

```

```

Query Match 56.2%; Score 18; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 PGT 3
Db 3 PGT 5

```

```

RESULT 10
US-08-459-888-4
; Sequence 4, Application US/08459888
; Patent No. 573651;
; GENERAL INFORMATION:
; APPLICANT: Baxter, Robert
; TITLE OF INVENTION: ACID-LABILE SUBUNIT (ALS) OF
; TITLE OF INVENTION: INSULIN-LIKE-GROWTH FACTOR (IGF) BINDING PROTEIN COMPLEX
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1 MB floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,888
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/213402
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/989962
; FILING DATE: 11-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/646779
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 52:PICID3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881

```

```

; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-459-888-4

```

```

Query Match 56.2%; Score 18; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 PGT 3
Db 3 PGT 5

```

```

RESULT 11
US-08-460-452-3
; Sequence 3, Application US/08460452
; Patent No. 5849687
; GENERAL INFORMATION:
; APPLICANT: Baxter, Robert
; TITLE OF INVENTION: ACID-LABILE SUBUNIT (ALS) OF INSULIN-LIKE-GROWTH FACTOR (IG.
; TITLE OF INVENTION: BINDING PROTEIN COMPLEX
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1 mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,452
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/213402
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/989962
; FILING DATE: 11-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/646779
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 52:PICID2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-460-452-3

```

```

Query Match 56.2%; Score 18; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 PGT 3
Db 3 PGT 5

```

```
RESULT 12
US-08-460-452-4
: Sequence 4, Application US/08460452
: Patent No. 5866360
: GENERAL INFORMATION:
: APPLICANT: Baxter, Robert
: TITLE OF INVENTION: ACID-LABILE SUBUNIT (ALS) OF INSULIN-LIKE-GROWTH FACTOR (IGF)
: TITLE OF INVENTION: BINDING PROTEIN COMPLEX
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1 mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/460-452
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/213402
: FILING DATE: 14-MAR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/989942
: FILING DATE: 11-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/646779
: FILING DATE: 18-JAN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Hasak, Janet E.
: REGISTRATION NUMBER: 28,616
: REFERENCE/DOCKET NUMBER: 521P1C1D2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1896
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 4:
: LENGTH: 5 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-460-452-4

Query Match 56.2%; Score 18; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGT 3
Db 3 PGT 5

RESULT 13
US-08-459-557-3
: Sequence 3, Application US/08459557
: Patent No. 5866360
: GENERAL INFORMATION:
: APPLICANT: Baxter, Robert
: TITLE OF INVENTION: ACID-LABILE SUBUNIT (ALS) OF
: TITLE OF INVENTION: INSULIN-LIKE-GROWTH FACTOR (IGF) BINDING PROTEIN COMPLEX
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1 MB floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459,557
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/213402
: FILING DATE: 14-MAR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/989962
: FILING DATE: 11-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/646779
: FILING DATE: 18-JAN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Hasak, Janet E.
: REGISTRATION NUMBER: 28,616
: REFERENCE/DOCKET NUMBER: 521P1C1D2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1896
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 3:
: LENGTH: 5 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-459-557-3

Query Match 56.2%; Score 18; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PGT 3
Db 3 PGT 5

RESULT 14
US-08-459-557-4
: Sequence 4, Application US/08459557
: Patent No. 5866360
: GENERAL INFORMATION:
: APPLICANT: Baxter, Robert
: TITLE OF INVENTION: ACID-LABILE SUBUNIT (ALS) OF
: TITLE OF INVENTION: INSULIN-LIKE-GROWTH FACTOR (IGF) BINDING PROTEIN COMPLEX
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1 MB floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459,557
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/213402
: FILING DATE: 14-MAR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/989962
: FILING DATE: 11-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/646779
: FILING DATE: 18-JAN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Hasak, Janet E.
: REGISTRATION NUMBER: 28,616
: REFERENCE/DOCKET NUMBER: 521P1C1D2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1896
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 3:
: LENGTH: 5 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-459-557-3
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```
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/989962
? FILING DATE: 11-DEC-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/646779
? FILING DATE: 18-JAN-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Hasak, Janet E.
? REGISTRATION NUMBER: 28,616
? REFERENCE/DOCKET NUMBER: 521P1C1D3
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415/225-1896
? TELEFAX: 415/952-9881
? TELEX: 910/371-7168
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? US-08-459-557-4

Query Match          56.2%; Score 18; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PGT 3
Db      3 PGT 5

Search completed: November 5, 2003, 17:49:17
Job time : 23 secs

? SEQUENCE CHARACTERISTICS:
? LENGTH: 5 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? US-08-459-209-3

Query Match          56.2%; Score 18; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PGT 3
Db      3 PGT 5

Search completed: November 5, 2003, 17:49:17
Job time : 23 secs

? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/989962
? FILING DATE: 11-DEC-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/646779
? FILING DATE: 18-JAN-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Hasak, Janet E.
? REGISTRATION NUMBER: 28,616
? REFERENCE/DOCKET NUMBER: 521P1C1D3
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415/225-1896
? TELEFAX: 415/952-9881
? TELEX: 910/371-7168
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? US-08-459-557-4

Query Match          56.2%; Score 18; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PGT 3
Db      3 PGT 5

RESULT 15
US 08-459-209-3
? Sequence 3, Application US/084592C3
? Patent No. 5936064
? GENERAL INFORMATION:
? APPLICANT: Baxter, Robert
? TITLE OF INVENTION: ACID-LABILE SUBUNIT (ALS) OF
? TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR (IGF) BINDING PROTEIN COMPLEX
? NUMBER OF SEQUENCES: 28
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Genentech, Inc.
? STREET: 460 Point San Bruno Blvd
? CITY: South San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 9408C
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.50 inch, 1 mb floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC DOS/MS DOS
? SOFTWARE: Patin (Genentech)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/459,209
? FILING DATE: 02-JUN-1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/213402
? FILING DATE: 14-MAR-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/989962
? FILING DATE: 11-DEC-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/646779
? FILING DATE: 18-JAN-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Hasak, Janet E.
? REGISTRATION NUMBER: 28,616
? REFERENCE/DOCKET NUMBER: 521P1C1D3
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415/225-1896
? TELEFAX: 415/952-9881
? TELEX: 910/371-7168
? INFORMATION FOR SEQ ID NO: 4:
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GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: November 5, 2003, 17:52:48 ; Search time 21 Seconds  
(without alignments)  
22.897 Million cell updates/sec

Title: US-09-914-088-7

Perfect score: 30

Sequence: 1 FTPT 5

Scoring table: BLCSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283309 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	53.3	5	2	PS0324
2	14	46.7	5	2	B37988
3	12	40.0	3	3	I78890
4	12	40.0	4	2	S53509
5	12	40.0	4	2	S17255
6	12	40.0	5	1	H0RCHA
7	12	40.0	5	2	A60411
8	11	36.7	4	2	A02147
9	11	36.7	5	2	P06444
10	9	30.0	5	2	E42364
11	9	30.0	5	2	E60274
12	8	26.7	5	2	A41225
13	8	26.7	5	2	I39964
14	8	26.7	5	2	I39966
15	8	26.7	5	2	I39965
16	8	26.7	5	2	G37196
17	8	26.7	5	2	P0714
18	8	26.7	5	3	JTC870
19	7	23.3	3	3	RHDTG
20	7	23.3	3	3	RHSHT
21	7	23.3	3	3	A92971
22	7	23.3	3	3	A338C2
23	7	23.3	3	3	A43391
24	7	23.3	4	2	A32039
25	7	23.3	4	2	PL0140
26	7	23.3	4	2	A34626
27	7	23.3	4	2	I51049
28	7	23.3	4	2	PT0240
29	7	23.3	4	2	PT0240

30 7 23.3 4 2 I54357  
31 7 23.3 4 2 PT0675  
32 7 23.3 5 2 A60521  
33 7 23.3 5 2 JN0862  
34 7 23.3 5 2 JN0860  
35 7 23.3 5 2 C41225  
36 7 23.3 5 2 B60274  
37 7 23.3 5 2 B22565  
38 7 23.3 5 2 PQ0009  
39 7 23.3 5 2 JS0119  
40 7 23.3 5 2 S53595  
41 7 23.3 5 2 S11127  
42 7 23.3 5 2 PT0267  
43 7 23.3 5 2 JT0520  
44 7 23.3 5 2 PT0669  
45 6 20.0 3 3 S68328

schwannomin - mous  
T-cell receptor be  
glycogen phosphory  
peptidyl-dipeptida  
peptidyl-dipeptida  
copper resistance  
major protein anti  
R-phycocerythrin al  
angiotensin-conver  
subesophageal gang  
hypothetical prote  
phosphoprotein, bo  
ig heavy chain CRD  
ig kappa chain V-I  
T-cell receptor be  
blood cell protein

## ALIGNMENTS

### RESULT 1

PS0324  
ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 02-Jul-1998  
C:Accession: PS0324  
R:Tsugeta, A.  
submitted to JIPID, April 1993  
A:Reference number: PS0206  
A:Accession: PS0324  
A:Molecule type: protein  
A:Residues: 1-5 <TSU>  
A:Experimental source: leaf, chlorophyll

Query Match 53.3% Score 16; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTPT 5  
| | |  
Db 1 FQAPT 5

### RESULT 2

B37988  
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)  
C:Species: Physarum polycephalum  
C:Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993  
C:Accession: B37988  
R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki, J. Biol. Chem. 265, 19898-19903, 1990  
A:Title: Purification and characterization of a novel intracellular acid proteinase f  
A:Reference number: A37988; MUID:9106C608; PMID:2246266  
A:Accession: B37988  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <MUR>

Query Match 46.7% Score 14; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PP 4  
| | |  
Db 3 PP 4

### RESULT 3

I78890  
tyrosine protein kinase - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: 176830  
 R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.  
 C:Organism: 9, 3437-3448, 1994  
 A:Title: Two distinct protein isoforms are encoded by mtk, a csk-related tyrosine protein  
 A:Reference number: 158407; MUID:9506060; PMID:7970753  
 A:Accession: 178890  
 A:Status: Preliminary; translated from GU/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-3 <RES>  
 A:Cross-references: GB:L33339; NID:9629536; PIR:AA64432.1; PID:9629539  
 C:Genetics:  
 A:Gene: p52ntk

Query Match 40.0%; Score 12; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PT 5  
 ||  
 DB 2 PT 3

RESULT 4  
 SB3528  
 starvation-induced ribonuclease - tomato  
 C:Species: Lycopersicon esculentum (tomato)  
 C:Date: 01-Aug-1994 #sequence\_revision 01-Sep-1995 #text\_change 07 May 1999  
 C:Accession: SB3508  
 R:Koeck, X.; Loeffler, A.; Abel, S.; Glund, K.  
 Plant Mol. Biol. 27, 477-485, 1995  
 A:Title: cDNA structure and regulatory properties of a family of starvation-induced ribonucleases  
 A:Reference number: SB3506; MUID:9520242; PMID:7894015  
 A:Accession: SB3508  
 A:Status: Preliminary  
 A:Molecule type: Protein  
 A:Residues: 1-4 <XOE>

Query Match 40.0%; Score 12; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PT 5  
 ||  
 DB 2 PT 3

RESULT 5  
 S17255  
 ribosomal protein, y11, mitochondrial, protein family 1, yeast (Saccharomyces cerevisiae)  
 C:Species: Saccharomyces cerevisiae  
 A:Variety: strain 0173  
 C:Date: 21-Apr-1993 #sequence\_revision 14-Sep-1994 #text\_change 07 May 1997  
 C:Accession: S17255  
 R:Graham, L.; Graack, H.R.; Kruff, V.; Chelli, T.; Schindler-Peterson, S.; Kitakawa, M.  
 FEBS Lett. 284, 51-56, 1991  
 A:Title: Extended N terminal sequencing of proteins of the large ribosomal subunit from  
 A:Reference number: S17255; MUID:91285186; PMID:176067  
 A:Accession: S17255  
 A:Molecule type: Protein  
 A:Residues: 1-4 <GRO>  
 C:Comment: A coding region for this protein could not be identified in the genome of Saccharomyces cerevisiae  
 C:Genetics:  
 A:Genome: nuclear  
 C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 40.0%; Score 12; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PT 3  
 ||  
 DB 3 PT 4

RESULT 6  
 HOROHA  
 proctolin - American cockroach  
 C:Species: Periplaneta americana (American cockroach)  
 C:Date: 29-Jul-1981 #sequence\_revision 29-Jul-1981 #text\_change 23-Aug-1996  
 C:Accession: A01644  
 R:Starratt, A.N.; Brown, B.E.  
 Life Sci. 17, 1253-1256, 1975  
 A:Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insect  
 A:Reference number: A9348; MUID:76074798; PMID:576  
 A:Accession: A01644  
 A:Molecule type: Protein  
 A:Residues: 1-5 <SRA>  
 A:Note: The synthetic peptide had the same chromatographic, electrophoretic, and phar  
 R:O'Shea, M.; Adams, M.S.  
 Science 213, 567-569, 1981  
 A:Title: Pentapeptide (proctolin) associated with an identified neuron.  
 A:Reference number: A94260; MUID:8125865; PMID:6113690  
 A:Contents: annotation; biological source  
 C:Comment: This peptide is found in the lateral white neurons, which occur in the co  
 innervate the striated hindgut muscles in insects and stimulate contraction of these  
 C:Superfamily: proctolin  
 C:Keywords: neuropeptide

Query Match 40.0%; Score 12; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PT 5  
 ||  
 DB 4 PT 5

RESULT 7  
 A60411  
 proctolin - Atlantic horseshoe crab  
 C:Species: Limulus polyphemus (Atlantic horseshoe crab)  
 C:Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 17-Mar-1999  
 C:Accession: A60411  
 R:Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt  
 Peptides 11, 205-211, 1990  
 A:Title: Identification of proctolin in the central nervous system of the horseshoe c  
 A:Reference number: A60411; MUID:92287800; PMID:2356151  
 A:Accession: A60411  
 A:Molecule type: protein  
 A:Residues: 1-5 <GRO>  
 C:Comment: This neuropeptide stimulates cardiac output and hindgut motility in the ho  
 C:Keywords: neuropeptide

Query Match 40.0%; Score 12; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PT 5  
 ||  
 DB 4 PT 5

RESULT 8  
 A02147  
 phagocytosis-stimulating peptide (tuftsin) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 03-Feb-1994  
 C:Accession: A02147  
 R:Nishio, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.  
 Biochem. Biophys. Res. Commun. 47, 172-179, 1972  
 A:Title: The characteristics, isolation and synthesis of the phagocytosis stimulating  
 A:Reference number: A02147; MUID:72187087; PMID:4112769  
 A:Accession: A02147  
 A:Molecule type: Protein  
 A:Residues: 1-4 <NIS>  
 A:Note: A peptide having the same structure, physical properties, and biological acti

R:Fidalgo, B.V.; Najjar, V.A.  
 Biochemistry 6, 3386-3392, 1967  
 A:Reference number: A37502; MUID:68091045; PMID:4163272  
 A:Contents: annotation: immunoglobulin class  
 C:Comment: An IgG (called leucokinin) binds reversibly to the cell membrane of neutrophils.  
 n is essential for maximum stimulation of the phagocytic activity of neutrophils.  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 36.7%; Score 11; DB 2; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTP 4  
 |  
 |  
 Db 1 TKP 3

## RESULT 9

PT0644  
 T-cell receptor beta chain V-D-J region (111-10) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0644

J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711559  
 A:Accession: PT0644  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-5 <FE>  
 A:Experimental source: newborn thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 36.7%; Score 11; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2  
 |  
 |  
 Db 4 FT 5

## RESULT 10

E42364  
 flagellar protein fliC - Salmonella typhimurium (fragment)  
 C:Species: Salmonella typhimurium  
 C:Date: 24-Jul-1992 #sequence\_revision 24-Jul-1992 #text\_change 12-Sep-1993  
 C:Accession: E42364  
 R.Vogler, A.P.; Homma, M.; Irikura, V.M.; MacTab, R.M.  
 J. Bacteriol. 173, 3564-3572, 1991  
 A:Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and secretion  
 A:Reference number: A42364; MUID:91258342; PMID:1646201  
 A:Accession: E42364  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-5 <VOG>  
 A:Cross-references: GB:M62408

Query Match 30.0%; Score 9; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTP 4  
 |  
 |  
 Db 3 TLP 5

## RESULT 11

E60274  
 major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)  
 C:Species: Mycobacterium tuberculosis  
 C:Date: 1; Dec-1992 #sequence\_revision 1; Dec-1992 #text\_change 30-Sep-1993

C:Accession: E60274  
 R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.  
 Infect. Immun. 59, 372-382, 1991  
 A:Title: Isolation and partial characterization of major protein antigens in the cult  
 A:Reference number: A60274; MUID:91099899; PMID:1898899  
 A:Accession: E60274  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <NAG>

Query Match 30.0%; Score 9; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPT 5  
 |  
 |  
 Db 3 PIT 5

## RESULT 12

A41225  
 copper resistance protein A - Pseudomonas syringae pv. tomato (fragment)  
 C:Species: Pseudomonas syringae pv. tomato  
 C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 24-Jun-1993  
 C:Accession: A41225

R:Cha, J.S.; Cooksey, D.A.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991  
 A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer  
 A:Reference number: A41225; MUID:92020961; PMID:1924351  
 A:Accession: A41225  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <CHA>

Query Match 26.7%; Score 8; DB 2; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TP 3  
 |  
 |  
 Db 4 SP 5

## RESULT 13

I39964  
 ribosomal protein S4 - Bacillus circulans (fragment)  
 C:Species: Bacillus circulans  
 C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 19-Jul-1996  
 C:Accession: I39964  
 R:Grundy, F.J.; Henkin, T.M.  
 J. Bacteriol. 174, 6763-6770, 1992  
 A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.  
 A:Reference number: I39963; MUID:93015735; PMID:1400226  
 A:Accession: I39964  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-5 <RES>  
 A:Cross-references: GB:M99041; NID:G143471  
 C:Genetics:  
 A:Gene: rpsD

Query Match 26.7%; Score 8; DB 2; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2  
 |  
 |  
 Db 4 YT 5

## RESULT 14

I39966  
 ribosomal protein S4 - Bacillus licheniformis (fragment)

C:Species: Bacillus licheniformis  
C:Date: 19-Jul-1996 #sequence\_revision: 19-Jul-1996 #text\_change: 19-Jul-1996  
C:Accession: I39966  
R:Grundy, F.J.; Henkin, T.M.  
J. Bacteriol. 174, 6763-6770, 1992  
A:Title: Characterization of the Bacillus subtilis tpsD regulatory target site.  
A:Reference number: I39963; MUID:93015735; PMID:1400226  
A:Accession: I39966  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-5 <RES>  
A:Cross references: GB:M99043; NID:g143473  
C:Genetics:  
A:Gene: tpsD

Query Match 26.7%; Score 8; DB 2; Length 5;  
Best Local Similarity 50.0%; Pref. No. 2; He+5;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FT 2  
Db 4 YT 5

Result 14  
I39965  
ribosomal protein S4 - Bacillus megaterium (fragment)  
C:Species: Bacillus megaterium  
C:Date: 19-Jul-1996 #sequence\_revision: 19-Jul-1996 #text\_change: 19-Jul-1996  
C:Accession: I39965  
R:Grundy, F.J.; Henkin, T.M.  
J. Bacteriol. 174, 6763-6770, 1992  
A:Title: Characterization of the Bacillus subtilis tpsD regulatory target site.  
A:Reference number: I39963; MUID:93015735; PMID:1400226  
A:Accession: I39965  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-5 <RES>  
A:Cross references: GB:M99042; NID:g143473  
C:Genetics:  
A:Gene: tpsD

Query Match 26.7%; Score 8; DB 2; Length 5;  
Best Local Similarity 50.0%; Pref. No. 2; He+5;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FT 2  
Db 4 YT 5

Search completed: November 5, 2003, 17:53:06  
Job time: 21 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:43:22 ; Search time 10 seconds  
(without alignments:  
23.513 Million cell updates/sec

Title: US-09-914-088-7

Perfect score: 30

Sequence: 1 FTPPT 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	40.0	4	1 RM01 YEAST	P16515 saccharomyces
2	12	40.0	5	1 PRCT PERAM	P01373 periplaneta
3	11	36.7	4	1 TUFT HUMAN	P01958 homo sapien
4	11	36.7	5	1 E103 LITRU	P82029 litorea rub
5	11	36.7	5	1 PAP2 FARMA	P81864 pardachirus
6	11	36.7	5	1 RE31 LITRU	P82072 litorea rub
7	11	36.7	5	1 RE32 LITRU	P82073 litorea rub
8	8	26.7	5	1 BPP7 BOVIN	P10425 boehrops in
9	8	26.7	5	1 PSK DAVIA	P18351 fuscus catc
10	7	23.3	3	1 THYL HIC	P11151 sus scrofa
11	7	23.3	4	1 DCXL PSETH	P10915 pseudoecoras
12	7	23.3	5	1 SUGA ACHEU	P19991 acheta dome
13	6	20.0	4	1 ACHL ACHEU	P15904 acheta na fu
14	6	20.0	4	1 FAR3 HERME	P42563 tirudo medi
15	6	20.0	4	1 FAR4 HERME	P42563 tirudo medi
16	6	20.0	4	1 FFKA ANTEL	P59705 anthopoeura
17	6	20.0	4	1 FLRF HERME	P42561 tirudo medi
18	6	20.0	4	1 FLRN ANTEL	P59707 anthopoeura
19	6	20.0	4	1 FMRF MACCN	P01162 macrocallis
20	6	20.0	4	1 FYRI ANTEL	P59706 anthopoeura
21	6	20.0	4	1 OCPI OCTMI	P59648 octopus min
22	6	20.0	5	1 AL14 CARMA	P81817 carcinus ma
23	6	20.0	5	1 E104 LITRU	P82103 litorea rub
24	6	20.0	5	1 FARP ARTIR	P41853 arthroposthi
25	6	20.0	5	1 RE11 LITRU	P82070 litorea rub
26	6	20.0	5	1 RE21 LITRU	P82071 litorea rub
27	6	20.0	5	1 TPIS CANEA	P54714 canis famli
28	6	20.0	5	1 UC22 MAIZE	P82628 zea mays (m
29	5	16.7	5	1 B10A CITFR	P13071 citrobacter
30	1	3.3	4	1 ECSI HUMAN	P02731 homo sapien
31	1	3.3	4	1 OCP3 OCTMI	P59649 octopus min
32	1	3.3	5	1 B10B CITFR	P12947 citrobacter
33	1	3.3	5	1 UF01 MOUSE	P16519 mus musculu

34 1 3.3 5 1 UXA4 CHLTR P38005 chlamydia t  
35 0 0.0 3 1 GRWY HUMAN P01157 homo sapien  
36 0 0.0 3 1 LUXE VIBFI P24272 vibrio flicc  
37 0 0.0 4 1 DCMS PSECH P19918 pseudomonas  
38 0 0.0 5 1 TRM3 ECOLI P13973 escherichia

#### ALIGNMENTS

##### RESULT 1

RM01 YEAST  
ID RM01 YEAST STANDARD; PRT; 4 AA.  
AC P36515;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).  
GN MRPL1.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91285106; PubMed=2060626;  
RA Grohmann L.; Graack H.-R.; Kruff V.; Choll T.; Goldschmidt-Reisin S.;  
RA Kitakawa M.;  
RT "Extended N-terminal sequencing of proteins of the large ribosomal  
subunit from yeast mitochondria.";  
RL FEBS Lett. 284:51-56(1991).  
DR PIR: S17255; S17255.  
DR SGI: L0002681; MRPL1.  
KW Ribosomal protein; Mitochondrion.  
FT NON TER 4 4  
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0C00000 CRC64;

Query Match 40.0%; Score 12; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TP 3  
||  
DB 3 TP 4

##### RESULT 2

PRCT PERAM  
ID PRCT PERAM STANDARD; PRT; 5 AA.  
AC P01373;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-FEB-1995 (Rel. 31, Last annotation update)  
DE Proctolin.  
OS Periplaneta americana (American cockroach),  
OS Limulus polyphemus (Atlantic horseshoe crab), and  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Hexapoda; Blattaria; Blattelloidea;  
OC Blattellidae; Periplaneta.  
OX NCBI\_TaxID=6978, 6850, 6759;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=P.americana;  
RX MEDLINE=76074708; PubMed=576;  
RA Starratt A.N.; Brown B.E.;  
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter  
in insects.";  
RL Life Sci. 17:1253-1256(1975).  
RN [2]  
RP BIOLOGICAL SOURCE.  
RC SPECIES=P.americana;  
RX MEDLINE=91225865; PubMed=6113690;

RA C'Shea M., Adams M.E.;  
 RT "Pentapeptide (proctolin) associated with an identified neuron."  
 RL Science 213:567-569(1981).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=C. polyphemus;  
 RX MEDLINE=90287803; PubMed=2356151;  
 RA Groome J.R., Tillinghast E.K., Towmey M.A., Vetrovs A.,  
 RA Watson W.H., III, Hunt E.F., Griffin P.R., Alexander C.E.,  
 RA Shabanowitz J.;  
 RT "Identification of proctolin in the central nervous system of the  
 RT horseshoe crab, Limulus polyphemus."  
 RC Peptides 11:205-211(1990).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=C. maenas;  
 RX MEDLINE=86232789; PubMed=2872661;  
 RA Stangier J., Dirksen H., Keller R.;  
 RT "Identification and immunocytochemical localization of proctolin in  
 RT pericardial organs of the shore crab, Carcinus maenas."  
 RL Peptides 7:67-72(1986).  
 RC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINGOUT MOTILITY.  
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.  
 CC THE CRAB PERICARDIAL ORGANS.  
 CC PIR: A01644; HORCHA.  
 DR PIR: A60411; A60411.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA; 649 MW; 71B767B54460C80 CRC64.

Query Match: 40.0%; Score 12; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PT 5  
 DB 4 PT 5

RESULT 4  
 TUFT HUMAN  
 ID TUFT HUMAN STANDARD; PRT; 4 AA.  
 AC P1858;  
 DT 21 JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Phagocytosis-stimulating peptide (Tuftsin).  
 OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catartida; Hominidae; Homo  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=72187087; PubMed=4112769;  
 RA Nishizuka K., Constantopoulos A., Sarch P.B., Najar V.A.;  
 RT "The characteristics, isolation and synthesis of the phagocytosis  
 RT stimulating peptide tuftsin."  
 RL Biochem. Biophys. Res. Commun. 47:172-179(1973).  
 RN [2]  
 RP SEQUENCE  
 RX MEDLINE=68091045; PubMed=4169272;  
 RA Fida'go B.V., Najjar V.A.;  
 RT "The physiological role of the lymphoid system VII: the stimulatory  
 RT effect of leucophilic gamma globulin (leuckokinin) on the phagocytic  
 RT activity of human polymorphonuclear leukocyte."  
 RL Biochemistry 6:3396-3392(1967).  
 CC -1- MISCELLANEOUS: AN IGG (CALLED LEUCKOKININ) BINDS REVERSIBLY TO THE  
 CC CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. DEMONSTRATION ON THE  
 CC MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.  
 CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC  
 CC ACTIVITY OF NEUTROPHILS.  
 DR PIR: A02187; A02147.  
 KW MW; 191150;

DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006909; P:phagocytosis; NAS.  
 SQ SEQUENCE 4 AA; 501 MW; 74176321C000000 CRC64;

Query Match: 36.7%; Score 11; DB 1; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTP 4  
 DB 1 TKP 3

RESULT 4  
 E703 LITRU  
 ID E703 LITRU STANDARD; PRT; 5 AA.  
 AC P82059;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Electrin 3.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 CX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella."  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 5  
 FT SEQUENCE 5 AA; 633 MW; 66876:F2C9A00000 CRC64;

Query Match: 36.7%; Score 11; DB 1; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTTP 4  
 DB 1 FWTP 4

RESULT 5  
 PAP2 PARMA  
 ID PAP2 PARMA STANDARD; PRT; 5 AA.  
 AC P61364;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Pardaxin II (PXII) (Fragment).  
 OS Pardachirus marmoratus (Red sea moles sole).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 OC Solioidei; Solidae; Pardachirus.  
 OX NCBI\_TaxID=31587;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=87057369; PubMed=3782138;  
 RA Lazarovici P., Primor N., Loew L.M.;  
 RT "Purification and pore-forming activity of two hydrophobic  
 RT polypeptides from the secretion of the red sea moles sole (Pardachirus  
 RT marmoratus)."  
 RL J. Biol. Chem. 261:16704-16713(1986).  
 CC -1- FUNCTION: Exhibits unusual shark repellent and surfactant

CC properties. Forms voltage-dependent, ion-permeable channels  
 CC in membranes. At high concentration causes cell membrane lysis.  
 CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PARAXIN FAMILY.  
 KW Toxin.

FT NON\_TER 5 5  
 SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 36.7%; Score 11; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTP 3  
 Db 3 FFP 5

## RESULT 6

RE31\_LITRU  
 ID RE31\_LITRU STANDARD; PRT; 5 AA.  
 AC P82072;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Rubellidin 3.1.  
 CS Litoria rubella (Desert tree frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae.  
 CC Pelodyadinae; Litoria.  
 CC NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE-Skin secretion;  
 RA Steitborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 'Litoria rubella'. The skin peptide profile as a probe for the study  
 of evolutionary trends of amphibians";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
 activity.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -1- MASS SPECTROMETRY: MW=655; METHOD=PEP.  
 KW Amphibian defense peptide; Amidation.  
 FT MCD\_RES 5 5  
 SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10000000 CRC64;

Query Match 36.7%; Score 11; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2  
 Db 4 FT 5

## RESULT 7

RE12\_LITRU  
 ID RE12\_LITRU STANDARD; PRT; 5 AA.  
 AC P82073;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Rubellidin 3.2.  
 CS Litoria rubella (Desert tree frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 CC Pelodyadinae; Litoria.  
 CC NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE-Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 'Litoria rubella'. Comparison with the skin peptides from Litoria  
 rubella";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
 activity.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 KW Amphibian defense peptide.  
 SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 36.7%; Score 11; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2  
 Db 4 FT 5

## RESULT 8

BPP7\_BOTIN  
 ID BPP7\_BOTIN STANDARD; PRT; 5 AA.  
 AC P30425;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S5,2 (SA) (Angiotensin-converting  
 enzyme inhibitor).  
 CS Bothrops insularis (Island Jararaca) (Queimada Jararaca).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 CC Viperidae; Crotalinae; Bothrops.  
 CC NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RA MEDLINE=9031557; PubMed=2386615;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -1- FUNCTION: This peptide both inhibits the activity of the  
 angiotensin-converting enzyme and enhances the action of  
 bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR: G37196; G37195  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MCD\_RES 1 1  
 SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 26.7%; Score 8; DB 1; Length 5;  
 Best Local Similarity 33.3%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTP 3  
 Db 3 WAP 5

## RESULT 9

PSK\_DAUCA  
 ID PSK\_DAUCA STANDARD; PRT; 5 AA.  
 AC P58261;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK  
 beta)].  
 OS Daucus carota (Carrot).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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CC Speimatiophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC Asteridae; campanulids; Apiales; Apiaceae; Daucus.
CX NCBI TaxID:4639;
[1]
RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
RC STRAINS=cv. US-Harumakigosun;
RX MEDLINE=20212743; PubMed=10750705;
RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kikayashi T.,
RA Kamada H., Sakagami Y.;
RT "A secreted peptide growth factor, physiosulfone, acting as a
RT stimulatory factor of carrot somatic embryo formation."
RJ Plant Cell Physiol. 41:27-32(2000).
CC -!- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE
CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC
CC EMBRYOS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A
CC PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
KW Growth factor; Sulfation.
FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
FT MCD_RES 1 1 SULFATION.
FT MCD_RES 3 3 SULFATION.
SQ SEQUENCE 5 AA; 687 MW; 76C1B504B30C000 CRC64;

Query Match 26.7%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 PT 2
DB 3 YT 4

RESULT 10
THYL_PIG STANDARD; EPT; 3 AA.
AC P01152;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thylolipin (Thyrotropin releasing hormone) (TPH) (Protein-lin).
OS Sus scrofa (Pig).
OS Ovis aries (Sheep).
OS Bombina orientalis (Oriental fire-bellied toad), and
OS Notoththalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CX NCBI TaxID:9924, 9940, 8346, 8316;
[1]
RP SEQUENCE.
RC SPECIES=Pig; TISSUE=Hypothalamus;
RX MEDLINE=7036150; PubMed=4984938;
RA Nair R.M.G., Barrett J.F., Bowers C.V., Schally A.V.;
RT "Structure of porcine thyrotropin releasing hormone";
RL Biochemistry 9:1103-1106(1970).
RN [2]
RP SYNTHESIS.
RC SPECIES=Pig;
RX MEDLINE=70369904; PubMed=4982117;
RA Boler J., Eitzmann F., Folkers K., Bowers C.V., Schally A.V.;
RT "The identity of chemical and hormonal properties of the thyrotropin
RT releasing hormone and pyroglutamate-histidyl-proline amide";
RL Biochem. Biophys. Res. Commun. 37:705-710(1969).
RN [3]
RP SEQUENCE.
RC SPECIES=Sheep; TISSUE=Hypothalamus;
RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R.,
RA Ward D.N.;
RT "The elucidation of the primary structure of the hypothalamic thyroid
RT stimulating hormone releasing factor of ovine origin by means of mass
RT spectrometry";
RL Org. Mass Spectrom. 5:221-228(1971).

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RN [4]
RP SYNTHESIS.
RC SPECIES=Sheep;
RX MEDLINE=70163386; PubMed=4985794;
RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
RA Guillemin R.;
RT "Characterization of ovine hypothalamic hypophysiotropic
RT TSH-releasing factor";
RL Nature 226:321-325(1970).
RN [5]
RP SEQUENCE.
RC SPECIES=B. orientalis; TISSUE=Skin;
RX MEDLINE=76138399; PubMed=815011;
RA Yasuhara T., Nakajima T.;
RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
RL Chem. Pharm. Bull. 23:1301-1303(1975).
RN [6]
RP SEQUENCE.
RC SPECIES=N. viridescens;
RX MEDLINE=75035605; PubMed=4214528;
RA Grimm-Joergensen Y., McKelvy J.F.;
RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
RT viridescens) brain in vitro. Isolation and characterization of
RT thyrotropin releasing factor";
RL J. Neurochem. 23:471-478(1974).
CC -!- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
CC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
CC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
DR PIR; A90919; RHTCTO.
DR PIR; A92971; A92971.
DR PIR; A93750; RHSH.
KW Amidation; Pyroglutamate carboxylic acid.
FT MCD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MCD_RES 3 3 AMIDATION.
SQ SEQUENCE 3 AA; 380 MW; 7761F68C00000000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 P 3
DB 3 P 3

RESULT 11
DCML_PSECH
ID DCML_PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit L) (CO-DH L) (Fragment).
GN CUTH.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hügendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydohydrogenic bacteria";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC acceptor.
CC -!- COFACTOR: Molybdenum (molybdopterin).
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.

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DR PIR; 250140, PL0140.  
 KW Oxidoreductase; Molybdenum.  
 FT NOK TER 4 4  
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F0003000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 P 3  
 |  
 Db 4 P 4

## RESULT 12

SUGA ACHDC STANDARD; PRT; 5 AA.

AC P19951; 1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Suboesophageal ganglion; pentapeptide.  
 OS Acheta domesticus (House cricket).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
 OC Acheta.  
 CX NCBI TaxID=6997;  
 RN [1]

## SEQUENCE

RA Wicker C., Wicker C.,  
 RT "Isolation and structure of a peptide isolated from the  
 RT suboesophageal ganglion of Acheta domesticus (Orthoptera).";  
 RL Comp. Biochem. Physiol. 88C:185-187(1987).  
 CC -1 SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL  
 CC GANGLIA.  
 DR PIR; JS0319; JS0319.  
 SQ SEQUENCE 5 AA; 476 MW; 69D76D5DD0B0C000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 P 3  
 |  
 Db 4 P 4

## RESULT 13

ACHI ACHFU STANDARD; PRT; 4 AA.

AC P35904; 1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Achatin-I.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Stgmurethra; Achatinoidea; Achatinidae; Achatina.  
 CX NCBI TaxID=6530;  
 RN [1]

## SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.

RC STRAIN=Perussac; TISSUE=Ganglion;  
 RX MEDLINE=8927355; PubMed=2597281;  
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li E.,  
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.  
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina  
 RT fulica Perussac containing a D-amino acid residue";  
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989)  
 RN [2]

## CHARACTERIZATION

RC STRAIN=Perussac; TISSUE=Heart atrium;  
 RX MEDLINE=91264856; PubMed=1675568;

RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
 RA Yoshida M., Harada A., Mureoka Y., Kobayashi M.;  
 RT "Purification of achatin-I from the atria of the African giant snail,  
 RT Achatina fulica, and its possible function.";  
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
 RN [3]

## X-RAY CRYSTALLOGRAPHY.

RP MEDLINE=93014529; PubMed=1399265;  
 RA Ishida T., In Y., Doi M., Yasuda-Kamatani Y., Minakata H.,  
 RA Iwashita T., Nomoto K.;  
 RT "Crystal structure and molecular conformation of achatin-I  
 RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a  
 RT D-amino acid residue.";  
 RL Int. J. Pept. Protein Res. 39:258-264(1992).  
 CC -1 FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY  
 CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY  
 CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE  
 CC HEART BEAT HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.  
 CC PIR; A32480; A32480.  
 DR Hormone; D-amino acid.  
 FT MOD RES 2 2 D-PHENYLALANINE.  
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810030000 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 P 1  
 |  
 Db 2 P 2

## RESULT 14

FAR3 HIRME STANDARD; PRT; 4 AA.

ID AC P42562;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide YLRF-amide.  
 OS Hirudo medicinalis (Medicinal leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
 CX NCBI TaxID=6421;  
 RN [1]

## SEQUENCE.

RP MEDLINE=92195954; PubMed=1686933;  
 RA Evans S.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of RFamide neuropeptides in the medicinal leech.";  
 RL Peptides 12:897-908(1991).  
 CC -1 SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 4 4 AMIDATION.  
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 P 1  
 |  
 Db 4 P 4

## RESULT 15

FAR4 HIRME STANDARD; PRT; 4 AA.

ID AC P42563;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide like neuropeptide YMRP-amide.

```

CS Hirudo medicinalis (Medicinal leech);
CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Atychtedellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID:6421;
RR
RF SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933.
RA Evans B.O., Pohl J., Kartsonis M.A., Colaneri E.J.
RT "Identification of RFamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -! SIMILARITY: BELONGS TO THE FARP (FMRFamide RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MCD RES 4 AMINATION.
SQ SEQUENCE 4 AA; 616 YK; 69CA568B3C00000 CRC64;

Query Match 25.0%; Score 67 DB 1; Length 4;
Best Local Similarity 100.0%; Pred.No. 1; Score 5;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 F 1
Db 4 F 4

```

Search Completed: November 5, 2003, 17:04:17  
 Job time: 10 secs

GenCore version 5.1.6

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OM protein - protein search, using sw mode:

Run on: November 5, 2003, 17:52:17 : Search time 33 seconds  
 (without alignments:  
 39,099 Million cell updates/sec

Title: US-09-914-088-7

Perfect score: 30

Sequence: 1 FRPT 5

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 810525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 5

Post processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database :

SPTREMBL\_23.\*  
 1: sp\_archaea.\*  
 2: sp\_bacteria.\*  
 3: sp\_fungi.\*  
 4: sp\_human.\*  
 5: sp\_invertebrate.\*  
 6: sp\_mammal.\*  
 7: sp\_mhc.\*  
 8: sp\_organelle.\*  
 9: sp\_phase.\*  
 10: sp\_plant.\*  
 11: sp\_rodent.\*  
 12: sp\_virus.\*  
 13: sp\_vertebrate.\*  
 14: sp\_unclassified.\*  
 15: sp\_virus.\*  
 16: sp\_bacteriap.\*  
 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by BLAST to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	23.1	5	P83308	P83308 gallus gall
2	5	16.7	5	P83073	P83073 bacillus ce
3	0	0.0	4	Q08433	Q08433 rattus sp.
4	0	0.0	5	Q99207	Q99207 hordeum vul

## ALIGNMENTS

RESULT 1  
 P83308 PRELIMINARY; PRT; 5 AA.  
 AC P83308  
 DT 01-JUN-2002 (TEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)

DE FMRFamide-like neuropeptide (LPLRF-amide).  
 OS Gallus gallus (Chicken)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN (1)  
 RP SEQUENCE. AND SYNTHESIS.  
 RC TISSUE=Brain;  
 RA PubMed=6137771;  
 RA Dockray G.J.; Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;  
 RT "A novel active pentapeptide from chicken brain identified by  
 RT antibodies to FMRFamide.";  
 RL Nature 305:329-330(1983).  
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 23.3%; Score 7; DB 13; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 P 3  
 Db 2 P 2

## RESULT 2

P83073 PRELIMINARY; PRT; 5 AA.  
 AC P83073;  
 DT 01-OCT-2001 (TEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TEMBLrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TEMBLrel. 18, Last annotation update)  
 DE 88 kDa protein (Fragment).  
 OS Bacillus cereus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1396;  
 RN (1)  
 RP SEQUENCE.  
 RC STRAIN=NCIMB 11796;  
 RA Browne N., Dowds B.C.A.;  
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
 FT MCM TER 5  
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 16.7%; Score 5; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 T 2  
 Db 4 T 4

## RESULT 3

Q08433 PRELIMINARY; PRT; 4 AA.  
 ID Q08433  
 AC Q08433;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
 DE Bilirubin UDP-glucuronosyltransferase (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Gunn;  
 RX MEDLINE=91282759; PubMed=1840486;

RA Sato H., Aono S., Kashiwazata S., Koizumi O.,  
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the  
 RL hyperbilirubinemic Gunn rat.",  
 RL Biochem Biophys Res Commun. 177:1161-1164 (1991).  
 CR EMBL: S18636; AAL19259.1; -;  
 KW Transferase.  
 FT NON TER  
 SQ SEQUENCE 4 AA; 473 MW; 633732C42C000000 CRC64;

Query Match 0.0%; Score 0; DB 11; Length 4;  
 Best Local Similarity 0.0%; Pred. No. 8.3e+05;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 T 2  
 DB 1 N 1

## RESULT 4

Q99007 PRELIMINARY; PRT; 5 AA.  
 AT Q99007;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Alpha amylase (Fragment).  
 GN AMY1 GENE.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID:4511;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91329704; PubMed=1831055;  
 RA Jacobsen J.V., Close T.J.;  
 RT "Control of transient expression of chimaeric genes by gibberellic  
 R1 acid and abscisic acid in protoplasts prepared from mature barley  
 R2 aleurone layers.";  
 RL Plant Mol. Biol. 16:713-721 (1991).  
 DR EMBL: X54643; CAA38455.1; -;  
 FT NON TER  
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F0C000 CRC64;

Query Match 0.0%; Score 0; DB 10; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 8.3e+05;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 F 1  
 DB 1 N 1

Search completed: November 5, 2003, 17:55:23  
 Job time : 33 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CorpuGen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2003, 17:48:47 ; Search time 40 Seconds  
(without alignments)  
19,841 Million cell updates/sec

Title: US-09-914-088-7

Perfect score: 30

Sequence: 1 FPPPT 5

Scoring Table: BLCSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 20275

Minimum DB seq length: 0

Maximum DB seq length: 5

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1980.DAT.\*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1981.DAT.\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1982.DAT.\*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1983.DAT.\*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1984.DAT.\*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1985.DAT.\*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1986.DAT.\*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1987.DAT.\*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1988.DAT.\*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1989.DAT.\*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1990.DAT.\*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1991.DAT.\*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1992.DAT.\*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1993.DAT.\*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1994.DAT.\*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1995.DAT.\*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1996.DAT.\*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1997.DAT.\*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1998.DAT.\*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb/AA1999.DAT.\*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb/AA2000.DAT.\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	5	21	IGF C-epsilon-2 do
2	30	100.0	5	22	peptide P7 derived
3	30	100.0	5	23	Human IGE immunog
4	24	80.0	4	19	Neuroactive peptid
5	24	80.0	4	23	Neuroactive peptid
6	24	80.0	4	23	Portion of the cor
7	24	80.0	5	20	Neuroactive peptid
8	19	63.3	3	19	NMDA receptor bind
9	19	63.3	3	19	NMDA receptor bind

10	19	63.3	3	23	Contiguous hydroxy
11	19	63.3	4	15	Prolyl endopeptida
12	19	63.3	4	23	N. meningitidis LC
13	19	63.3	4	23	Gum arabic glycopr
14	19	63.3	4	23	Contiguous hydroxy
15	19	63.3	5	11	Polypeptide accomp
16	19	63.3	5	15	SV40 T antigen cdc
17	19	63.3	5	15	PHF-tau epitope.
18	19	63.3	5	16	PHF-tau epitope.
19	19	63.3	5	16	AAAR76939
20	19	63.3	5	17	AAW06981
21	19	63.3	5	18	N-acetylglucosam
22	19	63.3	5	19	Peptide determined
23	19	63.3	5	19	Human thrombopoiet
24	19	63.3	5	19	EVH1 ligand motif.
25	19	63.3	5	20	Portion of the cor
26	19	63.3	5	22	Amino acid sequenc
27	19	63.3	5	22	Ena/VASP homology
28	19	63.3	5	22	"L domain" amino a
29	19	63.3	5	22	Colostrinin deriv
30	19	63.3	5	22	Colostrinin peptid
31	19	63.3	5	22	Colostrinin peptid
32	19	63.3	5	22	Ewe colostrinin pe
33	19	63.3	5	23	Zyxine VASP bindin
34	19	63.3	5	23	Peptide sequence e
35	19	63.3	5	23	Colostrinin consti
36	19	63.3	5	23	Colostrinin consti
37	19	63.3	5	23	Neural cell regula
38	19	63.3	5	23	Peptide amiro acid
39	19	63.3	5	23	Peptide CycE-5mer
40	19	63.3	5	24	Triketone-inhibito
41	18	60.0	5	19	PPGF retropeptide
42	18	60.0	5	20	Neutrophil-activat
43	18	60.0	5	22	Phosphorylated pep
44	17	56.7	5	16	Immune stimulating
45	17	56.7	5	17	Soybean pepsin dig

ALIGNMENTS

RESULT 1

AAAB25913

ID AAAB25913 standard; Peptide; 5 AA.

XX AAAB25913;

XX 05-JAN-2001 (first entry)

XX IGF C-epsilon-2 domain surface exposed epitope peptide P7 SEQ ID NO:7.

XX Epitope; murine; human; immunoglobulin E; IGE; C-epsilon-2 domain;

XX allergic disease; immunophylaxis; immunotherapy; anti-allergic;

XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;

XX allergy; atopy.

XX Homo sapiens.

XX WO2000050460-A1.

XX 31-AUG-2000.

XX 22-FEB-2000; 2000WO-EP01455.

XX 25-FEB-1999; 99GB-0004405.

XX 23-MAR-1999; 99GB-0007151.

XX 07-MAY-1999; 99GB-0010537.

XX 07-MAY-1999; 99GB-0010538.

XX 07-AUG-1999; 99GB-0018594.

XX 07-AUG-1999; 99GB-0018603.

XX 07-SEP-1999; 99GB-0021046.

XX 07-SEP-1999; 99GB-0021047.

XX 29-OCT-1999; 99GB-0025619.

PR 23-NOV-1999; 99GB-0027698.  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX  
PI Dyson M, Friede M, Greenwood J, Hewitt E, Larent A, Mason S;  
XX Randall R, Turnell WG, Van Mechelen MF, Vinals De Bassols YC;  
XX WPI: 2000-522073/53.  
XX  
XX Peptides useful for treating, preventing and ameliorating allergic  
XX diseases, comprising an isolated surface exposed group of a specific  
XX domain from immunoglobulin E.  
XX  
XX Claim 8; Page 5; 129pp; English.  
XX  
XX The present invention describes a peptide (I) comprising an isolated  
XX surface exposed group/epitope (E) of C-epsilon-2 domain (D) of  
XX immunoglobulin E (IgE), or its mimotope. Also described are: (i) an  
XX immunogen (II) for treating allergy comprising (i); (2) a vaccine (iii)  
XX for treating allergies comprising (iii); (3) a ligand (iv) capable of  
XX recognising E; (4) a pharmaceutical composition (PC) comprising (iv);  
XX (5) a peptide (ia) capable of being recognised by (iv); (6) an immunogen  
XX (IIa) comprising (ia); and (7) producing (III) by producing (ii) (i)  
XX can have anti-allergic and immunosuppressive activities, and can be used  
XX as a vaccine and histamine release inhibitor. (2), (iii) and (iii) are  
XX useful in medicine and in the manufacture of medicaments for treating  
XX and preventing allergies. (iv) is useful for identifying mimotopes of pl,  
XX in medicine and also in manufacturing medicaments for treating  
XX allergies. (i) is useful in diagnostics and in the affinity purification  
XX of circulating anti-IgE antibodies from blood. (ii), (iii) and PC are  
XX useful for treating a patient susceptible to or suffering from allergies.  
XX (iv) is also useful in diagnosing atopy. AAB25907 to AAB26039 represent  
XX peptide sequences which are used in the exemplification of the present  
XX invention.  
XX  
XX Sequence 5 AA;  
SQ

Query Match 100.0%; Score 30; RB 21; Length: 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+5;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPPT 5  
DB 1 FTPPT 5  
RESULT 2  
AAU16638  
ID AAU16638 standard; Peptide; 5 AA.  
XX  
XX AAU16638;  
XX  
XX 07-NOV-2001 (first entry)  
XX  
XX Peptide P7 derived from Cepsilon2 region of human IgE.  
XX  
XX Human; linkage technology; conjugated compound; carrier vehicle;  
XX epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
XX IgE mediated disease; antibody response.  
XX  
XX Homo sapiens.  
XX  
XX WO200145745-A2.  
XX  
XX 28-JUN-2001.  
XX  
XX 21-DEC-2000; 2000WO-GB04935.  
XX  
XX 21-DEC-1999; 99GB-0030233.  
XX  
XX 22-FEB-2000; 2000GB-0004036.  
XX  
XX 22-AUG-2000; 2000GB-0020707.  
XX  
XX 22-AUG-2000; 2000GB-0020708.

XX  
PA (ACAM-) ACAMBIS RES LTD.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Fliin N, Johnson T;  
XX  
XX WPI: 2001-521967/57.  
XX  
XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
XX mediated diseases.  
XX  
XX Example 4; Page 21; 48pp; English.  
XX  
XX The present invention relates to linkage methodology for use in the  
XX conjugation of compounds (e.g. peptides) to carrier vehicles  
XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
XX biological and immunological constructs. The invention provides a  
XX method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
XX protein) for use in a pharmaceutical composition or a vaccine. The  
XX invention describes peptides derived from or mimotopes of the  
XX Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
XX (IgE) which are used to produce conjugated compounds. The compounds or  
XX compositions of the invention are useful in the manufacture of a  
XX medicament for the treatment of IgE mediated diseases. The invention  
XX allows for controlled conjugation of a peptide epitope (antigen) to a  
XX protein so as to form an immunogenic conjugate which may be able to  
XX raise a protective antibody response in an animal or human patient.  
XX AAU16632-AAU16913 represent peptides derived from or mimotopes of  
XX the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
XX  
XX Sequence 5 AA;  
SQ

Query Match 100.0%; Score 30; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPPT 5  
DB 1 FTPPT 5  
RESULT 3  
ABC03223  
ID ABC03223 standard; Peptide; 5 AA.  
XX  
XX ABC03223;  
XX  
XX 02 SEP 2002 (first entry)  
XX  
XX Human IgE immunogenic peptide SEQ ID NO: 7.  
XX  
XX Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
XX vaccine; anti-allergic.  
XX  
XX Homo sapiens.  
XX  
XX WO200216409-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-EP09576.  
XX  
XX 22-AUG-2000; 2000GB-0020717.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX  
XX Friede M, Mason S, Turnell WG, Vinals Bassols YC;  
XX  
XX WPI: 2002-489648/52.  
XX  
XX Conjugate for use in vaccine for treatment of allergy, comprises  
XX disulfide bridge cyclized peptide and immunogenic carrier.  
XX

XX Claim 4; Page 9; 45pp; English.

XX The present invention relates to conjugates suitable for use in vaccines,

XX where the conjugate comprises a disulphide bridge cyclised peptide and an

XX immunogenic carrier. The vaccines can be used in the treatment of

XX allergies. The present sequence is a peptide immunogen derived from human

XX immunoglobulin E (IgE) suitable to be cyclised and used in the invention.

SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 23; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPT 5

Db 1 FTPT 5

RESULT 4

AAW47113

ID AAW47113 standard; peptide; 4 AA.

AC AAW47113;

XX 18-MAY-1998 (first entry)

XX NMCA receptor binding neuroactive peptide 13.

XX NMCA receptor; neuroactive; glycine co-agonist; learning; memory;

XX N-methyl-D-aspartate; pharmaceutical.

OS Synthetic.

OS Rattus sp.

XX WC9743306-A1.

PD 26-NOV-1997.

XX 16-MAY-1997; 97WO-US09667.

XX 17-MAY-1996; 96US-0649272.

XX (NEUR ) NEUROTHEAPEUTICS LP.

XX Colley PA, Moskal JR, Yamamoto H;

XX WPI; 1998-008795/01.

XX New neuro-active polypeptide(s) for enhancing learning and memory -

XX have NMCA receptor agonist activity at the glycine binding site

XX Claim 1; Page 23; 38pp; English.

XX This neuroactive peptide can bind to a N-methyl-D-aspartate (NMDA)

XX receptor and is included in a pharmaceutical composition comprising an

XX effective NMDA receptor binding amount of a polypeptide. The products

XX bind to the NMDA receptor at the glycine co-agonist site and effect at

XX least the same biological activity from the NMDA receptor as the binding

XX of glycine. They can be used as NMDA receptor agonists for enhancing

XX learning and memory. They can also be used for the isolation and

XX characterisation of NMDA receptor activity, NMDA receptor tissue

XX localisation and correlation with disease, injury or other

XX pharmacological effects.

SQ Sequence 4 AA;

Query Match 80.0%; Score 24; DB 13; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TPPT 5

Db 1 TPPT 4

RESULT 5

AAE29186

ID AAE29186 standard; peptide; 4 AA.

AC AAE29186;

XX 27-JAN-2003 (first entry)

XX Neuroactive peptide, NT-13.

XX Therapy; hypoxia; neuropathic pain; central nervous system; analgesic;

XX cognitive enhancement; neuroactive peptide; neuroprotective; vasotropic;

XX N-methyl-D-aspartate receptor; NMDA; peptide therapy; nootropic; NT-13.

OS Unidentified.

XX WO200272609-A2.

XX 19-SEP-2002.

XX 12-MAR-2002; 2002WO-US07427.

XX 12-MAR-2001; 2001US-275083P.

XX (NYXI-) NVXIS NEURO THERAPIES INC.

XX Moskal JR;

XX WPI; 2002-759835/82.

XX Preventing or treating hypoxia or its effects on the central nervous

XX system, or neuropathic pain in a human, by administering neuroactive

XX peptides or compounds competing with the peptide for binding to

XX N-methyl-D-aspartate receptor -

XX Claim 1; Page 49; 64pp; English.

XX The invention relates to a method for preventing and/or treating hypoxia,

XX neuropathic pain or the effects of hypoxia on the central nervous system,

XX or producing cognitive enhancement in a mammal. The method comprises

XX administering a composition containing neuroactive peptides (designated

XX NT1, NT2, NT3, NT4, NT5, NT6, NT7 or NT8); or a compound that competes

XX with NT8 for binding to the N-methyl-D-aspartate (NMDA) receptor. The

XX method is useful for preventing and/or treating hypoxia, neuropathic pain

XX or the effects of hypoxia on the central nervous system, in a mammal

XX (particularly a human). The method is also useful for producing cognitive

XX enhancement in a mammal. The invention is used in peptide therapy. The

XX present sequence is a neuroactive peptide.

SQ Sequence 4 AA;

Query Match 80.0%; Score 24; DB 23; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TPPT 5

Db 1 TPPT 4

RESULT 6

AAW50692

ID AAW50692 standard; Peptide; 4 AA.

AC AAW50692;

XX 08-APR-2002 (first entry)

XX Neuroactive peptide NT-13, for hypoxia treatment.

XX Neuroactive peptide; NT-13; hypoxia; ischaemia; therapy;  
KW N-methyl-D-aspartate; NMDA; agonist; antihypoxic.  
XX Synthetic.  
OS WO200198367-A2.  
XX  
XX 27-DEC-2001.  
XX  
XX 22-JUN-2001; 2001WO-US:9839.  
XX  
XX 22 JUN-2000; 2000US-213614P.  
XX  
XX (NYX1-) NYXIS NEURO THERAPEUTICS INC.  
XX  
XX Moskal JR, Yamamoto H, Colley PA;  
XX WPI; 2002-098225/13.  
XX  
XX N-PSDB; ABA91366, ABA91367, ABA91369, ABA91369.  
XX  
XX Use of peptide or amino acid compositions for the treatment of hypoxia  
PT and ischaemia -  
XX  
XX Claim 1; Page 31; 41pp; English.  
XX  
XX The present sequence is that of neuroactive peptide NT-13, which  
XX is capable of binding to the N-methyl-D-aspartate (NMDA) receptor.  
XX NT-13 is one of a set of NT family peptides (see ABA90690-92) that  
XX can be used to treat hypoxia and ischaemia. A method of treating  
XX hypoxia by administering a peptide or amino acid composition  
XX comprising a neuroactive peptide, DNA molecules encoding the  
XX neuroactive peptides, and a method of treating the effects of  
XX hypoxia in the central nervous system by administering a  
XX neuroactive peptide, especially NT-13, are claimed. The  
XX neuroactive peptides may be cyclized and may contain (preferably  
XX conservative) amino acid substitutions. NT-13 was shown to be a  
XX partial agonist in a pharmacological NMDA-specific function  
XX assay, a partial agonist in voltage clamp experiments in an  
XX cocycle expression system, and a partial agonist in a behavioural  
XX NMDA-specific function assay.  
XX  
XX  
SQ Sequence 4 AA;  
Query Match 80.0%; Score 24; DB 23; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 TPPT 5  
DB 1 TPPT 4  
RESULT 7  
AAV42926  
ID AAV42926 standard; peptide; 5 AA.  
XX  
XX AAV42926;  
XX  
XX 20-DEC-1999 (first entry)  
XX  
XX Portion of the core peptide in the hinge region of IgA1.  
XX  
XX Immunoglobulin; IgA1; hinge; core; nephropathy; diagnosis.  
XX  
XX Homo sapiens.  
XX  
XX WO990663-A1.  
XX  
XX 07 OCT-1999.  
XX  
XX 25-MAR-1999; 99WO-JP01525.  
XX

PR 31-MAR-1998; 98JP-0101759.  
XX  
XX (ASAH) ASAHI KASEI KOGYO KK.  
XX (KOKU/) KOKUBO T.  
XX  
XX Kokubo T, Arai K, Toma K;  
XX WPI; 1999-591373/50.  
XX  
XX Quick, convenient examination of IgA nephropathy by determining  
PT antibody recognizing core peptides in the hinge region of IgA1 -  
XX  
XX Disclosure; Page 5; 32pp; Japanese.  
XX  
XX A new method is disclosed for diagnosing IgA nephropathy by determining  
XX an antibody recognising the core peptide in the hinge region of IgA;  
XX contained in a liquid specimen, e.g. blood, serum, plasma, saliva or  
XX urine. The method is quick, convenient, safe and may be automated. Since  
XX there is no need for renal biopsy, the patients suffer little mental  
XX stress, and there is no risk of perirenal bleeding. The present sequence  
XX represents a portion of the core peptide in the hinge region of IgA1.  
XX  
XX Sequence 5 AA;  
SQ  
Query Match 80.0%; Score 24; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 TPPT 5  
DB 1 TPPT 4  
RESULT 8  
AAW47114  
ID AAW47114 standard; peptide; 3 AA.  
XX  
XX AAW47114;  
XX  
XX 19-MAY-1998 (first entry)  
XX  
XX NMDA receptor binding neuroactive peptide 14.  
XX  
XX NMDA receptor; neuroactive; glycine co-agonist; learning; memory;  
XX N-methyl-D aspartate; pharmaceutical.  
XX  
XX Synthetic.  
XX Rattus sp.  
XX  
XX WO9743306 A1.  
XX  
XX 20-NOV-1997.  
XX  
XX 16-MAY-1997; 97WC-US08667.  
XX  
XX 17-MAY-1996; 96US-0649272.  
XX  
XX (NEUR-) NEUROTERAPEUTICS LP.  
XX  
XX Colley PA, Moskal JR, Yamamoto H;  
XX WPI; 1998-038795/01.  
XX  
XX New neuro active polypeptide(s) for enhancing learning and memory -  
PT have NMDA receptor agonist activity at the glycine binding site  
XX  
XX Claim 5; Page 24; 38pp; English.  
XX  
XX This neuroactive peptide can bind to a N-methyl-D-aspartate (NMDA)  
XX receptor and is included in a pharmaceutical composition comprising an  
XX effective NMDA receptor binding amount of a polypeptide. The products  
XX bind to the NMDA receptor at the glycine co-agonist site and effect at  
XX least the same biological activity from the NMDA receptor as the binding



CC of glycine. They can be used as NMDA receptor agonists for enhancing  
 CC learning and memory. They can also be used for the isolation and  
 CC characterisation of NMDA receptor activity, NMDA receptor tissue  
 CC localisation and correlation with disease, injury or other  
 CC pharmacological effects.

XX SQ Sequence 3 AA;

Query Match 63.3%; Score 19; DB 19; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TPP 4  
 |||  
 Db 1 TPP 3

#### RESULT 9

AAW47115  
 ID AAW47115 standard; peptide; 3 AA.

XX AC AAW47115;  
 XX DT 18-MAY-1998 (first entry)  
 XX DE NMDA receptor binding neuroactive peptide 15.  
 XX KW NMDA receptor; neuroactive; glycine co-agonist; learning; memory;  
 XX KW N-methyl-D-aspartate; pharmaceutical.  
 XX OS Synthetic.  
 XX OS Rattus sp.  
 XX PN WO9743306-A1.  
 XX PD 20-NOV-1997.

XX PF 16-MAY-1997; 97WO-US08667.  
 XX PR 17-MAY-1996; 96US-0649272.  
 XX PA (NEUR-) NEUROTHERAPEUTICS LP.  
 XX P; Colley PA, Moskal JR, Yamamoto H;  
 XX DR WPI; 1998 008735/01.  
 XX PI New neuro-active polypeptide(s) for enhancing learning and memory -  
 XX PT have NMDA receptor agonist activity at the glycine binding site.

XX PS Claim 5; Page 24; 38pp; English.

XX CC This neuroactive peptide can bind to a N-methyl D-aspartate (NMDA)  
 CC receptor and is included in a pharmaceutical composition comprising an  
 CC effective NMDA receptor binding amount of a polypeptide. The products  
 CC bind to the NMDA receptor at the glycine co-agonist site and effect at  
 CC least the same biological activity from the NMDA receptor as the binding  
 CC of glycine. They can be used as NMDA receptor agonists for enhancing  
 CC learning and memory. They can also be used for the isolation and  
 CC characterisation of NMDA receptor activity, NMDA receptor tissue  
 CC localisation and correlation with disease, injury or other  
 CC pharmacological effects.

XX SQ Sequence 3 AA;

Query Match 63.3%; Score 19; DB 19; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPT 5  
 |||  
 Db 1 PPT 3

#### RESULT 10

ABB78522  
 ID ABB78522 standard; Peptide; 3 AA.

XX AC ABB78522;  
 XX DT 09-JUL-2002 (first entry)  
 XX DE Contiguous hydroxyproline sequence SEQ ID NO:213.  
 XX KW Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;  
 XX KW HRP; repetitive proline-rich protein; RRP; arabinogalactan protein;  
 XX KW AGP; plant gum.  
 XX OS Acacia senegal.  
 XX OS Synthetic.  
 XX PN WO200178503-A2.  
 XX PD 25-OCT-2001.

XX PF 12-APR-2001; 2001WO-US12336.  
 XX PR 12-APR-2000; 2000US-0547693.  
 XX PA (UYOH-) UNIV OHIO.  
 XX PI Kieliszewski MJ;  
 XX DR WPI; 2002-04:307/05.

XX PT Nucleic acids and proteins useful for producing hydroxy-proline rich  
 XX PT glycoproteins in plants -  
 XX PS Claim 9; Page 122; 326pp; English.  
 XX CC The present invention describes synthetic genes encoding plant gums and  
 CC other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic  
 CC acids that encode them. The nucleic acids, proteins and methods from the  
 CC present invention may be used to produce HRGPs, repetitive proline-rich  
 CC proteins (RPPs) and arabinogalactan-proteins (AGPs) in plants via  
 CC recombinant methodologies. Also described is the expression of synthetic  
 CC genes designed from repetitive peptide sequences, such as glycoproteins  
 CC (including the peptide sequences of gum arabic glycoprotein (GAGP)).  
 CC AB251730 to AB251849 and ABB78401 to ABB78544 represent sequences used  
 CC in the exemplification of the present invention.

XX SQ Sequence 3 AA;

Query Match 63.3%; Score 19; DB 23; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TPP 4  
 |||  
 Db 1 TPP 3

XX PS Claim 9; Page 122; 326pp; English.

XX CC The present invention describes synthetic genes encoding plant gums and

XX CC other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic  
 XX CC acids that encode them. The nucleic acids, proteins and methods from the  
 XX CC present invention may be used to produce HRGPs, repetitive proline-rich  
 XX CC proteins (RPPs) and arabinogalactan-proteins (AGPs) in plants via  
 XX CC recombinant methodologies. Also described is the expression of synthetic  
 XX CC genes designed from repetitive peptide sequences, such as glycoproteins  
 XX CC (including the peptide sequences of gum arabic glycoprotein (GAGP)).  
 XX CC AB251730 to AB251849 and ABB78401 to ABB78544 represent sequences used  
 XX CC in the exemplification of the present invention.

XX SQ Sequence 3 AA;

#### RESULT 11

AAR45401  
 ID AAR45401 standard; peptide; 4 AA.

XX AC AAR45401;

XX DT 11-JUL-1994 (first entry)  
 XX DE Polyl endopeptidase inhibitor peptide-10.

XX KW Corn; maize; prolly endopeptidase; dementia; gamma-zein;  
 XX KW protease inhibitor; Alzheimer's Disease.  
 XX OS Synthetic.

XX JP5531072-A.  
 XX 14 DEC-1993.  
 XX 27-MAY-1992; 92JP-0160354.  
 XX 27-MAY 1992; 92JP-0160354.  
 XX (AGENCY OF IND SCI & TECHNOLOGY.  
 XX (SHOJA SANGYO CO.  
 XX WPI, 1994-022840/03.  
 XX Prolyl endopeptidase inhibitors for treating dementia are  
 XX prepared by hydrolysis of corn protein.  
 XX Claim 1; Page 2; 8pp; Japanese.  
 XX This peptide is one of 10 claimed peptides having prolyl  
 XX endopeptidase inhibitory activity; the peptide is expected to be of  
 XX use for the prophylaxis and treatment of dementia. The peptide is  
 XX synthesised by standard methods.  
 XX Sequence 4 AA;  
 XX  
 XX Query Match 63.3%; Score 19; DB 15; Length 4;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 TPP 4  
 DB 1 TPP 3  
 XX  
 XX RESULT 12  
 XX AB547154  
 XX ID AB547154 standard; Peptide; 4 AA.  
 XX AC ABP47354;  
 XX DT 19-AUG-2002 (first entry)  
 XX DE N. meningitidis LOS peptidic mimotope related peptide #12.  
 XX KW Neisseria meningitidis; meningococcus; meningococcal; varicella; LOS;  
 XX KW lipopolysaccharide; monoclonal antibody; antibacterial; infection;  
 XX KW antiinflammatory; meningococcal disease.  
 XX CS Neisseria meningitidis.  
 XX OS Synthetic.  
 XX PN WO200228859 A2.  
 XX 11 APR-2002.  
 XX DT 03-OCT-2001; 2001WO-EP11409.  
 XX FR 03 (AT-2000; 2000GB-0024250.  
 XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX De Bolle XT, Larsson J, Lohet Y, Mouton PY, Pochon J, Vost P;  
 XX WPI, 2002-475596/51.  
 XX Novel mimotope of Neisseria meningitidis surface, for treating  
 XX meningococcal disease, comprising a peptide epitope obtainable by  
 XX screening peptide library with a specific monoclonal antibody.  
 XX Example 5; Page 37; 55pp; English.  
 XX The present invention describes mimotopes (1) of a surface of N. M.

CC of meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis  
 CC comprising a peptide epitope obtained by screening a peptide library  
 CC with a monoclonal antibody (MAB) like 4B12C10, H44/24, H44/58, H44/7C  
 CC or H44/78. (1) is antigenically cross-reactive with MAB. (1) have  
 CC antibacterial and antiinflammatory activities, and can be used in  
 CC vaccines. MAB is useful in the identification of (1). (1) or MAB are  
 CC useful as a medicament, and also in the manufacture of a medicament for  
 CC treating or preventing meningococcal disease. (1) and MAB are useful  
 CC for treating a patient suffering from or susceptible to meningococcal  
 CC disease by administering (1) or MAB to the patient. (1) is useful in  
 CC a diagnostic assay for meningococcal infection to detect antibodies  
 CC against 13, 7, 9, LOS and to detect the presence of 13, 7, 9 immunotype  
 CC meningococcus in a sample from a patient. ABN88464 to ABN88487 and  
 CC ABP47326 to ABP47754 represent sequences used in the exemplification  
 CC of the present invention.  
 XX  
 XX Sequence 4 AA;  
 XX  
 XX Query Match 63.3%; Score 19; DB 23; Length 4;  
 XX Best Local Similarity 75.0%; Pred. No. 9.3e+05;  
 XX Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 TPP 4  
 DB 1 RPP 4  
 XX  
 XX RESULT 13  
 XX AB578491  
 XX ID AB578491 standard; Peptide; 4 AA.  
 XX AC ABP78491;  
 XX DT 09-JUL-2002 (first entry)  
 XX DE Gum arabic glycoprotein (GAGP) peptide motif SEQ ID NO:178.  
 XX KW Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;  
 XX KW HRGP; repetitive proline rich protein; RRP; arabinogalactan protein;  
 XX KW AGP; plant gum.  
 XX OS Acacia senegal.  
 XX OS Synthetic.  
 XX PN WO200178503-A2.  
 XX 25-OCT-2001.  
 XX DT 12-APR 2001; 2001WO US12336.  
 XX PR 12-APR-2001; 2001US-054743.  
 XX PA (UYCH-) UNIV CHIO.  
 XX Kieleszewski XG;  
 XX WPI: 2002-041307/05.  
 XX Nucleic acids and proteins useful for producing hydroxy-proline rich  
 XX glycoproteins in plants.  
 XX Claim 5; Page 121; 326pp; English.  
 XX The present invention describes synthetic genes encoding plant gums and  
 XX other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic  
 XX acids that encode them. The nucleic acids, proteins and methods from the  
 XX present invention may be used to produce HRGPs, repetitive proline-rich  
 XX proteins (RPPs) and arabinogalactan-proteins (AGPs) in plants via  
 XX recombinant methodologies. Also described is the expression of synthetic  
 XX genes designed from repetitive peptide sequences, such as glycoproteins  
 XX including the peptide sequences of gum arabic glycoprotein (GAGP).  
 XX AB:51730 to AB:51849 and AB:78401 to AB:78544 represent sequences used  
 XX in the exemplification of the present invention.

```

XX SQ Sequence 4 AA;
Query Match 63.3%; Score 19; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

OY 2 TPP 4
   |||
DB 1 TPP 3

RESULT 14
ABR78523
ID ABR78523 standard; Peptide; 4 AA.
XX
AC ABR78523;
XX
DT 09-JUN-2002 (first entry)
XX
DE Contiguous hydroxyproline sequence SEQ ID NO:214.
XX
KW Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;
KW HRP; repetitive proline-rich protein; RRP; arabinogalactan protein;
KW AGP; plant gum.
XX
CS Acacia senegal.
OS Synthetic.
XX
PN WC20078503-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2C01WO-US12336.
XX
PR 12-APR 2000; 2C0JUS-0547693.
XX
PA (UYOH-) UNIV OH:O.
XX
PI Kieliszewski MJ.
XX
DR WPI; 2002-041307/05.
XX
PT Nucleic acids and proteins useful for producing hydroxy-proline rich
PT glycoproteins in plants -
PS Claim 9; Page 122; 326pp; English.
XX
CC The present invention describes synthetic genes encoding plant gums and
CC other hydroxyproline (Hyp)-rich glycoproteins (HRGs) and the nucleic
CC acids that encode them. The nucleic acids, proteins and methods from the
CC present invention may be used to produce HRGs, repetitive proline-rich
CC proteins (RPPs) and arabinogalactan-proteins (AGPs) in plants via
CC recombinant methodologies. Also described is the expression of synthetic
CC genes designed from repetitive peptide sequences, such as glycoproteins
CC (including the peptide sequences of gum arabic glycoprotein (GAGP)).
CC ABL51730 to ABL51849 and ABR78401 to ABR78544 represent sequences used
CC in the exemplification of the present invention.
XX
XX SQ Sequence 4 AA;
Query Match 63.3%; Score 19; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPP 4
   |||
DB 1 TPP 3

RESULT 15
AAR07911
ID AAR07911 standard; protein; 5 AA.

```

```

XX AAR07911;
XX
DT 18-FEB-1991 (first entry)
XX
DE Polypeptide accompanying fragment of the C-terminus of the p15
DE protein of HIV-1, HIV-2 or HTLV-1 used in vaccine composition.
XX
KW Human lymphotropic diseases; CD5; capsid protein.
XX
OS Synthetic.
XX
PN EP398707-A.
XX
PD 22-NOV-1990.
XX
PF 17-MAY-1990; 90EP-0305325.
XX
PR 17-MAY-1989; 89US-0353021.
XX
PA (SANG-) SANGSTAT MED CORP.
XX
PI Pouletty PJ, Stra K;
XX
DR WPI; 1990-350439/47.
XX
PT Polypeptide comprising core sequence E-P-T-A-P - used, along with
PT antibodies raised against it, for treatment and diagnosis of
PT human lymphotropic diseases.
XX
PS Claim 3; Page 5; 6pp; English.
XX
CC Peptide is used in composition with peptide derived from p15
CC protein of HIV-1, HIV-2 or HTLV-1.
CC Composition is useful in detection of human lymphotropic retrovirus.
CC Anti-idiotypic Abs and vaccines may be prepared, useful in
CC modulation and immunisation against human lymphotropic viruses.
CC See also AAR07908-10.
XX
XX SQ Sequence 5 AA;
Query Match 63.3%; Score 19; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPP 4
   |||
DB 3 TPP 5

Search completed: November 5, 2003, 17:54:15
Job time : 41 secs

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GenCore version 5.1.6  
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ON protein: - protein search, using sw model

Run on: November 5, 2003, 17:55:28 ; Search time 29 Seconds  
(without alignments)  
29.612 Million cell updates/sec

Title: US-09-914-088-7

Perfect score: 50

Sequence: 1 FTPPT 5

Scoring table: SLOSCM62

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 10465

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
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2: /cgn2\_6/prodata/2/pubaa/US07\_PUBCOMB.pep.  
3: /cgn2\_6/prodata/2/pubaa/US06\_PUBCOMB.pep.  
4: /cgn2\_6/prodata/2/pubaa/US06\_PUBCOMB.pep.  
5: /cgn2\_6/prodata/2/pubaa/US07\_PUBCOMB.pep.  
6: /cgn2\_6/prodata/2/pubaa/US07\_PUBCOMB.pep.  
7: /cgn2\_6/prodata/2/pubaa/US08\_PUBCOMB.pep.  
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11: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.  
12: /cgn2\_6/prodata/2/pubaa/US09\_PUBCOMB.pep.  
13: /cgn2\_6/prodata/2/pubaa/US10\_PUBCOMB.pep.  
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15: /cgn2\_6/prodata/2/pubaa/US10\_PUBCOMB.pep.  
16: /cgn2\_6/prodata/2/pubaa/US10\_PUBCOMB.pep.  
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19: /cgn2\_6/prodata/2/pubaa/US10\_PUBCOMB.pep.

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	5	12	US-10-082-014-278
2	30	100.0	5	12	US-10-372-076-112
3	19	63.3	4	15	US-10-185-815-99
4	19	63.3	4	15	US-10-062-623A-23
5	19	63.3	5	9	US-09-825-144-15
6	19	63.3	5	9	US-09-823-243-3
7	19	63.3	5	9	US-09-785-921A-15
8	19	63.3	5	10	US-09-861-687-3
9	19	63.3	5	12	US-10-247-853-2
10	19	63.3	5	12	US-10-247-853-3
11	19	63.3	5	12	US-10-192-361-42
12	19	63.3	5	15	US-10-281-652-12
13	18	60.0	5	15	US-10-252-406-27
14	16	53.3	4	15	US-10-211-088-124
15	15	53.3	5	15	US-10-206-699-49

16	53.3	5	15	US-10-206-699-186	Sequence 186, Appl
17	50.0	4	10	US-09-957-995A-15	Sequence 15, Appl
18	50.0	5	9	US-09-054-345-1	Sequence 1, Appl
19	50.0	5	9	US-09-858-754-9	Sequence 9, Appl
20	50.0	5	10	US-09-861-687-4	Sequence 4, Appl
21	50.0	5	12	US-10-316-253-59	Sequence 59, Appl
22	50.0	5	12	US-10-232-544-25	Sequence 25, Appl
23	50.0	5	12	US-10-302-817A-25	Sequence 25, Appl
24	50.0	5	14	US-10-099-895-15	Sequence 15, Appl
25	50.0	5	14	US-10-099-895-25	Sequence 25, Appl
26	50.0	5	15	US-10-237-850-27	Sequence 27, Appl
27	50.0	5	15	US-10-096-986-9	Sequence 9, Appl
28	50.0	5	15	US-10-255-733-1	Sequence 1, Appl
29	46.7	3	10	US-09-922-261-32	Sequence 32, Appl
30	46.7	4	9	US-09-873-737A-21	Sequence 21, Appl
31	46.7	4	9	US-09-803-126-17	Sequence 17, Appl
32	46.7	4	10	US-09-908-322-71	Sequence 71, Appl
33	46.7	4	10	US-09-916-940-3	Sequence 3, Appl
34	46.7	4	10	US-09-825-561A-70	Sequence 70, Appl
35	46.7	4	10	US-09-871-974-12	Sequence 12, Appl
36	46.7	4	11	US-09-783-931-71	Sequence 71, Appl
37	46.7	4	12	US-10-181-804A-15	Sequence 15, Appl
38	46.7	4	12	US-10-096-550-3	Sequence 3, Appl
39	46.7	4	12	US-10-352-704-21	Sequence 21, Appl
40	46.7	4	12	US-10-210-023-54	Sequence 54, Appl
41	46.7	4	12	US-10-299-991-5	Sequence 5, Appl
42	46.7	4	12	US-10-299-991-10	Sequence 10, Appl
43	46.7	4	12	US-10-299-991-11	Sequence 11, Appl
44	46.7	4	14	US-10-041-030-13	Sequence 13, Appl
45	46.7	4	15	US-10-235-552-3	Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-10-082-014-278  
; Sequence 278, Application US/10082014  
; Publication No. US20030195858A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL  
; FILE REFERENCE: ICC-130.0 4564/85124  
; CURRENT APPLICATION NUMBER: US/10/082,014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/930,915  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 278  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-278

Query Match 100.0% Score 30; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred.No.5.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTPPT 5  
Db 1 FTPPT 5

RESULT 2  
US-10-372-076-132  
; Sequence 132, Application US/10372076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Page, Mark  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS

FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/372,076  
PRIOR FILING DATE: 2003-02-21  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/080,299  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 132  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Homo sapiens  
US 10-372-076 132

Query Match 100.0% Score 30; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPT 5  
DB 1 FTPT 5

RESULT 3  
US-10-185-815-99  
Sequence 99, Application US/10185815  
Publication No. US20030096354A1  
GENERAL INFORMATION:  
APPLICANT: Flax Corporation, LLC  
APPLICANT: O'Mahony, Daniel  
APPLICANT: Lambkin, Imelda  
APPLICANT: Higgins, Lisa  
TITLE OF INVENTION: Peyer's Patch And/or M-Cell Targeting Ligands  
FILE REFERENCE: E1067-20093  
CURRENT APPLICATION NUMBER: US/10/185,815  
CURRENT FILING DATE: 2002-10-03  
PRIOR APPLICATION NUMBER: 60/302,591  
PRIOR FILING DATE: 2001-07-02  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 99  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: polypeptide ligand  
US-10-185-815-99

Query Match 63.3% Score 19; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTP 4  
DB 1 TTP 3

RESULT 4  
US-10-620-621A-23  
Sequence 23, Application US/10062621A  
Publication No. US20030108520A1  
GENERAL INFORMATION:  
APPLICANT: Borovsky, Dov  
APPLICANT: DeLoof, Arnold  
APPLICANT: Vethaert, Peter  
TITLE OF INVENTION: Neuropeptides and Their Use for Fast Control  
FILE REFERENCE: UF-216C1  
CURRENT APPLICATION NUMBER: US/10/620,621A  
CURRENT FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: 09/295,849  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: PCT/US00/10,134

PRIOR FILING DATE: 2000-04-18  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 23  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: NFF peptide  
FEATURE:  
NAME/KEY: Variant  
LOCATION: (1)-(14)  
OTHER INFORMATION: No. US20030108520A1 amidated amino acids  
US-10-620-621A-23

Query Match 63.3% Score 19; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5  
DB 2 PPT 4

RESULT 5  
US-09-825-144-15  
Sequence 15, Application US/09825144  
Patent No. US2002037286A1  
GENERAL INFORMATION:  
APPLICANT: Matthias Krause  
APPLICANT: Antonio S. Sechi  
APPLICANT: Frank B. Gertler  
APPLICANT: Jorgel Wetland  
TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
FILE REFERENCE: M0656/7565  
CURRENT APPLICATION NUMBER: US/09/825,144  
CURRENT FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: US 60/194,215  
PRIOR FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Fast-Seq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-825-144-15

Query Match 63.3% Score 19; DB 9; Length 5;  
Best Local Similarity 75.0%; Pred. No. 5.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTPT 4  
DB 1 FTPT 4

RESULT 6  
US-09-823-242-3  
Sequence 3, Application US/09823240  
Patent No. US20020048813A1  
GENERAL INFORMATION:  
APPLICANT: Frank B. Gertler  
APPLICANT: James E. Bear  
APPLICANT: Jurgel Wetland  
APPLICANT: Joseph Loureiro  
TITLE OF INVENTION: Methods and Products for Regulating Cell  
TITLE OF INVENTION: Motility  
FILE REFERENCE: M0656/7564 (HCL)  
CURRENT APPLICATION NUMBER: US/09/823,240  
CURRENT FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 60/194,564  
PRIOR FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 11

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US 09-823-240-3

Query Match      63.3%; Score 19; DB 9; Length 5;
Best Local Similarity 75.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FTPT 4
      1 1 1
Db      1 FTPT 4

RESULT 7
US-09-785-921A-15
; Sequence 15, Application US/C9785921A
; Patent No. US20020094334A1
; GENERAL INFORMATION:
; APPLICANT: Keener, William K.
; APPLICANT: Ward, Thomas E.
; FILE REFERENCE: LIT-PI-529
; TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
; CURRENT APPLICATION NUMBER: US/09/785,921A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO: 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Rous sarcoma virus
US 09-785-921A-15

Query Match      63.3%; Score 19; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PPT 5
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Db      3 PPT 5

RESULT 8
US-09-861-687-3
; Sequence 3, Application US/09861687
; Publication No. US20020193292A1
; GENERAL INFORMATION:
; APPLICANT: Markussen, Jan
; APPLICANT: Jonassen, Ib
; APPLICANT: Havelund, Sverdr
; APPLICANT: Brandt, Jakob
; APPLICANT: Kurtzhals, Peter
; APPLICANT: Harsen, Hertz Per
; APPLICANT: Kaarholm, Niels Christian
; TITLE OF INVENTION: INSULIN DERIVATIVES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. US20020193292A10 No. US20020193292A1disk of No. US200201932
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/C9/861,687
; FILING DATE: 21-May-2001

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/666,360
; FILING DATE: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 00 32 9 241 07 11
; TELEFAX: 00 32 9 241 07 99
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-247-853-2

Query Match      63.3%; Score 19; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FTPT 5
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Db      1 YTPKT 5

RESULT 9
US-10-247-853-2
; Sequence 2, Application US/10247853
; Publication No. US20030138972A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics sa.
; TITLE OF INVENTION: Monoclonal antibodies specific for PHF-tau,
; hybridomas secreting them, antigen recognition of these
; antibodies and their applications
; NUMBER OF SEQUENCES: 3
; STREET: Industriepark-Zwijnaarde 7, box 4
; CITY: Ghent
; COUNTRY: Belgium
; ZIP: B-9052
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/247,853
; FILING DATE: 02-No. US20030138972A1-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/666,360
; FILING DATE: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 00 32 9 241 07 11
; TELEFAX: 00 32 9 241 07 99
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-247-853-2

Query Match      63.3%; Score 19; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 TPP 4
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Db 3 TPP 5

RESULT 10
US-10-247-853-3
; Sequence 3, Application US/10247853
; Publication No. US20030138972A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics sa.
; TITLE OF INVENTION: Monoclonal antibodies specific for FGF-2a,
; hybridomas secreting them, antigen recognition of these
; antibodies and their applications
; NUMBER OF SEQUENCES: 3
; STREET: Industriepark-Zwijnaarde 7, box 4
; CITY: Ghent
; COUNTRY: Belgium
; ZIP: B-9052
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10247853
; FILING DATE: 02-Nov-02 US20030138972A1-1993
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: C8/666,360
; FILING DATE: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 00 32 9 241 07 11
; TELEFAX: 00 32 9 241 07 99
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US 10 247-853-3

Query Match 63.3%; Score 19; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPP 4
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Db 3 TPP 5

RESULT 11
US-10-292-381-47
; Sequence 47, Application US/10192381
; Publication No. US20030170807A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: WOLFEY, Paul
; APPLICANT: TU, Jian
; APPLICANT: XIAO, Bo
; APPLICANT: LEAHY, Daniel
; APPLICANT: BENKEN, Jutta
; APPLICANT: LANAHAN, Anthony
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HEMER 1b PROTEIN (AS
; FILE REFERENCE: JNU1580-4
; AMENDED)
; CURRENT APPLICATION NUMBER: US/10192381
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US/09/377,285
; PRIOR FILING DATE: 1999-08-18
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; PRIOR APPLICATION NUMBER: US 60/138,426
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,493
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,494
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/097,334
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 47
; LENGTH: 5
; TYPE: PPT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: optimal ligand
US-10-192-381-47

Query Match 63.3%; Score 19; DB 12; Length 5;
Best Local Similarity 75.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTTP 4
   |||
Db 1 FPPP 4

RESULT 12
US-10-281-652-12
; Sequence 12, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-12

Query Match 63.3%; Score 19; DB 15; Length 5;
Best Local Similarity 75.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTTP 4
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Db 1 FPPP 4

RESULT 13
US-10-252-408-27
; Sequence 27, Application US/10252408
; Publication No. US20030082736A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, Craig A.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
; FILE REFERENCE: A-71592
; CURRENT APPLICATION NUMBER: US/10/252,408
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; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US/08/436,824
; PRIOR FILING DATE: 1995-03-20
; PRIOR APPLICATION NUMBER: US 08/255,849
; PRIOR FILING DATE: 1994-06-08
; PRIOR APPLICATION NUMBER: US 07/860,710
; PRIOR FILING DATE: 1992-01-30
; PRIOR APPLICATION NUMBER: US 07/523,635
; PRIOR FILING DATE: 1990-05-10
; PRIOR APPLICATION NUMBER: US 07/421,417
; PRIOR FILING DATE: 1989-10-13
; PRIOR APPLICATION NUMBER: US 07/405,370
; PRIOR FILING DATE: 1989-09-11
; PRIOR APPLICATION NUMBER: US 07/403,242
; PRIOR FILING DATE: 1989-09-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Miscellaneous Structure
US-10-252-408-27

Query Match      60.0%; Score 18; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTP 3
   |||
Db 3 FTP 5

RESULT 14
US-10-211-088-128
; Sequence 128, Application US/1021108#
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A:el Fusion: Proteins And Assays For Molecular Bi
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
US-10-211-088-128

Query Match      53.3%; Score 16; DB 15; Length 4;
Best Local Similarity 50.0%; Pred. No. 5.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTPP 4
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Db 1 YTPP 4

RESULT 15
US-10-206-699-49
; Sequence 49, Application US/10206699
; Publication No. US20030100510A1
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; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,162
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-49

Query Match      53.3%; Score 16; DB 15; Length 5;
Best Local Similarity 75.0%; Pred. No. 5.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TPPT 5
   |||
Db 2 TPST 5

Search completed: November 5, 2003, 18:00:35
Job time : 29 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OX protein - protein search, using sw mode:

Run on: November 5, 2003, 17:53:28 : Search time 21 Seconds  
(without alignments)  
10.074 Million cell updates/sec

Title: US-09 914-088-7  
Perfect score: 10  
Sequence: 1 FRPPT 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 22629

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
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2: /cgn2\_6/prodata/1/aaa/5B\_COMB.pep:  
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5: /cgn2\_6/prodata/1/aaa/PCUS\_COMB.pep:  
6: /cgn2\_6/prodata/1/aaa/backfiles.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	80.0	4	1	US-08-649-272A-13
2	24	80.0	4	3	US-09-105-799-13
3	24	80.0	5	4	US-09-646-154-1
4	19	63.3	3	1	US-08-649-272A-14
5	19	63.3	3	1	US-08-649-272A-14
6	19	63.3	3	3	US-09-105-799-14
7	19	63.3	3	3	US-09-105-799-15
8	19	63.3	4	1	US-07-917-034A-5
9	19	63.3	4	1	US-08-122-546-1
10	19	63.3	4	2	US-08-764-938-1
11	19	63.3	4	3	US-09-195-868-18
12	19	63.3	4	3	US-09-131-052-1
13	19	63.3	4	3	US-09-131-053A-1
14	19	63.3	4	3	US-08-895-590-40
15	19	63.3	5	2	US-08-666-473-6
16	19	63.3	5	2	US-08-666-473-10
17	19	63.3	5	2	US-08-518-967-13
18	19	63.3	5	2	US-08-340-283-3
19	19	63.3	5	2	US-08-967-508-12
20	19	63.3	5	2	US-08-612-858-29
21	19	63.3	5	3	US-08-666-360-2
22	19	63.3	5	3	US-08-666-360-3
23	19	63.3	5	3	US-08-967-506-12
24	19	63.3	5	3	US-08-932-082-3
25	19	63.3	5	4	US-09-646-154-3
26	19	63.3	5	4	US-09-432-285-2
27	19	63.3	5	4	US-09-432-285-3

28	19	63.3	5	4	US-09-641-803-12	Sequence 12, Appl
29	19	63.3	5	4	US-08-897-556A-106	Sequence 106, App
30	19	63.3	5	4	US-08-877-605-339	Sequence 339, App
31	19	63.3	5	5	PCT-US94-02552-12	Sequence 12, Appl
32	18	60.0	5	2	US-08-347-335A-4	Sequence 4, Appli
33	18	60.0	5	3	US-08-974-735-2	Sequence 2, Appli
34	18	60.0	5	4	US-08-406-824A-27	Sequence 27, Appl
35	18	60.0	5	6	5395760-5	Patent No. 5395760
36	17	56.7	4	2	US-08-323-686-22	Sequence 22, Appl
37	17	56.7	4	3	US-08-886-886-38	Sequence 38, Appl
38	17	56.7	5	2	US-08-333-686-6	Sequence 6, Appli
39	16	53.3	5	2	US-08-437-013-22	Sequence 22, Appl
40	16	53.3	5	4	US-09-430-702-19	Sequence 19, Appl
41	15	50.0	4	1	US-07-917-034A-3	Sequence 3, Appli
42	15	50.0	4	1	US-08-325-509-48	Sequence 48, Appl
43	15	50.0	4	1	US-08-569-806-9	Sequence 9, Appli
44	15	50.0	4	2	US-08-441-871-27	Sequence 27, Appl
45	15	50.0	4	2	US-08-441-871-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1  
US-08-649-272A-13  
; Sequence 13, Application US/08649272A  
; Patent No. 5763393  
; GENERAL INFORMATION:  
; APPLICANT: MOSKAL, Joseph R  
; APPLICANT: YAMAMOTO, Hirotsuka  
; APPLICANT: COLLEY, Patricia A  
; TITLE OF INVENTION: Neuroactive Peptides  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BAKNER & ALLEGRETTI, LTD.  
; STREET: 10 S. Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/649,272A  
; FILING DATE: 17-MAY-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHAO, Mark  
; REGISTRATION NUMBER: 37,293  
; REFERENCE/DOCKET NUMBER: 95,1204  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1  
; OTHER INFORMATION: /note= "NT-13"  
US-08-649-272A-13

Query Match 80.0%; Score 24; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy

2 TPPT 5  
|||  
1 TPPT 4

## RESULT 2

US-09-105-799-13  
; Sequence 13, Application US/09105799  
; Patent No. 6107271  
; GENERAL INFORMATION:  
; APPLICANT: MOSKAL, Joseph R  
; APPLICANT: YAMAMOTO, Hirotsuka  
; APPLICANT: COLLEY, Patricia A  
; TITLE OF INVENTION: Neuroactive Peptides  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.  
; STREET: 10 S. Wacker Drive, Suite 3000  
; City: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/105,799  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/649,272  
; FILING DATE: 17-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHAO, Mark  
; REGISTRATION NUMBER: 37,293  
; REFERENCE/DOCKET NUMBER: 95,1204  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: No. 6107271 Relevant  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1  
; OTHER INFORMATION: /note= "NT 13"

US-09-105-799 13

Query Match 80.0%; Score 24; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy

2 TPPT 5  
|||  
1 TPPT 4

## RESULT 3

US-09-646-154-4  
; Sequence 4, Application US/09646154  
; Patent No. 6429024  
; GENERAL INFORMATION:  
; APPLICANT: KOKUBO, TOHRU  
; APPLICANT: ARAI, KENJI  
; APPLICANT: TOMA, KAZUNORI  
; TITLE OF INVENTION: TEST METHOD FOR IGA NEPHROPATHY  
; FILE REFERENCE: KP-9821

; CURRENT APPLICATION NUMBER: US/09/646,154  
; CURRENT FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: PCT/JP99/01525  
; PRIOR FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Formula amino  
; OTHER INFORMATION: acid sequence  
US-09-646-154-4

Query Match 80.0%; Score 24; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2 TPPT 5  
|||  
1 TPPT 4

Db

## RESULT 4

US-08-649-272A-14  
; Sequence 14, Application US/08649272A  
; Patent No. 5763393  
; GENERAL INFORMATION:  
; APPLICANT: MOSKAL, Joseph R  
; APPLICANT: YAMAMOTO, Hirotsuka  
; APPLICANT: COLLEY, Patricia A  
; TITLE OF INVENTION: Neuroactive Peptides  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.  
; STREET: 10 S. Wacker Drive, Suite 3000  
; City: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/649,272A  
; FILING DATE: 17-MAY 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHAO, Mark  
; REGISTRATION NUMBER: 37,293  
; REFERENCE/DOCKET NUMBER: 95,1204  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1  
; OTHER INFORMATION: /note= "NT-14"

US-08-649-272A-14

Query Match 63.3%; Score 19; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TPP 4  
 Db 1 TPP 3

## RESULT 5

US-08-649-272A-15  
 ; Sequence 15, Application US/08649272A  
 ; Patent No. 5763393  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MCSKAL, Joseph R  
 ; APPLICANT: YAMAMOTO, Hirotsuka  
 ; APPLICANT: COLLEY, Patricia A  
 ; TITLE OF INVENTION: Neuroactive Peptides  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER & ALLEGRETTI, LTD.  
 ; STREET: 10 S. Wacker Drive, Suite 3000  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/649,272A  
 ; FILING DATE: 17-MAY-1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CHAO, Mark  
 ; REGISTRATION NUMBER: 37,293  
 ; REFERENCE/DOCKET NUMBER: 95,1204  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-715-1234  
 ; TELEFAX: 312-715-1234  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: not relevant  
 ; MOLECULE TYPE: peptide  
 ; FEATURE:  
 ; NAME/KEY: Peptide  
 ; LOCATION: 1  
 ; OTHER INFORMATION: /note="NT-15"  
 US-08-649-272A-15

Query Match 63.3%; Score 19; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPT 5  
 Db 1 PPT 3

## RESULT 6

US-09-105-799-14  
 ; Sequence 14, Application US/09105799  
 ; Patent No. 6107271  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MCSKAL, Joseph R  
 ; APPLICANT: YAMAMOTO, Hirotsuka  
 ; APPLICANT: COLLEY, Patricia A  
 ; TITLE OF INVENTION: Neuroactive Peptides  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER & ALLEGRETTI, LTD.

STREET: 10 S. Wacker Drive, Suite 3000  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/105,799  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/649,272  
 FILING DATE: 17-MAY-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CHAO, Mark  
 REGISTRATION NUMBER: 37,293  
 REFERENCE/DOCKET NUMBER: 95,1204  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-715-1000  
 TELEFAX: 312-715-1234  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: No. 6107271 Relevant  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: 1  
 OTHER INFORMATION: /note="NT-14"  
 US-09-105-799-14

Query Match 63.3%; Score 19; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TPP 4  
 Db 1 TPP 3

## RESULT 7

US-09-105-799-15  
 ; Sequence 15, Application US/09105799  
 ; Patent No. 6107271  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MCSKAL, Joseph R  
 ; APPLICANT: YAMAMOTO, Hirotsuka  
 ; APPLICANT: COLLEY, Patricia A  
 ; TITLE OF INVENTION: Neuroactive Peptides  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER & ALLEGRETTI, LTD.  
 ; STREET: 10 S. Wacker Drive, Suite 3000  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/105,799  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/649,272  
FILING DATE: 17-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: CHAO, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 95,1204  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: NO. 6:07271 Relevant  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1  
OTHER INFORMATION: /note="NT-15"  
US-09 105 799.15

Query Match 63.3% Score 19; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5  
|||  
Db 1 PPT 3

## RESULT 8

US-07-917-034A-5  
Sequence 5, Application US/07917034A  
Patent No. 5427927  
GENERAL INFORMATION:  
APPLICANT: Meyer, Thomas, Pohlner, Cohnanes, Schumacher,  
APPLICANT: Ginter, Donny, Carola  
TITLE OF INVENTION: Process For The Enzymatic Cleavage  
TITLE OF INVENTION: of Recombinant Proteins Using Tga Proteases  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felte & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb standard  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/917,034A  
FILING DATE: 19920810  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PC7/EP91/00192  
FILING DATE: 1-Feb-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 40 39 415.6  
FILING DATE: 10-Dec-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 40 15 922.1  
FILING DATE: 17-May-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 40 15 921.3  
FILING DATE: 17-May-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 40 03 149.7  
FILING DATE: 3-Feb-1990  
ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5427927man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: HUBR 1018  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-917-034A-5

Query Match 63.3% Score 19; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5  
|||  
Db 1 PPT 3

## RESULT 9

US-08-122-546-1  
Sequence 1, Application US/08122546  
Patent No. 5591593  
GENERAL INFORMATION:  
APPLICANT: Courtenay-Luck, Nigel S  
TITLE OF INVENTION: MINIMCY RECOGNITION UNIT OF PEM MUCIN  
TITLE OF INVENTION: TANDEM REPEAT SPECIFIC MONOCLONAL ANTIBODY  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jules E Goldberg, Esq.  
STREET: 261 Madison Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/122,546  
FILING DATE: 09/29/93  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldberg, Jules E  
REGISTRATION NUMBER: 24,408  
REFERENCE/DOCKET NUMBER: JG-EPC-1069PCT  
TELEPHONE: (212) 986-4090  
TELEFAX: (212) 818-9479  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-122-546-1

Query Match 63.3% Score 19; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5  
|||  
Db 2 PPT 4

RESULT 10  
US-08-764-938-1  
; Sequence 1, Application US/08764938  
; Patent No. 5833943  
; GENERAL INFORMATION:  
; APPLICANT: Courtenay-Luck, Nigel S  
; TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OF PEM MUCIN  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jules E Goldberg, Esq.  
; STREET: 261 Madison Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DCS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08764.938  
; FILING DATE: December 13, 1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldberg, Jules E  
; REFERENCE/DOCKET NUMBER: JG-EPC-1069PCT/C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 986-4090  
; TELEFAX: (212) 818-9479  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
US-08-764-938-1

Query Match 63.3%; Score 19; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5  
111  
DB 2 PPT 4

RESULT 11  
US-09-195-868-18  
; Sequence 18, Application US/09195868  
; Patent No. 609621  
; GENERAL INFORMATION:  
; APPLICANT: KAVANAUGH MD, MICHAEL  
; APPLICANT: POT PH.D., DAVID  
; APPLICANT: WILLIAMS MDPH, LEWIS T.  
; TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: 4560 HORTON STREET  
; CITY: EMERYVILLE  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09195,868  
; FILING DATE:  
; CLASSIFICATION:  
; APPLICATION NUMBER: US/09195,868  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FIRESTONE, LEIGH H.  
; REGISTRATION NUMBER: 36,831  
; REFERENCE/DOCKET NUMBER: 1182,004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-923-2707  
; TELEFAX: 510-655-3542  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-195-868-18

Query Match 63.3%; Score 19; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5  
111  
DB 1 PPT 3

RESULT 12  
US-09-131-052-1  
; Sequence 1, Application US/09131052  
; Patent No. 6107469  
; GENERAL INFORMATION:  
; APPLICANT: Courtenay-Luck, Nigel S  
; TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OF PEM MUCIN  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jules E Goldberg, Esq.  
; STREET: 261 Madison Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10016-2391  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DCS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09131,052  
; FILING DATE: August 7, 1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldberg, Jules E  
; REFERENCE/DOCKET NUMBER: JG-EPC-1069C-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 986-4090  
; TELEFAX: (212) 818-9479  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

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1  FRAGMENT TYPE: internal
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4  Query Match 63.3%; Score 19; DB 3; Length 4;
5  Best Local Similarity 100.0%; Pred. No. 2.5e+05;
6  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
7
8  QY 3 PPT 5
9  |||
10 DB 2 PPT 4
11
12 RESULT 13
13 US-09-131 053A-1
14 Sequence 1, Application US/09131053A
15 Patent No. 6174691
16 GENERAL INFORMATION:
17 APPLICANT: Courtenay-Luck, Nigel S
18 TITLE OF INVENTION: MINIMUM RECOMBINATION UNIT OF THE MUCIN
19 NUMBER OF SEQUENCES: 18
20 CORRESPONDENCE ADDRESS:
21 ADDRESSEE: Jules E Goldberg, Esq.
22 STREET: 261 Madison Avenue
23 CITY: New York
24 STATE: New York
25 COUNTRY: USA
26 ZIP: 10016-2391
27 COMPUTER READABLE FORM:
28 MEDIUM TYPE: Floppy disk
29 COMPUTER: IBM PC compatible
30 OPERATING SYSTEM: PC-DOS/MS-DOS
31 SOFTWARE: Patent In Release #1.0, Version #1.25
32 CURRENT APPLICATION DATA:
33 APPLICATION NUMBER: US/09/131 053A
34 FILING DATE: August 7, 1998
35 CLASSIFICATION:
36 ATTORNEY/AGENT INFORMATION:
37 NAME: Goldberg, Jules E
38 REFERENCE/DOCKET NUMBER: JG-EM-10690-2
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: (212) 986-4092
41 TELEFAX: (212) 818-9479
42 INFORMATION FOR SEQ ID NO: 1:
43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 4 amino acids
45 TYPE: amino acid
46 STRANDEDNESS: single
47 TOPOLOGY: linear
48 MOLECULE TYPE: peptide
49 HYPOTHETICAL: NO
50 ANTI-SENSE: NO
51 FRAGMENT TYPE: internal
52 US 09 131 053A-1
53
54 Query Match 63.3%; Score 19; DB 3; Length 4;
55 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
56 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
57
58 QY 3 PPT 5
59 |||
60 DB 2 PPT 4
61
62 RESULT 14
63 US 09-895-590-42
64 Sequence 40, Application US/08895590
65 Patent No. 6207410
66 GENERAL INFORMATION:
67 APPLICANT: Hall, Linda M.
68 ADDRESSEE: Ren, Dejian
69 STREET: Zheng, Wei
70 CITY: Subaid, Manuel Nareel Paul
71
72 TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
73 NUMBER OF SEQUENCES: 101
74 CORRESPONDENCE ADDRESS:
75 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
76 STREET: 699 Prince Street
77 CITY: Alexandria
78 STATE: VA
79 COUNTRY: USA
80 ZIP: 22314-3187
81 COMPUTER READABLE FORM:
82 MEDIUM TYPE: Floppy disk
83 COMPUTER: IBM PC compatible
84 OPERATING SYSTEM: PC-DOS/MS-DOS
85 SOFTWARE: Patent In Release #1.0, Version #1.30
86 CURRENT APPLICATION DATA:
87 APPLICATION NUMBER: US/08/895,590
88 FILING DATE:
89 CLASSIFICATION:
90 PRIOR APPLICATION DATA:
91 APPLICATION NUMBER: US/08/374,888
92 FILING DATE: 19-JAN-1995
93 ATTORNEY/AGENT INFORMATION:
94 NAME: McGowan, Malcolm M.
95 REGISTRATION NUMBER: 39,300
96 REFERENCE/DOCKET NUMBER: 022650-263
97 TELECOMMUNICATION INFORMATION:
98 TELEPHONE: 703-836-6620
99 TELEFAX: 703-836-2021
100 INFORMATION FOR SEQ ID NO: 40:
101 SEQUENCE CHARACTERISTICS:
102 LENGTH: 4 amino acids
103 TYPE: amino acid
104 TOPOLOGY: linear
105 MOLECULE TYPE: protein
106 US-08-895-590-40
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108 Query Match 63.3%; Score 19; DB 3; Length 4;
109 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
110 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
111
112 QY 2 PPT 4
113 |||
114 DB 2 PPT 4
115
116 RESULT 15
117 US-08-666-473-6
118 Sequence 6, Application US/08666473
119 Patent No. 6443713
120 GENERAL INFORMATION:
121 APPLICANT: YOSHIDA, Aritio
122 ADDRESSEE: TAKEUCHI, YAKUO
123 TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
124 TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
125 NUMBER OF SEQUENCES: 114
126 CORRESPONDENCE ADDRESS:
127 ADDRESSEE: Foley & Lardner
128 STREET: 3000 K Street, N.W., Suite 500
129 CITY: Washington
130 STATE: D.C.
131 COUNTRY: USA
132 ZIP: 20007-5109
133 COMPUTER READABLE FORM:
134 MEDIUM TYPE: Floppy disk
135 COMPUTER: IBM PC compatible
136 OPERATING SYSTEM: PC-DOS/MS-DOS
137 SOFTWARE: Patent In Release #1.0, Version #1.30
138 CURRENT APPLICATION DATA:
139 APPLICATION NUMBER: US/08/666,473
140 FILING DATE: 19 SEP 1996
141 CLASSIFICATION:
142 ATTORNEY/AGENT INFORMATION:

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APPLICATION NUMBER: WO PCT/JP95/02238  
FILING DATE: 01-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-22:01  
FILING DATE: 09-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-2691:1  
FILING DATE: 31-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16897/837  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 9C4136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08 666-473-6

Query Match 63.3%; Score 19; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

Cy 2 TPP 4  
|||  
Db 2 TPP 4

Search completed: November 5, 2003, 17:56.31  
Job time : 22 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw mode:

Run on: November 5, 2003, 17:59:59 ; Search time 13 Seconds  
(without alignments)  
96.169 Million cell updates/sec

Title: US-09-914-088-8

Perfect score: 68

Sequence: 1 CLEGGQVMDVLL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 1925

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	32.4	7	B34818	vicilin 57K chain
2	21	30.9	8	A28719	thymic humoral fac
3	21	30.9	10	G58501	48K bile/gallblad
4	20	29.4	9	A60427	macrophage cyto
5	20	29.4	10	GXHU1	gastric juice pep
6	20	29.4	11	PS0259	19K protein 3225
7	19	27.9	12	PN0160	ribosomal protein
8	18	26.5	13	A33660	osteoclast functi
9	18	26.5	13	S47357	T-cell antigen rec
10	18	26.5	13	S66235	sperr motility inh
11	17	25.0	6	P70604	T-cell receptor be
12	17	25.0	6	PT0857	T-cell receptor be
13	17	25.0	7	PT0543	T-cell receptor be
14	17	25.0	10	S10926	inhibin beta-A cha
15	17	25.0	10	PC4442	cytochrome c553
16	17	25.0	10	PH1592	Ig H chain V-D-J r
17	17	25.0	12	G49410	complex polypept
18	17	25.0	12	C58502	58K bile and gallb
19	17	25.0	12	S43013	hypothetical prote
20	17	25.0	12	S36899	ribosomal protein
21	17	25.0	12	PH1611	Ig H chain V-D-J r
22	17	25.0	12	PH1581	Ig H chain V-D-J r
23	16	23.5	9	A37027	macrophage chemot
24	16	23.5	10	A32543	cardioexcitatory n
25	16	23.5	10	A56633	neomycin suppressin
26	16	23.5	10	A32195	Na+/K+-exchanging
27	16	23.5	11	S19301	endo-1.4-beta-xyla
28	16	23.5	11	A34243	H-hydrophorin - Ja
29	16	23.5	12	T46794	hypothetical prote

30 16 23.5 12 2 JQ2108 hypothetical 1.4K  
31 16 23.5 12 2 JQ2118 hypothetical 1.4K  
32 16 23.5 12 2 PH1172 T-cell receptor al  
33 16 23.5 13 2 S65612 tubulin alpha-chain  
34 15 22.1 6 2 B34835 dnAA protein - Pse  
35 15 22.1 10 2 C26997 unspecific monocoy  
36 15 22.1 10 2 PH0807 T-cell receptor al  
37 15 22.1 10 2 PH0946 T-cell receptor be  
38 15 22.1 10 2 E86128 hypothetical prote  
39 15 22.1 11 2 S14087 parasporal crystal  
40 15 22.1 11 2 S18385 NADP-cytochrome P4  
41 15 22.1 11 2 H84382 hypothetical prote  
42 15 22.1 12 2 S29764 alpha-macroglobuli  
43 15 22.1 12 2 S48209 zinc-metallophosph  
44 15 22.1 12 2 I40663 bma protein - Clos  
45 15 22.1 12 2 PH1587 Ig H chain V-D-J r

#### ALIGNMENTS

##### RESULT 1

B34818

vicilin 57K chain - Pigeon pea (fragment)

C:Species: Cajanus cajan (pigeon pea)

C:Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 30-Sep-1993

C:Accession: B34818

R:Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.

Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990

A:Title: Unusual denaturation properties of vicilin from Cajanus cajan.

A:Reference number: A34818; MUID:90165956; PMID:2306256

A:Accession: B34818

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MAW>

Query Match 32.4%; Score 22; DB 2; Length 7;

Best Local Similarity 60.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLEGG 5

DB 3 CMESG 7

##### RESULT 2

A28719

thymic humoral factor gamma 2 - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 18-Jun-1993

C:Accession: A28719

R:Burststein, Y.; Buchner, V.; Pecht, M.; Trainin, N.

Biochemistry 27, 4066-4071, 1988

A:Title: Thymic humoral factor gamma-2: purification and amino acid sequence of an im

A:Reference number: A28719; MUID:88326920; PMID:3261994

A:Accession: A28719

A:Molecule type: protein

A:Residues: 1-8 <BUR>

Query Match 30.9%; Score 21; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEDG 5

DB 1 LEDG 4

##### RESULT 3

G58501

48K bile/gallbladder stone protein - unidentified bacterium (fragment)

C:Species: unidentified bacterium

C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998



C:Accession: G54501

R:Rinette, J.P.; Binette, M.B.

A:Submitted to the Protein Sequence Database, October 1996

A:Description: The proteins of kidney and gallbladder stones.

A:Reference number: A58501

A:Accession: G58501

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <BIN>

A:Experimental source: human bile and gallbladder stones

A>Note: 1 Ser and 4-Glu were also found

Query Match 30.9%; Score 21; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 1; 1e-03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0;

QY 2 LEDGQVM 8

DB 4 VEDGKAL 10

#### RESULT 4

A60427

A:Macrophage cytotoxicity-inducing factor, 29K - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 12-Feb-1993 #sequence\_revision: 12-Feb-1993 #text\_change 18-Jun-1993

C:Accession: A60427

R:Cones, C.M.; Prince, C.A.; Williams, J.S.

Exp. Hematol. 19, 704-709, 1991

A>Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducing

A:Reference number: A60427; MUID:91372355; PMID:1929970

A:Accession: A60427

A:Molecule type: protein

A:Residues: 1-9 <GBR>

A>Note: the sequence from the text on page 705 is inconsistent with that from page 708

C:Keywords: cytokine

Query Match 29.4%; Score 20; DB 2; Length 9;  
Best Local Similarity 86.0%; Pred. No. 2; 1e-04;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 IENQ 6

DB 4 LEDSQ 9

#### RESULT 5

GXHU

A:Gastric juice peptide - human

C:Species: Homo sapiens (man)

C>Date: 20-Jun-2000 #sequence\_revision: 20-Jun-2000 #text\_change 20-Jun-2000

C:Accession: A01628

R:Heathcote, J.G.; Washington, R.J.

Int. J. Protein Res. 2, 117-126, 1973

A>Title: Peptides of normal human gastric juice

A:Reference number: A01628; MUID:75150463; PMID:464848

A:Accession: A01628

A:Molecule type: protein

A:Residues: 1-10 <HEA>

A>Note: a second peptide lacking 1 Leu, but otherwise identical in composition with the

C:Superfamily: unassigned animal peptides

C:Keywords: stomach

Query Match 29.4%; Score 20; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2; 1e-03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LEDGQVMDS 10

DB 1 LAAGKVERSD 10

#### RESULT 6

PS0259

A:39K protein 3225 - rice (strain Nihonbare) (fragment)

C:Species: Oryza sativa (rice)

C>Date: 03-Feb-1994 #sequence\_revision: 03-Feb-1994 #text\_change 11-Apr-1995

C:Accession: PS0259

R:Tsugita, A.; Kano, M.

submitted to JIPID, April, 1993

A:Reference number: PS0209

A:Accession: PS0259

A:Molecule type: protein

A:Residues: 1-11 <TSC>

A:Experimental source: callus

C:Comment: molecular weight 39K, pI 5.7.

Query Match 29.4%; Score 20; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 2; 2e-03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDGQVM 8

DB 4 EDGPV 9

#### RESULT 7

PN0160

A:Ribosomal protein S16 - fungus (Fusarium sporotrichioides) (fragment)

C:Species: Fusarium sporotrichioides

C>Date: 05-Aug-1994 #sequence\_revision: 05-Aug-1994 #text\_change 11-Nov-1994

C:Accession: PN0160

R:Fukaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.

submitted to JIPID, May 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporot

A:Reference number: PN0160

A:Molecule type: protein

A:Residues: 1-12 <FUK>

C:Keywords: protein biosynthesis; ribosome

Query Match 27.9%; Score 19; DB 2; Length 12;  
Best Local Similarity 80.0%; Pred. No. 3; 5e-03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 VMDVD 11

DB 6 VMDVD 10

#### RESULT 8

A03660

A:Osteoclast functional antigen alpha chain - green monkey (fragment)

C:Species: Cercopithecus aethiops (green monkey, grivet)

C>Date: 10-Mar-1990 #sequence\_revision: 10-Mar-1990 #text\_change 23-Mar-1995

C:Accession: A03660

R:Davies, J.; Warwick, J.; Totty, N.; Philp, R.; Helfrich, M.; Horton, M.

J. Cell. Biol. 109, 1817-1826, 1989

A>Title: The osteoclast functional antigen, implicated in the regulation of bone resor

A:Reference number: A03660; MUID:90009054; PMID:2477382

A:Accession: A03660

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <DAV>

A:Experimental source: a green monkey kidney Vero cell line

Query Match 26.5%; Score 18; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 5; 7e-03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 MVDVD 11

DB 3 LDVDC 6

#### RESULT 9

```
S47357
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47357
R:Lehrer, P.J.
submitted to the EMBL Data Library, August, 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47357
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-23 <USH>
A:Cross-references: EMBL:Z35691; NID:9527451; PIDD:CAA84750.1; PIDD:3527452
C:Keywords: T-cell receptor

Query Match 26.5%; Score 18; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 5.7e+03;
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CLEDGQVMD 9
| | |
Db 1 CASSGRSTD 9

RESULT 13
S46235
sperm motility inhibitor protein - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S46235
R:Iwamoto, T.; Hiroaki, H.; Furutachi, Y.; Wada, K.; Satoh, M.; Osada, T.; Gao
FEBS Lett. 368, 420-424, 1995
A:Title: Cloning of boar SPMI gene which is expressed specifically in seminal vesicle an
A:Reference number: S46233; MUID:95361914; PMID:7635190
A:Accession: S46235
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <WA>
A:Note: Pro-6 was also found

Query Match 26.5%; Score 18; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDGQVM 8
| | |
Db 7 DDGQV 12

RESULT 11
PT0604
T-cell receptor beta chain V-D-J region (121-1K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0604
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0604
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 25.0%; Score 17; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DQG 6
| | |
Db 4 DQG 6

RESULT 12
PT0657
T-cell receptor beta chain V-D-J region (121-1K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0657
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0657
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 25.0%; Score 17; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DQG 6
| | |
Db 4 DQG 6

RESULT 13
PT0543
T-cell receptor beta chain V-D-J region (126-1BE) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0543
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0543
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-7 <FEE>
A:Experimental source: day 18 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 25.0%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DQG 6
| | |
Db 4 DQG 6

RESULT 14
SI0926
inhibin beta-A chain - African clawed frog (fragment)
N:Alternate names: activin A; mesoderm-inducing factor
C:Species: Xenopus laevis (African clawed frog)
C:Date: 18-Feb-1994 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: SI0926
R:Smith, J.C.; Price, B.M.J.; van Nimmen, K.; Huylebroeck, D.
Nature 345, 729-731, 1990
A:Title: Identification of a potent Xenopus mesoderm-inducing factor as a homologue o
A:Reference number: SI0926; MUID:90294906; PMID:2113615
A:Accession: SI0926
A:Molecule type: protein
A:Residues: 1-10 <NAT>
C:Superfamily: inhibin
C:Keywords: hormone

Query Match 25.0%; Score 17; DB 2; Length 10;
| |
```

Best Local Similarity 75.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 4 DGV 7  
DB 5 DGV 8

RESULT 15  
PC4442  
cytochrome c553 - Desulfovibrio desulfuricans (fragment)  
C:Species: Desulfovibrio desulfuricans  
C:Date: 28-Mar-1998 #sequence\_revision 28-Mar-1998 #text\_change 07 May-1999  
C:Accession: PC4442  
R:Rubert, C.; Leroy, G.; Bianco, P.; Forest, E.; Pruschi, M.; Della, A.  
Biochem. Biophys. Res. Commun. 242, 213-218, 1998  
A:Title: Characterization of the cytochromes C from Desulfovibrio desulfuricans G201.  
A:Reference number: PC4442; XUID:9810281; PMID:9439638  
A:Accession: PC4442  
A:Molecule type: protein  
A:Residues: 1-10 <ADB>  
A:Experimental source: strain G201  
C:Comment: This protein is involved in the formate reduction pathway.

Query Match 25.0%; Score 17; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 EDG 5  
DB 2 EDG 4

Search completed: November 5, 2003, 18:04:16  
Job time : 14 secs

GenCore version 5.1.6  
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OM protein protein search, using sw model

Run on: November 5, 2003, 17:56:33 ; Search time 9.5 seconds  
(without alignments)  
64,352 Million cell updates/sec

Title: US-09-914-088-8  
Perfect score: 68  
Sequence: 1 CLECGQVMDVDLL 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127963 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 596

Minimum DB seq length: 0  
Maximum DB seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	29.4	10	1 GAGU HUMAN	P01359 homo sapien
2	19	27.9	12	1 V23K WSSV	P82005 white spot
3	18	26.5	8	1 ACT_CARRA	P80729 carcinus ra
4	17	25.0	10	1 APE_CARGI	P80474 capnocytop
5	17	25.0	13	1 UHA1 HUMAN	P40928 homo sapien
6	16	23.5	8	1 PLP BRANA	P81727 brassica ra
7	16	23.5	10	1 FARP_LOCMI	P38553 Locusta mig
8	16	23.5	10	1 LOMS_EUMA	P21144 leucophaea
9	16	23.5	10	1 XALE_KLEFN	P55564 klebsiella
10	16	23.5	12	1 HS9A_RAT	P42993 rattus norv
11	16	23.5	13	1 GER2_HORVI	P28526 hordeum vul
12	15	22.1	9	1 D1_NEPNO	P24816 nephrops no
13	15	22.1	10	1 PPCK_FASHE	P30525 fasciola he
14	15	22.1	10	1 SPI_HALRO	Q10997 halocynthia
15	15	22.1	12	1 XYL1_STRVN	P14405 streptomyce
16	15	22.1	13	1 GER1_HORVU	P28525 hordeum vul
17	14	20.6	9	1 FARD_CALVO	P41868 calliphora
18	14	20.6	10	1 UPA2_HUMAN	P13088 homo sapien
19	14	20.6	11	1 CA21_LITIC	P82091 litoria cit
20	14	20.6	11	1 RR2_CONAM	P42341 conopholis
21	14	20.6	12	1 CXAI_CONIM	P50382 conus imper
22	14	20.6	12	1 PA2B_VIPBO	P11859 vipera berb
23	14	20.6	13	1 ACT7_SOYBN	P15527 glycine max
24	14	20.6	13	1 ADFB_TENMO	P83109 tenebrio mo
25	14	20.6	13	1 IDFA_CANFA	P54816 canis famil
26	14	20.6	13	1 TEJA_BANJA	P83307 rana japoni
27	14	20.6	13	1 UN10_CLOPA	P81345 clostridium
28	13.5	19.9	9	1 UF02_MOUSE	P38640 mus musculu
29	13	19.1	8	1 WPI_PERAT	P83195 perkinsus a
30	13	19.1	9	1 DNFI_LOCM	P16319 Locusta mig
31	13	19.1	9	1 IPVR_RHOVI	P22992 rhodopseudo
32	13	19.1	9	1 RE42_LITRU	P82075 litoria rub
33	13	19.1	9	1 UPA6_HUMAN	P30062 homo sapien

34 13 19.1 10 1 COXO\_RAT P80432 rattus norv  
35 13 19.1 10 1 SP34\_DICMU P81545 dictyostell  
36 13 19.1 10 1 UXA6\_CHLIR P38007 chlamydia c  
37 13 19.1 10 1 VEG6\_BACSU P80699 bacillus su  
38 13 19.1 11 1 CA21\_LITIC P82087 litoria cit  
39 13 19.1 11 1 FARP\_PENMO P83321 penaeus mon  
40 13 19.1 11 1 RRPL\_CHAV P13179 chandipura  
41 13 19.1 12 1 CD14\_LITXA P56245 litoria xan  
42 13 19.1 12 1 HCYB\_MEGCR Q10584 megathura c  
43 13 19.1 12 1 OPS3\_DROVI P17645 drosophila  
44 13 19.1 12 1 FIBB\_RABIT P14478 oryctolagus  
45 13 19.1 13 1

## ALIGNMENTS

RESULT 1  
GAGU\_HUMAN  
ID GAGU\_HUMAN STANDARD; PRT; 10 AA.  
AC P01358;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Gastric juice peptide.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75150968; PubMed=5538385;  
RA Heathcote J.G.; Washington R.J.;  
RT "Peptides of normal human gastric juice."  
RL Int. J. Protein Res. 2:117-126(1970).  
DR PIR; AC1628; GXHU1.  
DR MIM; 137220;  
DR GO; GO:0007586; P:digestion; NAS  
FT PEPTIDE 1 10 GASTRIC JUICE PEPTIDE 1.  
FT PEPTIDE 2 10 GASTRIC JUICE PEPTIDE 2.  
SQ SEQUENCE 10 AA; 1004 MW; CFEEC6AB02C3387D CRC64;  
  
Query Match 29.4%; Score 20; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.1e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2 LEDGQVMDVD 11  
| | | | |  
DB 1 LAAGKVEDSD 10

RESULT 2  
V23K\_WSSV  
ID V23K\_WSSV STANDARD; PRT; 12 AA.  
AC P82005;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 23 kDa structural polyprotein (Fragment).  
OS White spot syndrome virus (WSSV).  
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.  
OX NCBI TaxID=92652;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=South Carolina;  
RX MEDLINE=20214217; PubMed=10752552;  
RA Wang Q.; Foulos B.T.; Lightner D.V.;  
RT "Protein analysis of geographic isolates of shrimp white spot syndrome virus."  
RL Arch. Virol. 145:263-274(2000).  
CC -!- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.  
FT NON\_TER :2 12  
SQ SEQUENCE 12 AA; 1323 MW; 0C0F41E91D51A724 CRC64;

```
RT factor";
RL Microbiology 141:3087-3093(1995).
CC -!- FUNCTION: AMINOPEPTIDASE WHICH HYDROLYZES SUBSTRATES WITH FREE N-
CC TERMINAL AMINO ACID RESIDUES BUT NOT N-TERMINAL BLOCKED ONES
CC OPTIMUM ACTIVITY IS MEASURED AT PH 7.5. MAY BE IMPORTANT IN THE
CC NUTRITION AND PATHOGENESIS OF THE ORGANISM IN THE HUMAN ORAL
CC CAVITY.
CC -!- COFACTOR: REQUIRES MAGNESIUM OR CALCIUM.
KW Hydrolase; Amino peptidase; Magnesium; Calcium.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1306 MW; 0CC0A6DB43772694 CRC64;

Query Match 25.0%; Score 17; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 DVDLL 13
DB 1 DVMXL 5

RESULT 5
UHA1_HUMAN STANDARD; PRT; 13 AA.
ID UHA1_HUMAN
AC P40928;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of heart (Spot 4304) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.7, ITS MW IS: 35.5 kDa.
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1380 MW; 6617BA7A1E06AB1B CRC64;

Query Match 25.0%; Score 17; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EDG 5
DB 7 EDG 9

RESULT 6
PLP_BRANA STANDARD; PRT; 8 AA.
ID PLP_BRANA
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Placental lipid-associated protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN 1
RP SEQUENCE.
RC STRAIN=CV_T0PAZ; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;
```

```
Query Match 27.9%; Score 19; DB 1; Length 12;
Best Local Similarity 27.3%; Pred. No. 1.9e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LGGQWMDVL 12
DB 1 MFGNLTNDV 11

RESULT 3
ACT_CARMA STANDARD; PRT; 8 AA.
ID ACT_CARMA
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin (Fragment).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eulacostraca; Eucarida; Decapoda; Ploccymata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN 1
RP SEQUENCE.
RA Lachaise F., Sornet G., Carpentier G., Granjeon E., Webster S.,
RA Baghdassarian D.;
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
RL Endocrine 5:23-32(1996)
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBICITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 6.8, ITS MW IS: 46 kDa.
CC -!- SIMILARITY: Belongs to the actin family.
DR InterPro; IPR034001; Actin.
DR InterPro; IPR034001; Actin like.
DR PROSITE; PS00406; ACTINS_1; PARTIAL.
DR PROSITE; PS00432; ACTINS_2; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT-LIKE; PARTIAL.
KW Structural protein.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 976 MW; 1424005AB32CAAB3 CRC64;
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Query Match 24.5%; Score 18; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 DVDL 12
DB 3 DVC: 6

RESULT 4
APE_CAPGI STANDARD; PRT; 10 AA.
ID APE_CAPGI
AC P83374;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Amino peptidase (SC 3.4.11.-) (Fragment).
OS Capnocytophaga gingivalis.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=1017;
RN 1
RP SEQUENCE.
RC STRAIN=ATCC 33624;
RX MEDLINE=96118234; PubMed=8574402;
RA Spratt L.A., Greenman G., Schaffer A.G.;
RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence
```

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RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Dantant A.P.,
RA Murphy D.J.:
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RL Pollen coat of Brassica napus."
RL Planta 208:588-598(1999).
CC -!- FUNCTION: MAY PLAY A STRUCTURAL ROLE IN THE ELAIOPLAST, A TAPETUM-
CC SPECIFIC ELASTIDIAL LIPID ORGANELLE
CC -!- TISSUE SPECIFICITY: TAPETUM OF ANTHEIRS.
FT NCN TER 8
SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 23.5%; Score 16; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 VMDVD 11
DB 1111
VIDVN 5

RESULT 7
FARP.LOCMI STANDARD; PRT; 10 AA.
ID FARP.LOCMI
AC P38553;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Schistocerca gregaria (PVDHFLRF-amide) (Cardioexcitatory neuropeptide).
OS Locusta migratoria (Migratory locust), and
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004, 7010;
RN [1]
RP SEQUENCE
RC SPECIES=L.migratoria; TISSUE=Brain;
RX MEDLINE=93324430; PubMed=7687352;
RA Schoofs L., Holman G.M., Paemen L., Veehaert E., Avelinckx M.,
de Loof A.;
RT "Isolation, identification, and synthesis of PVDHFLRFamide
RT (Schistocerca gregaria) in Locusta migratoria and its association with the
RT male accessory glands, the salivary glands, the heart, and the
RT oviduct."
RL Peptides 14:409-421(1993).
RN [2]
RP SEQUENCE
RC SPECIES=S.gregaria; TISSUE=Thoracic nervous system.
RX MEDLINE=89246543; PubMed=2719702;
RA Robb S., Packman L.C., Evans P.D.;
RT "Isolation, primary structure and bioactivity of FMRFamide, a
RT FMRF-amide-like neuropeptide from the locust, Schistocerca
RT gregaria."
RL Biochem. Biophys. Res. Commun. 160:850-856(1999).
CC -!- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL
CC OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND
CC OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVARY SECRETION.
CC -!- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS,
CC THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A32543.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 23.5%; Score 16; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DVD 11
DB 1111
VIDVN 5

RESULT 8
LCMS.LEUMA STANDARD; PRT; 10 AA.
ID LCMS.LEUMA
AC P21144; P41497;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucomyosuppressin (LMS) (Leu-MS).
OS Leucomyosuppressin (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucomyosuppressin,
RT an insect neuropeptide that inhibits spontaneous contractions of the
RT cockroach hindgut."
RL Comp. Biochem. Physiol. 85C:329-333(1986).
CC -!- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH
CC PROCTODEUM (HINDGUT).
KW Neuropeptide; Amidation; Pyroliidone carboxylic acid
FT MOD_RES 1 1
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1275 MW; D3C45229D2C1EAB2 CRC64;

Query Match 23.5%; Score 16; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DVD 11
DB 1111
VIDVN 5

RESULT 9
MALE.KLEPN STANDARD; PRT; 10 AA.
ID MALE.KLEPN
AC Q05564;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 33, Last annotation update)
DE Maltose-binding periplasmic protein (Maltodextrin-binding protein);
DE (KMBP) (Fragmental).
GN MALE
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1033-SP14 / KAY2026;
RX MEDLINE=93211295; PubMed=9459773;
RA Bachellier S., Perrin D., Hofnung M., Gilson E.;
RT "Bacterial interspersed mosaic elements (BIMES) are present in the
RT genome of Klebsiella."
RL Mol. Microbiol. 7:537-544(1993).
CC -!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE
CC TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND
CC CHEMOTAXIS TOWARD MALTOOLIGOSACCHARIDES.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
CC PROTEIN FAMILY 1.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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RESULT 13
PECK_FASHE STANDARD; PRT; 10 AA.
AC P80525;
CT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DI 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative phosphoenolpyruvate carboxylase [GTP] EC 4.1.1.32
DE (Phosphoenolpyruvate carboxylase) (PEPCK) (Newly excysted juvenile
DE protein 1) (Fragment)
OS Fasciola hepatica (Liver fluke)
CC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
CC Echinostomida; Echinostomata; Fascioloidae; Fasciolidae;
CC NCBI_TaxID=6192;
RN [1]
RP SEQUENCE.
RX MEDLINE=95366993; PubMed=7639732;
RA Kalcevic J., Ashman K., Meusen E.;
RT "Fasciola hepatica: rapid identification of newly excysted juvenile
RT proteins.";
RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
CC -1- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
CC + CO(2)
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP]
CC FAMILY.
DR InterPro: IPR003364; PEP carboxykin.
DR PROSITE: PS00505; PEPCK GTP; PARTIAL.
KW Lyase; Decarboxylase; GTP-binding.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1069 MW; 839346187AA9C97A CRC64;

Query Match 22.1%; Score 15; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DQGVN 8
DB 6 DGEAV 10

RESULT 14
SPI_HALRO STANDARD; PRT; 10 AA.
AC Q10997;
CT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DI 15-DEC-1998 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (Fragment)
OS Halcynethia toretzi (Sea squirt)
CC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
CC Stolidobranchia; Pyrosidae; Halcynethia.
CC NCBI_TaxID=7729;
RN [1]
RP SEQUENCE.
TX ISSUE=Hemolymph;
RX MEDLINE=96321333; PubMed=8759295;
RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
RT "Purification and characterization of a 58,000 Da proteinase
RT inhibitor from the hemolymph of a solitary ascidian, Halcynethia
RT toretzi.";
RL Comp. Biochem. Physiol. 114B:1-9(1996).
CC -1- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN; PARTIAL.
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA) CRC64;

Query Match 22.1%; Score 15; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.4e+03;

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Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 EDQQ 6
DB 3 KDGE 6

RESULT 15
XYLA_STRVN STANDARD; PRT; 12 AA.
ID XYLA_STRVN
AC P14405;
CT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Xylose isomerase (EC 5.3.1.5) (Fragment)
GN XYLA.
OS Streptomyces violaceoruber.
CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
CC Streptomycineae; Streptomycetaceae; Streptomyces.
CC NCBI_TaxID=1935;
RN [1]
RP SEQUENCE.
RX STRAIN=LMG 7183;
RX MEDLINE=90104230; PubMed=2604694;
RA Vangrypeere W., Ange C., Kersters-Hilderson H., Tempat P.;
RT "Single active-site histidine in D-xylose isomerase from Streptomyces
RT violaceoruber. Identification by chemical derivatization and peptide
RT mapping.";
RL Biochem. J. 263:195-199(1989).
CC -1- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
CC -1- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
DR HAMAP: MF_00455; 1.
DR InterPro: IPR001998; Xylose isom.
DR PROSITE: PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
DR PROSITE: PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
KW isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.
FT NON_TER 1 1
FT ACT_SITE 5 5
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1375 MW; E749268EB1AAAAA1 CRC64;

Query Match 22.1%; Score 15; DB 1; Length 12;
Best Local Similarity 63.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 DVGII 13
DB 6 DDCDI 10

Search completed: November 5, 2003, 18:02:29
Job time : 10.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:59:29 ; Search time 27.5 Seconds

(without alignments)  
121.989 Million cell updates/sec

Title: US-09-914-088-8

Perfect score: 68

Sequence: CLEGGQVMDVLL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 266

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

```

Pred. No. is the number of results predicted by CompuGen to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	36.8	9	11 Q9QZAB	Q9QZAB mus musculus
2	20	29.4	12	12 Q89243	Q89243 woodchuck h
3	19	27.9	9	4 Q96P97	Q96P97 homo sapien
4	19	27.9	9	10 Q8LPT5	Q8LPT5 zea mays (m
5	19	27.9	10	10 Q8LPT7	Q8LPT7 zea mays (m
6	19	27.9	12	10 Q8LPT6	Q8LPT6 zea mays (m
7	19	27.9	13	12 Q9PXB5	Q9PXB5 duck hepatic
8	18	26.5	11	6 Q9TRX0	Q9TRX0 sus scrofa
9	18	26.5	11	7 Q29831	Q29831 homo sapien
10	18	26.5	11	11 P97755	P97755 rattus norv
11	18	26.5	12	4 Q9NTR7	Q9NTR7 homo sapien
12	18	26.5	13	5 Q9TWR4	Q9TWR4 titiys serr
13	17	25.0	8	4 Q9P285	Q9P285 homo sapien
14	17	25.0	8	11 Q9QV15	Q9QV15 rattus sp.
15	17	25.0	11	6 P83128	P83128 bos indicus
16	17	25.0	11	13 Q9QWA2	Q9QWA2 gallus gall

17	17	25.0	12	2	Q932U8	Q932U8 acinetobact
18	17	25.0	12	2	Q52112	Q52112 acinetobact
19	17	25.0	12	2	Q8GMV1	Q8GMV1 acinetobact
20	17	25.0	12	2	Q8GMT8	Q8GMT8 acinetobact
21	17	25.0	12	2	Q8GML2	Q8GML2 acinetobact
22	17	25.0	12	10	Q9S938	Q9S938 beta vulgar
23	17	25.0	13	4	Q9UP58	Q9UP58 homo sapien
24	17	25.0	13	7	Q19690	Q19690 homo sapien
25	17	25.0	13	8	Q94RE2	Q94RE2 leptomonas
26	16	23.5	8	13	Q90493	Q90493 eophaaltria
27	16	23.5	9	6	Q9XT05	Q9XT05 macropus ru
28	16	23.5	9	10	Q42452	Q42452 triticum ae
29	16	23.5	9	10	Q9FSZ2	Q9FSZ2 cicer ariet
30	16	23.5	10	13	Q8L7F5	Q8L7F5 hevea bras
31	16	23.5	10	10	P82938	P82938 hordeum vul
32	16	23.5	10	11	Q9QV57	Q9QV57 mus sp. pro
33	16	23.5	11	5	Q23876	Q23876 dictyosteli
34	16	23.5	11	10	Q19784	Q19784 gossypium h
35	16	23.5	11	11	Q9QVF6	Q9QVF6 mus musculu
36	16	23.5	12	4	Q9UGS1	Q9UGS1 homo sapien
37	16	23.5	12	6	P81127	P81127 bos indicus
38	16	23.5	13	4	Q8WY56	Q8WY56 homo sapien
39	16	23.5	13	10	Q9S8N1	Q9S8N1 hordeum vul
40	15	22.1	7	4	Q15897	Q15897 homo sapien
41	15	22.1	8	11	Q9ET18	Q9ET18 mus spratus
42	15	22.1	8	11	Q9ET17	Q9ET17 mus caroli
43	15	22.1	8	11	Q9ET16	Q9ET16 mesocricetu
44	15	22.1	9	1	Q50832	Q50832 methanococc
45	15	22.1	9	2	P72149	P72149 pseudomonas

#### ALIGNMENTS

RESULT :

Q9QZAB PRELIMINARY; PRT; 9 AA.  
AC Q9QZAB: Q9QZAB:2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE C-type lectin DCU1 (Fragment).  
GN DCU1  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Gorski K., Huang X., Tseng S.-Y., Rattis F., Pardoll D., Tsuchiya H.;  
RT "Dendritic cell regulation of DCU1 mRNA expression."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF192526; AAF04843.1; .  
DR MGI; MGI:2136650; DCU1.  
KW Lectin.  
FT NON\_TER  
SQ SEQUENCE 9 AA; 994 MW; 342161ABI72EBAB7 CRC64;

Query Match 36.8%; Score 25; DB 11; Length 9;  
Best Local Similarity 66.7%; Pred. No. 8.3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY i CLEGGQ 6  
|||  
Db 4 CLEGG 9

RESULT 2

Q89243 PRELIMINARY; PRT; 12 AA.  
ID Q89243  
AC Q89243;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

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DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Core protein (Fragment).
CS Woodchuck hepatitis B virus.
CC Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.
CX NCBI_TaxID=35269;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W64;
RX MEDLINE=87219879; PubMed=3582979;
RA Eliceble J., Moroy T., Trepo C., Tiollais F., Buchdala M.A.;
RT "Nucleotide sequence of the woodchuck hepatitis virus surface antigen
RNAs and the variability of three overlapping viral genes.";
RL Gene 500:207-214(1986).
DR EMBL; M15954; AAA69576.1; -
DR InterPro; IPR02006; Hepatitis_core.
DR Pfam; PF03906; Hepatitis_core.1.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1388 MW; 22ABC172F2132B47 CRC64;

Query Match 29.4%; Score 20; DB 12; Length 12;
Best Local Similarity 75.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 MDVD 11
DB 11
DB 1 MDVD 4

RESULT 3
Q96P97 PRELIMINARY; PRT; 9 AA.
AC Q96P97;
DT 01 DEC-2001 (TrEMBLrel. 19, Created)
DT 01 DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01 DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Reptin52 Protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kang H.S., Park Y.J., Jung H.M., Kim D.Y., Han T.L., Kim Y.H.;
RT "Characterization of rPA-responsive genes in G47 cells using ordered
RT differential display PCR."
RL Submitted (JUL 2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401216; AAL02172.1; -
FT NON_TER 1
SQ SEQUENCE 9 AA; 981 MW; 5CDDAA682AB1873 CRC64;

Query Match 27.9%; Score 19; DB 47; Length 9;
Best Local Similarity 60.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GQVMD 9
DB 3 GETMD 7

RESULT 4
Q9LPT5 PRELIMINARY; PRT; 9 AA.
AC Q9LPT5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta-expansin-like protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Punicoidae; Andropogoneae; Zea.
CX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines."
RL Submitted (APR 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094308; AAM21834.1; -
FT NON_TER 1
SQ SEQUENCE 9 AA; 977 MW; 5C55B2D2CB1AAAA3 CRC64;

Query Match 27.9%; Score 19; DB 10; Length 9;
Best Local Similarity 42.9%; Pred. No. 8.3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDQVMD 9
DB 2 KDEVVD 8

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RP SEQUENCE FROM N.A.
RC STRAIN=CV. C123;
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.;
RA Morgante M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines."
RL Submitted (APR 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094310; AAM21836.1; -
FT NON_TER 1
SQ SEQUENCE 9 AA; 977 MW; 5C55B2D2CB1AAAA3 CRC64;

Query Match 27.9%; Score 19; DB 10; Length 9;
Best Local Similarity 42.9%; Pred. No. 8.3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDQVMD 9
DB 2 KDEVVD 8

RESULT 5
Q8LPT7 PRELIMINARY; PRT; 10 AA.
AC Q8LPT7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta-expansin-like protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Punicoidae; Andropogoneae; Zea.
CX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.;
RA Morgante M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines."
RL Submitted (APR 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094308; AAM21834.1; -
FT NON_TER 1
SQ SEQUENCE 10 AA; 1048 MW; 5C55B7DCB1AAAA3 CRC64;

Query Match 27.9%; Score 19; DB 10; Length 10;
Best Local Similarity 42.9%; Pred. No. 8.4e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDQVMD 9
DB 3 KDEVVD 9

RESULT 6
Q8LPT6 PRELIMINARY; PRT; 12 AA.
AC Q8LPT6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta-expansin-like protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Punicoidae; Andropogoneae; Zea.
CX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.;
RA Morgante M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in

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RT elite-raize inbred lines.";
RJ Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094309; AAM21835.1;
FT NON_TER 1
SQ SEQUENCE 12 AA; 1260 MW; 5055EDBD451AAAA3 CRC64;

Query Match 27.9%; Score 19; DB 10; Length 12;
Best Local Similarity 42.9%; Pred. No. 1.e+04;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 EDGQVMD 9
DB 5 KODEVVD 11

RESULT 7
Q9PX85 PRELIMINARY; PRT; 13 AA.
AC Q9PX85
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE 170 kDa DHBV pre-S region binding protein (Fragment).
OS Duck hepatitis B virus (DHBV).
OC Viruses; Retroviruses; Hepadnaviridae; Avihepadnavirus.
CX NCBI_TaxID=12639;
RN [1]
RX MEDLINE=96013813; PubMed=7474130;
RA Tong S., Li J., Wands J.R.;
RT "Interaction between duck hepatitis B virus and a 170-kilodalton
RT cellular protein is mediated through a neutralizing epitope of the pre-
RT S region and occurs during viral infection.";
RL J. Virol. 69:7106-7112(1995).
SQ SEQUENCE 13 AA; 1397 MW; DC478FE0149C0772 CRC64;

Query Match 27.9%; Score 19; DB 12; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.e+04;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEDGVV 7
DB 1 VREGKV 6

RESULT 8
Q9TRX0 PRELIMINARY; PRT; 11 AA.
AC Q9TRX0
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Lanosterol 14 alpha-demethylase, cytochrome P 45014X (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CX NCBI_TaxID=9823;
RN [1]
RX MEDLINE=91316123; PubMed=1859829;
RA Sono H., Sonoda Y., Sato Y.;
RT "Purification and characterization of cytochrome P 45014X (lanosterol:
RT 14 alpha-demethylase) from pig liver microsomes.";
RL Biochim. Biophys. Acta 1078:388-394(1991).
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1084 MW; 8A7ASCBC2AA72661 CRC64;

Query Match 26.5%; Score 18; DB 6; Length 11;
Best Local Similarity 44.4%; Pred. No. 1.4e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GQVMDVLL 13

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```

DB 1 GLLTGLDULL 9

RESULT 9
Q29831 PRELIMINARY; PRT; 11 AA.
AC Q29831
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Gene fragment encoding human histocompatibility antigen HLA-DR alpha
DE (exon 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=83169718; PubMed=6403940;
RA Das H.K., Biro P.A., Cohen S.N., Erlich H.A., von Gabain A.,
RA Lavrance S.K., Lemaux P.G., McDevitt H.O., Peterlin B.M., Schulz M.F.,
RA Sood A.K., Weissman S.M.;
RT "Use of synthetic oligonucleotide probes complementary to genes for
RT human HLA-DR alpha and beta as extension primers for the isolation of
RT 5' specific clones.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1531-1535(1983).
DR EMBL; V09525; CAA23784.1;
SQ SEQUENCE 11 AA; 1230 MW; 9378714E0865B1EA CRC64;

Query Match 26.5%; Score 18; DB 7; Length 11;
Best Local Similarity 37.5%; Pred. No. 1.4e+04;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CLEDGQV 8
DB 3 CDHSGRVL 10

RESULT 10
P97755 PRELIMINARY; PRT; 11 AA.
AC P97755
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE Secretogranin II (SGII) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RX MEDLINE=96143805; PubMed=8756552;
RA Jones L.C., Day R.N., Pittler S.J., Valentine D.L., Scammell J.G.;
RT "Cell-specific expression of the rat secretogranin II promoter.";
RL Endocrinology 137:3815-3822(1996).
DR EMBL; AF107301;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1298 MW; 3E4E8DA446C1B5A7 CRC64;

Query Match 26.5%; Score 18; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLE 3
DB 1 CLE 3

RESULT 11
Q5NTR7 PRELIMINARY; PRT; 12 AA.

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```
AC QNTW7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created);
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update);
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update);
DE C378NIC.1 (Eyes absent (Drosophila) homolog 4) (Fragment);
GN EY44;
CS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Dunn M.;
RL Submitted (MAY 2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121959; CAB92069.1;
FT NCN_TER 12
SQ SEQUENCE 12 AA; 1394 MW; C15EA7952D472AB6 CRC64;

Query Match 26.5%; Score 18; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEDGQ 6
DB : MEDSQ 5

RESULT 12
QNTW4
ID QNTW4 PRELIMINARY; PRT; 13 AA.
AC QNTW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created);
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update);
DE Peptide T-BRADYKININ potentiator.
OS Tityus serrulatus (Brazilian scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Ruthenidae; Tityidae; Tityus.
OX NCBI_TaxID=6887;
RN [1];
RP SEQUENCE.
RX MEDLINE=9424945; PubMed=8212046;
RA Ferreira L.A., Alves E.W., Henriques O.E.;
RC "Peptide T, a novel bradykinin potentiator isolated from Tityus
R serrulatus scorpion venom.";
RL Toxicon 31:941-947(1993).
SQ SEQUENCE 13 AA; 1694 MW; 3539E06443E23005 CRC64;

Query Match 26.5%; Score 18; DB 4; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.3e+04;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 EDGQMDVD 11
DB 2 KGGYPVEYD 10

RESULT 13
QNP395
ID QNP395 PRELIMINARY; PRT; 8 AA.
AC QNP395;
DT 01-OCT-2000 (TrEMBLrel. 15, Created);
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update);
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update);
DE Clotting factor VIII (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Shibata M., Shima M., Morichika S., Yoshida A.;
RC "Human clotting factor VIII gene, junction region, 1 kb upstream of
```

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RT exon 4 through 7.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; ABC40872; BAA34312.1;
FT NCN_TER 1
SQ SEQUENCE 8 AA; 866 MW; 1C16987AAB05BDD3 CRC64;

Query Match 25.0%; Score 17; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EDG 5
DB 4 EDG 6

RESULT 14
QNPV15
ID QNPV15 PRELIMINARY; PRT; 8 AA.
AC QNPV15;
DT 01-MAY-2000 (TrEMBLrel. 13, Created);
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update);
DE 18 kDa cell growth factor (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1];
RP SEQUENCE.
RX MEDLINE=92028975; PubMed=1656977;
RA Milner P.G.;
RC "Simian sarcoma virus transformation of normal rat kidney fibroblasts
RT is associated with markedly increased basic fibroblast growth factor
R expression.";
RL Biochem. Biophys. Res. Commun. 180:423-430(1991).
FT NCN_TER 1
SQ SEQUENCE 8 AA; 907 MW; B0787AAB07673AFA CRC64;

Query Match 25.0%; Score 17; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EDG 5
DB 5 EDG 7

RESULT 15
P83128
ID P83128 PRELIMINARY; PRT; 11 AA.
AC P83128;
DT 01-JUN-2002 (TrEMBLrel. 21, Created);
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update);
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update);
DE Pregnancy-associated glycoprotein (Fragment).
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9915;
RN [1];
RP SEQUENCE, AND GLYCOSYLATION.
RC TISSUE=Placenta;
RA Sousa N.M., Remy B., El Amri B., Figueiredo J.R., Beckers J.F.;
RC "Characterization of pregnancy-associated glycoproteins extracted from
RT zebu (Bos indicus) placentas removed at different gestational
R periods.";
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -1- EFM: GLYCOSYLATED.
KW Glycoprotein.
FT NCN_TER 1; 11
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SO SEQUENCE 1: AA; 1234 MW; CE8EA47EA0586B5D CRC64;  
Query Match 25.0%; Score 17; DB 6; Length 11;  
Best Local Similarity 30.0%; Pred. No. 2.1e+04;  
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
Qy 4 DQGVMDVLL 13  
Lh 1 DKNAVIGDLI 10

Search completed: November 5, 2003, 18:03:38  
Job time : 29.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 5, 2003, 17:56:03 ; Search time 34.5 Seconds  
(without alignment's)  
59.810 Million cell updates/sec

Title: US-09-914-088-8

Perfekt score: 68

Sequence: 1 CLEDCQVMDVLL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 299364

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	13	21	Antiallergy peptid
2	68	100.0	13	21	PI mimotope peptid
3	68	100.0	13	22	Peptide P15 deriv
4	68	100.0	13	22	IgE peptide #6. M
5	68	100.0	13	23	Human IgE immunoge
6	64	94.1	13	21	PI mimotope peptid
7	64	94.1	13	22	Peptide P15q deriv
8	64	94.1	13	22	Human IgE cyclic i
9	55	80.9	13	21	PI mimotope peptid

10	55	80.9	13	22	AAU16641	Peptide P15p deriv
11	55	80.9	13	23	ABJ00226	Human IgE immunoge
12	51	75.0	10	21	AAB25929	PI mimotope peptid
13	51	75.0	10	22	AAU16654	Peptide P15t deriv
14	51	75.0	10	23	ABJ00228	Human IgE immunoge
15	50	73.5	13	23	ABC00541	Human IgE cyclic i
16	47	69.1	9	21	AAB20867	Immunoglobulin E
17	47	69.1	9	21	AAB25907	IgE C-epsilon-2 do
18	47	69.1	9	22	AAU16632	Peptide P1 derived
19	47	69.1	9	22	AAB51023	IgE peptide #1. M
20	47	69.1	9	23	ABJ00217	Human IgE immunoge
21	45	66.2	10	24	AAB35057	Immunoglobulin E (
22	35	51.5	9	24	AAB35091	Human immunoglobul
23	34	50.0	7	21	AAB25923	PI mimotope peptid
24	34	50.0	7	22	AAU16648	Peptide P15s deriv
25	34	50.0	7	23	ABJ00227	Human IgE immunoge
26	34	50.0	9	24	AAB35076	Human immunoglobul
27	34	50.0	10	24	AAB35062	Immunoglobulin E (
28	33	48.5	11	21	AAB26010	Human IgE C-epsilo
29	33	48.5	11	22	AAU16735	Peptide ESB:/6etc
30	33	48.5	11	23	ABJ00265	Human IgE immunoge
31	31	45.6	11	19	AAB40426	Human CYP3A4 speci
32	30	44.1	9	24	AAB35101	Human immunoglobul
33	30	44.1	12	21	AAB25949	PI mimotope (PTAb
34	30	44.1	12	21	AAB26040	Human IgE C-epsilo
35	30	44.1	12	22	AAU16674	Peptide #15 deriv
36	30	44.1	12	22	AAU16765	Peptide EED147/173
37	30	44.1	12	23	ABJ00337	Human IgE cyclic i
38	30	44.1	12	23	ABJ00386	Human IgE cyclic i
39	29	42.6	9	24	AAB35082	Human immunoglobul
40	29	42.6	10	22	AAG84444	Arabidopsis thalia
41	29	42.6	10	22	AAG84446	Arabidopsis thalia
42	28	41.2	7	23	AAE14481	Oplophorus gracili
43	28	41.2	9	23	ABJ12891	Human 125P5C8 epit
44	28	41.2	10	23	AAB71434	Cobra CVF1 factor
45	28	41.2	10	23	ABG60432	Selective targetin

#### ALIGNMENTS

RESULT 1  
AAB20872  
ID AAB20872 standard; peptide; 13 AA.  
AC AAB20872;  
XX  
XX 03-JAN-2001 (first entry)  
XX  
DE Antiallergy peptide mimotope sequence SEQ ID NO:10.  
XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier;  
XX prostate cancer; Haemophilus influenzae; vaccine; infectious disease;  
XX malaria; cytostatic; antiallergic; nootropic; neuroprotective;  
XX protozoacide; Alzheimer's disease; allergy.  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Modified-site 13  
FT /note= "amidated"  
XX  
XX WO200050077-A1.  
XX  
XX 31-AUG-2000.  
XX  
XX 22-FEB-2000; 2003WO-EP01457.  
XX  
XX 25-FEB-1999; 99GB-0004405.  
XX 25-FEB-1999; 99GB-0004408.  
XX 25-FEB-1999; 99GB-0004412.  
XX 13-AUG-1999; 99GB-0019260.  
XX

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 (PEPT-) PEPTIDE THERAPEUTICS LTD.

PA Coste M, Lobet Y, Van-Mechelen XP, Verriest C;  
 PI WP1; 2000-572040/53.  
 XX Immunogens and vaccine comprising the immunogen useful for preventing  
 XX and treating infectious diseases e.g. malaria and chronic disease e.g.  
 XX cancer, comprises peptide and carrier from protein E of influenzae -  
 XX  
 PS Claim 10; Page 36; 53pp; English.

CC The present invention describes an immunogen (I) comprising a peptide  
 CC (Ia) and a carrier (Ib) derived from protein E of Haemophilus influenzae  
 CC or its fragment. Also described are: (1) a vaccine comprising (I), and  
 CC an excipient; (2) preparation of (I), comprising conjugating a peptide  
 CC to protein E or its fragment; and (3) preparation of a vaccine of (I),  
 CC comprising formulating (I) with an excipient. (I) has cytostatic,  
 CC anti-allergic, neurotropic, neuroprotective and proto-oncogene activities.  
 CC (I) and the vaccine are useful for the manufacture of a medicament for  
 CC preventing and treating infectious diseases such as malaria or chronic  
 CC disease such as cancer, Alzheimer's disease or allergy in a patient.  
 CC Unlike prior art immunogens, (I) induces high levels of anti-peptide  
 CC immune responses while inducing a moderate humoral response against the  
 CC carrier. The present sequence represents a specifically claimed  
 CC mimotope peptide sequence, which can be used in an immunogen of the  
 CC present invention.

XX  
 SQ Sequence 13 AA;  
 Query Match: 100.0%; Score 68; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00013;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEGGQVMDVLL 13  
 Db 1 CLEGGQVMDVLL 13  
 |||||

RESULT 2  
 AAB26914  
 ID AAB26914 standard; Peptide; 13 AA.  
 AC AAB26914.  
 XX  
 XX OS-JAN-2001 (first entry)  
 XX  
 XX P1: mimotope peptide P115 SEQ ID NO: 13.  
 XX Epitope: mimotope; human; immunoglobulin E (IgE) binding 2 domain;  
 KW allergic disease; immunoprophylaxis; immunotherapy; and allergy;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy.  
 XX  
 CS Homo sapiens.  
 XX  
 XX WQ2000050460 A1.  
 XX  
 XX 31 AUG-2003.  
 XX  
 XX 22-FEB-2003; 2000WO-EP01455.  
 XX  
 XX 25-FEB-1999; 99GB-0004405.  
 XX 29-MAR-1999; 99GB-0007151.  
 XX 07-MAY-1999; 99GB-0010537.  
 XX 07-MAY-1999; 99GB-0010538.  
 XX 07-AUG-1999; 99GB-0018594.  
 XX 07-AUG-1999; 99GB-0018603.  
 XX 07-SEP-1999; 99GB-0021046.  
 XX 07-SEP-1999; 99GB-0021047.  
 XX 29-OCT-1999; 99GB-0025619.  
 XX 23-NOV-1999; 99GB-0027698.

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 (PEPT-) PEPTIDE THERAPEUTICS LTD.

PA Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;  
 PI Randall R, Turnell WG, Van-Mechelen MP, Vinals De Baesols IC;  
 XX WP1; 2000-572073/53.  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 XX diseases, comprising an isolated surface exposed group of a specific  
 XX domain from immunoglobulin E.

PS Claim 14; Page 9; 129pp; English.

CC The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (E1) of C-epsilon-2 domain (D) of  
 CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an  
 CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III);  
 CC for treating allergies comprising (II); (3) a ligand (IV) capable of  
 CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
 CC (IIa) comprising (Ia); and (7) producing (III) by producing (II). (I)  
 CC can have anti-allergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (II), (III) and (IV) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (IV) is useful for identifying mimotopes of P1,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (II) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (I), (II), (III) and PC are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.

XX  
 SQ Sequence 13 AA;  
 Query Match: 100.0%; Score 68; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00013;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEGGQVMDVLL 13  
 Db 1 CLEGGQVMDVLL 13  
 |||||

RESULT 3  
 AAU16639  
 ID AAU16639 standard; Peptide; 13 AA.  
 XX AAU16639.  
 XX  
 XX 07-NOV-2001 (first entry)  
 XX  
 XX Peptide P15 derived as mimotope of Cepsilon2 region of human IgE.  
 XX Human; linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WQ200145745-A2.  
 XX  
 XX 28-JUN-2001.  
 XX  
 XX 21-FEB-2000; 2000WO-GR34935.  
 XX  
 XX 21-DEC-1999; 99GB-0030233.  
 XX 22-FEB-2000; 2000GB-0034096.  
 XX 22-AUG-2000; 2000GB-0020707.  
 XX 21-AUG-2000; 2000GB-0020708.

PA (ACM-) ACNVEIS RES LTD.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX PI P:inn N, Johnson T;  
XX WPI; 2001-521967/57.  
XX DR A linkage comprising an immunogenic conjugate useful treatment of IgE  
PT mediated diseases -  
XX  
XX Example 4; Page 21; 48pp; English.  
XX  
XX The present invention relates to linkage methodology for use in the  
CC conjugation of compounds (e.g. peptides) to carrier vehicles  
CC (e.g. macromolecules, polymers, dendrimers, proteins); to produce  
CC biological and immunological constructs. The invention provides a  
CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
CC protein) for use in a pharmaceutical composition or a vaccine. The  
CC invention describes peptides derived from or mimotopes of the  
CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
CC (IgE) which are used to produce conjugated compounds. The compounds or  
CC compositions of the invention are useful in the manufacture of a  
CC medicament for the treatment of IgE mediated diseases. The invention  
CC allows for controlled conjugation of a peptide epitope (antigen) to a  
CC protein so as to form an immunogenic conjugate which may be able to  
CC raise a protective antibody response in an animal or human patient.  
CC AAU1632-AAU16913 represent peptides derived from or mimotopes of  
CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
XX  
XX Sequence 13 AA;  
SQ

Query Match 100.0%; Score 68; DB 22; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00013;  
Matches 13; Conservative 0; Mismatches 0; Indels 3; Gaps 0;  
QY 1 CLEDGQVMDVLL 13  
DB 1 CLEDGQVMDVLL 13

RESULT 4  
AAB51028  
ID AAB51028 standard; Peptide; 13 AA.  
XX AC AAB51028;  
XX DT 21-MAR-2001 (first entry)  
XX DE IgE peptide #6.  
XX KW Vaccine; immunoglobulin E; IgE; anti-allergy.  
XX CS Mammalia.  
XX PN WC200074716-A2.  
XX PD 14-DEC-2000.  
XX PF 06 JUN-2000; 2000WO-EP05164.  
XX PR 08-JUN-1999; 99GB-0013327.  
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX PI Prieels J;  
XX WPI; 2001-091150/10.  
XX  
XX New vaccine comprising allergy peptides linked by an inert carrier,  
PT useful for boosting an anti-allergy immune response in an individual  
PT susceptible to an allergic response  
XX  
XX Claim 5; Page 20; 26pp; English.

XX  
CC The present invention relates to a composition comprising allergy  
CC peptides linked by an inert carrier. The allergy peptides are derived  
CC from Immunoglobulin E (IgE) or IgE receptor. The present peptide is one  
CC such peptide from IgE. The composition is useful as a vaccine or for  
CC manufacturing a medicament for the prophylaxis or treatment of allergy.  
CC In particular, for boosting an anti-allergy immune response in an  
CC individual susceptible to an allergic response.  
XX  
XX Sequence 13 AA;  
SQ

Query Match 100.0%; Score 68; DB 22; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00013;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CLEDGQVMDVLL 13  
DB 1 CLEDGQVMDVLL 13

RESULT 5  
ABJ00224  
ID ABJ00224 standard; Peptide; 13 AA.  
XX AC ABJ00224;  
XX DT 02-SEP-2002 (first entry)  
XX DE Human IgE immunogenic peptide SEQ ID NO: 8.  
XX KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
XX OS vaccine; antiallergic.  
XX OS Homo sapiens.  
XX PN WO200216409-A2.  
XX PD 28-FEB-2002.  
XX PF 17-AUG-2001; 2001WO-EP09576.  
XX PR 22-AUG-2000; 2000GB-0020717.  
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX PI Friede M, Mason S, Turnell WG, Vinals Bassols VC;  
XX DR WPI; 2002-489648/52.  
XX  
XX Conjugate for use in vaccine for treatment of allergy, comprises  
PT disulfide bridge cyclized peptide and immunogenic carrier -  
XX  
XX Claim 4; Page 9; 45pp; English.  
XX  
XX The present invention relates to conjugates suitable for use in vaccines,  
CC where the conjugate comprises a disulphide bridge cyclized peptide and an  
CC immunogenic carrier. The vaccines can be used in the treatment of  
CC allergies. The present sequence is a peptide immunogen derived from human  
CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
XX  
XX Sequence 13 AA;  
SQ

Query Match 100.0%; Score 68; DB 23; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00013;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CLEDGQVMDVLL 13  
DB 1 CLEDGQVMDVLL 13

RESULT 6





```

RESULT 8.
ID ABJ00312 standard; Peptide; 13 AA.
XX AC ABJ00312;
XX DT 02-SEP-2002 (first entry)
XX DE Human IgE cyclic immunogenic peptide SEQ ID NO: 96.
XX KW immunogen; human; IgE; immunoglobulin E; allergy; this-ether linkage;
XX KW vaccine; antiallergic; cyclic.
XX OS Homo sapiens.
XX PN WO200216439-A2.
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-EP09576.
XX PR 22-AUG-2000; 2000GB-0020717.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI Friede M, Mason S, Turnell WG, Vinals Bassols YC;
XX WP1; 2002-489648/52.
XX PT Conjugate for use in vaccine for treatment of allergy, comprises
XX PT disulfide bridge cyclized peptide and immunogenic carrier.
XX PS Claim 4; Page 11; 45pp; English.
XX CC The present invention relates to conjugates suitable for use in vaccines,
XX CC where the conjugate comprises a disulphide bridge cyclised peptide and an
XX CC immunogenic carrier. The vaccines can be used in the treatment of
XX CC allergies. The present sequence is a cyclic peptide immunogen derived
XX CC from human immunoglobulin E (IgE) suitable for use in the invention.
XX SQ Sequence 13 AA;
Query Match 94.1%; Score 64; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CLEGGQVMDVDL 12
Db 1 CLEGGQVMDVDL 12
RESULT 9
ID AAB25916 standard; Peptide; 13 AA.
XX AC AAB25916;
XX DT 05-JAN-2001 (first entry)
XX DE P1 mimotope peptide P15p SEQ ID NO:10.
XX KW Epitope; mimotope; human; immunoglobulin E; IgE; C epsilon 2 domain;
XX KW allergic disease; immunoprophylaxis; immunotherapy; antiallergic;
XX KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;
XX KW allergy; atopy.
XX OS Homo sapiens.
XX PN WC2000050460 A1.
XX PD 31-AUG-2000.
XX PF 17-AUG-2001; 2001WO-EP09576.
XX PR 22-AUG-2000; 2000GB-0020717.
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI Friede M, Mason S, Turnell WG, Vinals Bassols YC;
XX WP1; 2002-489648/52.
XX PT Conjugate for use in vaccine for treatment of allergy, comprises
XX PT disulfide bridge cyclized peptide and immunogenic carrier.
XX PS Claim 4; Page 11; 45pp; English.
XX CC The present invention relates to conjugates suitable for use in vaccines,
XX CC where the conjugate comprises a disulphide bridge cyclised peptide and an
XX CC immunogenic carrier. The vaccines can be used in the treatment of
XX CC allergies. The present sequence is a cyclic peptide immunogen derived
XX CC from human immunoglobulin E (IgE) suitable for use in the invention.
XX SQ Sequence 13 AA;
Query Match 94.1%; Score 64; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CLEGGQVMDVDL 12
Db 1 CLEGGQVMDVDL 12

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PF 22-FEB-2000; 2000WO-EP01455.
XX 25-FEB-1999; 99GB-0004405.
XX 29-MAR-1999; 99GB-0007151.
XX 07-MAY-1999; 99GB-0010517.
XX 07-MAY-1999; 99GB-0010518.
XX 07-AUG-1999; 99GB-0018594.
XX 07-AUG-1999; 99GB-0018603.
XX 07-SEP-1999; 99GB-0021046.
XX 29-SEP-1999; 99GB-0021047.
XX 29-OCT-1999; 99GB-0025619.
XX 23-NOV-1999; 99GB-0027698.
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;
XX PI Randall R, Turnell WG, Van Mechelen MP, Vinals De Bassols YC;
XX WP1; 2000-572073/53.
XX PT Peptides useful for treating, preventing and ameliorating allergic
XX PT diseases, comprising an isolated surface exposed group of a specific
XX PT domain from immunoglobulin E.
XX PS Disclosure; Page 9; 129pp; English.
XX CC The present invention describes a peptide (I) comprising an isolated
XX CC surface exposed group/epitope (E1) of C-epsilon-2 domain (3) of
XX CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an
XX CC immunogen (II) for treating allergy comprising (1); (2) a vaccine (III)
XX CC for treating allergies comprising (II); (3) a ligand (IV) capable of
XX CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);
XX CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen
XX CC (IIa) comprising (Ia); and (7) producing (III) by producing (II). (7)
XX CC can have antiallergic and immunosuppressive activities, and can be used
XX CC as a vaccine and histamine release inhibitor. (1), (II) and (III) are
XX CC useful in medicine and in the manufacture of medicaments for treating
XX CC and preventing allergies. (IV) is useful for identifying mimotopes of P1,
XX CC in medicine and also in manufacturing medicaments for treating
XX CC allergies. (I) is useful in diagnostics and in the affinity purification
XX CC of circulating anti-IgE antibodies from blood. (I), (III) and PC are
XX CC useful for treating a patient susceptible to or suffering from allergies.
XX CC (IV) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent
XX CC peptide sequences which are used in the exemplification of the present
XX CC invention.
XX SQ Sequence 13 AA;
Query Match 90.9%; Score 55; DB 21; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 LEDGQVMDVDL 12
Db 2 LEDGQVMDVDL 12
RESULT 10
AAU1664;
ID AAU16641 standard; Peptide; 13 AA.
XX AC AAU1664;
XX DT 07-NOV-2001 (first entry)
XX DE Peptide P15p derived as mimotope of Cepsilon2 region of human IgE.
XX KW Human; linkage technology; conjugated compound; carrier vehicle;
XX KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;
XX KW IgE mediated disease; antibody response.
XX OS Homo sapiens.

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OS Synthetic.
XX PN W0200145745-A2.
XX PC 28 JUN-2002.
XX PF 21-FEB-2000; 2000WC GR04935.
XX PP 21-FEB-1999; 99GB-C030233.
XX PR 22-FEB-2000; 2000GB-C004036.
XX PS 22-AUG-2000; 2000GB-C020752.
XX PT 22-AUG-2000; 2000GB-C020758.
XX PA (ACAM-) ACAMBIS RES LTD.
XX PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
XX PI Finn N. Johnson T;
XX PS WP1: 2001-521947/57.
XX PT A linkage comprising an immunogenic conjugate useful treatment of IgE
XX PT mediated diseases.
XX PS Example 4; Page 21; 49pp; English.
XX CC The present invention relates to linkage methodology for use in the
XX CC conjugation of compounds (e.g. peptides) to carrier vehicles
XX CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce
XX CC biological and immunological constructs. The invention provides a
XX CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a
XX CC protein) for use in a pharmaceutical composition or a vaccine. The
XX CC invention describes peptides derived from or mimotopes of the
XX CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E
XX CC (IgE) which are used to produce conjugated compounds. The compounds or
XX CC compositions of the invention are useful in the manufacture of a
XX CC medicament for the treatment of IgE-mediated diseases. The invention
XX CC allows for controlled conjugation of a peptide epitope (antigen) to a
XX CC protein so as to form an immunogenic conjugate which may be able to
XX CC raise a protective antibody response in an animal or human patient.
XX CC AA11632-AA11691 represent peptides derived from C1 mimotopes of
XX CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.
XX PS Sequence 13 AA;
XX CC
XX CC Query Match 80.9%; Score 55; DB 22; Length 13;
XX CC Best Local Similarity 100.0%; Pred. No. 0.018;
XX CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC QY 2 LEDGQVMDVL 12
XX CC DQ 11111111
XX CC DB 2 LEDGQVMDVL 12
XX CC
XX CC RESULT 12
XX CC AAB25929
XX CC ID AAB25929 standard; Peptide: 10 AA.
XX CC
XX CC AC AAB25929;
XX CC DT C5-JAN-2001 (first entry)
XX CC DE P1 mimotope peptide P1st SEQ ID NO:23.
XX CC
XX CC KW Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;
XX CC KW allergic disease; immunophylaxis; immunotherapy; antiallergic;
XX CC KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;
XX CC KW allergy; atopy.
XX CC OS Homo sapiens.
XX CC PN W0200050460-A1.
XX CC PD 31-AUG-2000.
XX CC PF 22-FEB-2000; 2000WC-EP01455.
XX CC
XX CC PR 25-FEB-1999; 99GB-C004425.
XX CC PR 29-MAR-1999; 99GB-C007151.
XX CC PR 07-MAY-1999; 99GB-C010537.
XX CC PR 07-MAY-1999; 99GB-C010538.
XX CC PR 07-AUG-1999; 99GB-C018594.
XX CC PR 07-AUG-1999; 99GB-C018603.
XX CC PR 07-SEP-1999; 99GB-C021046.
XX CC PR 07-SEP-1999; 99GB-C021047.
XX CC PR 29-OCT-1999; 99GB-C025619.
XX CC PR 23-NOV-1999; 99GB-C027698.
XX CC
XX CC PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
XX CC PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX CC
XX CC Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;
XX CC Randall R, Turnell WG, Van Mechelen MP, Vinals De Bassols YC;
XX CC WP1: 2000-572074/53.

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XX PR 22-AUG-2000; 2000GB-C020717.
XX PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI Friede M, Mason S, Turnell WG, Vinals Bassols YC;
XX PS WP1: 2002-489648/52.
XX CC Conjugate for use in vaccine for treatment of allergy, comprises
XX CC disulfide bridge cyclised peptide and immunogenic carrier.
XX PS Claim 4; Page 9; 45pp; English.
XX CC The present invention relates to conjugates suitable for use in vaccines,
XX CC where the conjugate comprises a disulphide bridge cyclised peptide and an
XX CC immunogenic carrier. The vaccines can be used in the treatment of
XX CC allergies. The present sequence is a peptide immunogen derived from human
XX CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.
XX PS Sequence 13 AA;
XX CC
XX CC Query Match 80.9%; Score 55; DB 23; Length 13;
XX CC Best Local Similarity 100.0%; Pred. No. 0.018;
XX CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC QY 2 LEDGQVMDVL 12
XX CC DQ 11111111
XX CC DB 2 LEDGQVMDVL 12
XX CC
XX CC RESULT 12
XX CC AAB25929
XX CC ID AAB25929 standard; Peptide: 10 AA.
XX CC
XX CC AC AAB25929;
XX CC DT C5-JAN-2001 (first entry)
XX CC DE P1 mimotope peptide P1st SEQ ID NO:23.
XX CC
XX CC KW Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;
XX CC KW allergic disease; immunophylaxis; immunotherapy; antiallergic;
XX CC KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;
XX CC KW allergy; atopy.
XX CC OS Homo sapiens.
XX CC PN W0200050460-A1.
XX CC PD 31-AUG-2000.
XX CC PF 22-FEB-2000; 2000WC-EP01455.
XX CC
XX CC PR 25-FEB-1999; 99GB-C004425.
XX CC PR 29-MAR-1999; 99GB-C007151.
XX CC PR 07-MAY-1999; 99GB-C010537.
XX CC PR 07-MAY-1999; 99GB-C010538.
XX CC PR 07-AUG-1999; 99GB-C018594.
XX CC PR 07-AUG-1999; 99GB-C018603.
XX CC PR 07-SEP-1999; 99GB-C021046.
XX CC PR 07-SEP-1999; 99GB-C021047.
XX CC PR 29-OCT-1999; 99GB-C025619.
XX CC PR 23-NOV-1999; 99GB-C027698.
XX CC
XX CC PA (SMIK-) SMITHKLINE BEECHAM BIOLOGICALS.
XX CC PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX CC
XX CC Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;
XX CC Randall R, Turnell WG, Van Mechelen MP, Vinals De Bassols YC;
XX CC WP1: 2000-572074/53.

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XX Peptides useful for treating, preventing and ameliorating allergic  
PT Diseases, comprising an isolated surface exposed group of a specific  
PT domain from immunoglobulin E -  
XX  
XX  
PS Disclosure; Page 9; 129pp; English.  
XX  
XX The present invention describes a peptide (I) comprising an isolated  
CC surface exposed group/epitope (E1) of C-epsilon-2 domain (D) of  
CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an  
CC immunogen (II) for treating allergy comprising (i), (2) a vaccine (III)  
CC for treating allergies comprising (II), (3) a ligand (IV) capable of  
CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
CC (Iia) comprising (Ia); and (7) producing (III) by producing (II). (I)  
CC can have anti-allergic and immunosuppressive activities, and can be used  
CC as a vaccine and histamine release inhibitor. (II), (III) and (IV) are  
CC useful in medicine and in the manufacture of medicaments for treating  
CC and preventing allergies. (IV) is useful for identifying mimotopes of E1,  
CC in medicine and also in manufacturing medicaments for treating  
CC allergies. (I) is useful in diagnostics and in the affinity purification  
CC of circulating anti-IgE antibodies from blood. (II), (III) and PC are  
CC useful for treating a patient susceptible to or suffering from allergies.  
CC (IV) is also useful in diagnosing atopy. AA425307 to AA436093 represent  
CC peptide sequences which are used in the exemplification of the present  
CC invention.  
XX  
XX SQ Sequence 10 AA;  
Query Match 75.0%; Score 51; DB 21; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 10; Conservative C; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LEDGQVMVDV 11  
DB 1 LEDGQVMVDV 10  
RESULT 13  
AAU16654  
ID AAU16654 standard; Peptide; 10 AA.  
AC AAU-6654;  
XX  
XX 07-NOV-2001 (first entry)  
XX Peptide P13c derived as mimotope of Cepsilon2 region of human IgE.  
XX Human; linkage technology; conjugated compound; carrier vehicles;  
KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
KW IgE mediated disease; antibody response.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS WC26C145745-A2.  
XX  
XX 28-JUN-2001.  
XX  
XX 21-DEC-2000; 2000WO-GB04935.  
XX  
XX 21-DEC-1999; 99GB-0030233.  
PR 22-FEB-2000; 2000GB-0004096.  
PR 22-AUG-2000; 2000GB-0020767.  
PR 22-AUG-2000; 2000GB-0020768.  
XX  
XX (ACAV-) ACAMBIS RES LTD.  
PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
XX F1:rm N, Johnson. T;  
XX WPI; 2001-521967/57.  
XX

PT A linkage comprising an immunogenic conjugate useful treatment of IgE  
PT mediated diseases -  
XX  
XX Example 4; Page 21; 48pp; English.  
XX  
XX The present invention relates to linkage methodology for use in the  
CC conjugation of compounds (e.g. peptides) to carrier vehicles  
CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
CC biological and immunological constructs. The invention provides a  
CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
CC protein) for use in a pharmaceutical composition or a vaccine. The  
CC invention describes peptides derived from or mimotopes of the  
CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
CC (IgE) which are used to produce conjugated compounds. The compounds or  
CC compositions of the invention are useful in the manufacture of a  
CC medicament for the treatment of IgE mediated diseases. The invention  
CC allows for controlled conjugation of a peptide epitope (antigen) to a  
CC protein so as to form an immunogenic conjugate which may be able to  
CC raise a protective antibody response in an animal or human patient.  
CC AAU16632-AAU16913 represent peptides derived from or mimotopes of  
CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
XX  
XX SQ Sequence 10 AA;  
Query Match 75.0%; Score 51; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LEDGQVMVDV 11  
DB 1 LEDGQVMVDV 10  
RESULT 14  
ABJ00228  
ID ABJ00228 standard; Peptide; 10 AA.  
XX  
XX ABJ00228;  
XX  
XX 02-SEP-2002 (first entry)  
XX Human IgE immunogenic peptide SEQ ID NO: 12.  
XX Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
KW vaccine; anti-allergic.  
XX  
XX Homo sapiens.  
OS WO200016409-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-EP09576.  
XX  
XX 22-AUG-2000; 2000GB-3020717.  
XX  
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX  
XX Friede M, Mason S, Turnell WG, Vinals Bassols YC;  
XX WPI; 2002-489648/52.  
XX  
XX Conjugate for use in vaccine for treatment of allergy, comprises  
PT disulfide bridge cyclized peptide and immunogenic carrier -  
XX  
XX Claim 4; Page 9; 45pp; English.  
XX  
XX The present invention relates to conjugates suitable for use in vaccines,  
CC where the conjugate comprises a disulfide bridge cyclised peptide and an  
CC immunogenic carrier. The vaccines can be used in the treatment of  
CC allergies. The present sequence is a peptide immunogen derived from human  
CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention.  
CC

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XX SQ Sequence 10 AA;
Query Match 75.0%; Score 51; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKDGQWMD 11
   |||||
DB 1 LKDGQWMD 10

RESULT 15
AB020541
ID AB020541 standard; Peptide; 10 AA.
XX AC AB020541;
XX DT 02-SEP-2002 (first entry)
XX DE Human IgE cyclic immunogenic peptide SEQ ID NO: 105.
XX KK Immunogen; human; IgE; immunoglobulin E; allergy; thio ether linkage;
XX KW vaccine; anti-allergic; cyclic.
XX CS Homo sapiens.
XX PK WP020216409-A2.
XX PD 29-SEP-2002.
XX FF 17 AUG-2001; 2001WO-EP29576.
XX PR 22-AUG-2000; 2000GB 0020717.
XX PA (SMR) SYNTHKONE BBSCHAM BIOMEDICALS.
XX PB (PPT) PEPTIDE THERAPEUTICS LTD
XX PC Fride M, Mason S, Turnell WJ, Vinals Bassalis YJ.
XX PE WPI: 2001 489648/52.
XX PT Conjugate for use in vaccine for treatment of allergy, comprises
XX PR disulfide bridge cyclized peptide and immunogenic carrier.
XX PS Claim 4; Page 16; 45pp; English.
XX CC The present invention relates to conjugates of a cyclic peptide vaccine,
XX CC which the conjugate comprises a disulfide bridge cyclized peptide and an
XX CC immunogenic carrier. The vaccine can be used in the treatment of
XX CC allergies. The present sequence is a cyclic peptide conjugate derived
XX CC from human immunoglobulin E (IgE) suitable for use in the invention.
XX SQ Sequence 10 AA;
Query Match 73.5%; Score 50; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLKDGQWMD 9
   |||||
DB 1 CLKDGQWMD 9

Search completed: November 5, 2003, 16:01:56
Job time : 34.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OX protein - protein search, using sw model

Run on: November 5, 2003, 19:03:44 ; Search time 22 seconds  
(without alignments)  
101.488 Million cell updates/sec

Title: US-09-914-088-8  
Perfect score: 68  
Sequence: 1 CLEGGQVMDVDLL 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 644079 segs, 171749292 residues

Total number of hits satisfying chosen parameters: 99933

Minimum DB seq length: 0  
Maximum DB seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by us-09-914-088-8 to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	49	72.1	10	12	US-10-372-076-136
3	47	69.1	9	12	US-10-082-014-273
4	47	69.1	9	12	US-10-372-076-127
5	45	66.2	10	12	US-10-144-188-55
6	34	50.0	10	12	US-10-144-188-60
7	29	42.6	10	12	US-09-572-270A-1084
8	29	42.6	10	12	US-09-572-270A-1080
9	28	41.2	7	10	US-09-842-164-12
10	28	41.2	10	10	US-09-925-442-1
11	27	39.7	13	11	US-09-862-151-1
12	26	38.2	10	11	US-09-572-404B-2983
13	25.5	37.5	12	11	US-09-922-568-2
14	25	36.8	10	15	US-10-155-922-72
15	25	36.8	11	11	US-09-863-049A-77

Sequence 11, Appl  
Sequence 2, Appl1  
Sequence 6, Appl1  
Sequence 10, Appl  
Sequence 14, Appl  
Sequence 18, Appl  
Sequence 22, Appl  
Sequence 434, App  
Sequence 556, App  
Sequence 475, App  
Sequence 475, App  
Sequence 502, App  
Sequence 613, App  
Sequence 502, App  
Sequence 602, App  
Sequence 513, App  
Sequence 8, Appl  
Sequence 22, Appl  
Sequence 1418, App  
Sequence 47, Appl  
Sequence 55, Appl  
Sequence 20, Appl  
Sequence 1189, App  
Sequence 535, App  
Sequence 633, App  
Sequence 458, App  
Sequence 591, App  
Sequence 102, App  
Sequence 196, App  
Sequence 504, App  
Sequence 163, App

ALIGNMENTS

RESULT 1  
US-10-082-014-282  
; Sequence 282, Application US/10082014  
; Publication No. US2003018585A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL  
; FILE REFERENCE: ICC-130.0 4364/85124  
; CURRENT APPLICATION NUMBER: US/10/082.014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/930,915  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 282  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-014-282

Query Match 72.1%, Score 49; DB 12; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.03;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LEDGQVMDVD 11  
Db 1 MEDGQVMDVD 10

RESULT 2  
US-10-372-076-136  
; Sequence 136, Application US/10372076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Page, Mark  
; APPLICANT: Friede, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS

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? FILE REFERENCE: 4564/87179
? CURRENT APPLICATION NUMBER: US/10/372,076
? CURRENT FILING DATE: 2003-02-21
? PRIOR APPLICATION NUMBER: 10/080,299
? PRIOR FILING DATE: 2002-02-21
? PRIOR APPLICATION NUMBER: 10/082,014
? PRIOR FILING DATE: 2002-02-22
? NUMBER OF SEQ ID NOS: 308
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 136
? LENGTH: 10
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-372-076 136
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Query Match 72.1%; Score 49; DB 12; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0%;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 2 LEDGQVMDVD 11
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Db 1 MEDGQVMDVD 10
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RESULT 3
US-10-082-014-273
? Sequence 273, Application US/10082014
? Publication No. US2003018588A1
? GENERAL INFORMATION:
? APPLICANT: Barker, Ashley J.
? TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
? FILE REFERENCE: ICC-130.9 4564/85124
? CURRENT APPLICATION NUMBER: US/10/082,014
? CURRENT FILING DATE: 2002-02-22
? PRIOR APPLICATION NUMBER: 09/930,915
? PRIOR FILING DATE: 2001-08-15
? NUMBER OF SEQ ID NOS: 290
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 273
? LENGTH: 9
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-082-014-273
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Query Match 69.1%; Score 47; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 0.0%;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EDGQVMDVD 11
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Db 1 EDGQVMDVD 9
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RESULT 4
US-10-372-076-127
? Sequence 127, Application US/10372076
? Publication No. US20030196645A1
? GENERAL INFORMATION:
? APPLICANT: Fiedle, Mark
? APPLICANT: Fiedle, Martin
? TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
? FILE REFERENCE: 4564/87179
? CURRENT APPLICATION NUMBER: US/10/372,076
? CURRENT FILING DATE: 2003-02-21
? PRIOR APPLICATION NUMBER: 10/080,299
? PRIOR FILING DATE: 2002-02-21
? PRIOR APPLICATION NUMBER: 10/082,014
? PRIOR FILING DATE: 2002-02-22
? NUMBER OF SEQ ID NOS: 308
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 127
? LENGTH: 9
? TYPE: PRT
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? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-372-076-127
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Query Match 69.1%; Score 47; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 3 EDGQVMDVD 11
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Db 1 EDGQVMDVD 9
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RESULT 5
US-10-144-188-55
? Sequence 55, Application US/10144188
? Publication No. US20030170212A1
? GENERAL INFORMATION:
? APPLICANT: Cai, Zeling
? APPLICANT: Jackson, Michael R.
? APPLICANT: Peterson, Per A.
? APPLICANT: Shi, Weixing
? APPLICANT: Kong, Yan
? APPLICANT: Degraw, Juli
? TITLE OF INVENTION: EX-VIVO Priming For Generating Cytotoxic T Lymphocytes Specif
? FILE REFERENCE: PR10010 ORT-1627
? CURRENT APPLICATION NUMBER: US/10/144,188
? CURRENT FILING DATE: 2002-05-13
? PRIOR APPLICATION NUMBER: 60/291,300
? PRIOR FILING DATE: 2001-05-15
? NUMBER OF SEQ ID NOS: 60
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 55
? LENGTH: 10
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Peptide antigen
US-10-144-188-55
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Query Match 66.2%; Score 45; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 LEDGQVMDVD 10
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Db 2 LEDGQVMDVD 10
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RESULT 6
US-10-144-188-60
? Sequence 60, Application US/10144188
? Publication No. US20030170212A1
? GENERAL INFORMATION:
? APPLICANT: Cai, Zeling
? APPLICANT: Jackson, Michael R.
? APPLICANT: Peterson, Per A.
? APPLICANT: Shi, Weixing
? APPLICANT: Kong, Yan
? APPLICANT: Degraw, Juli
? TITLE OF INVENTION: EX-VIVO Priming For Generating Cytotoxic T Lymphocytes Specif
? FILE REFERENCE: PR10010 ORT-1627
? CURRENT APPLICATION NUMBER: US/10/144,188
? CURRENT FILING DATE: 2002-05-13
? PRIOR APPLICATION NUMBER: 60/291,300
? PRIOR FILING DATE: 2001-05-15
? NUMBER OF SEQ ID NOS: 60
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 60
? LENGTH: 10
? TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide antigen
US-10-144 188-63

Query Match          50.0%; Score 34; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GQVMDVD 12
DB 1 GQVMDVD 7

RESULT 7
US-09-572-270A-1084
; Sequence 1084; Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572.270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1084
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in (AVA-P1 OR T4120.100) AND AVA-P2
US-09-572-270A-1084

Query Match          42.6%; Score 29; DB 12; Length 10;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GQVMDVD 11
DB 2 GQVLEVD 8

RESULT 8
US-09-572-270A-1086
; Sequence 1086; Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572.270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1086
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in (AVA-P1 OR T4120.100) AND AVA-P2
US-09-572-270A-1086

Query Match          42.6%; Score 29; DB 12; Length 10;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GQVMDVD 11
DB 3 GQVLEVD 9

RESULT 9
US-09-842-164-12
; Sequence 12; Application US/09842164
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; Patent No. US20020102687A1
; GENERAL INFORMATION:
; APPLICANT: INOUE, Satoshi
; TITLE OF INVENTION: Luciferase and Photoprotein
; FILE REFERENCE: 206497US0
; CURRENT APPLICATION NUMBER: US/09/842.164
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: JAPAN 2000-125053
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Oplophorus gracilirostris
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(7)
; OTHER INFORMATION: PRT, 35 kDa protein, partial
US-09-842-164-12

Query Match          41.2%; Score 28; DB 10; Length 7;
Best Local Similarity 71.4%; Pred. No. 5.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GQVMDVD 11
DB 1 GQVMDMD 7

RESULT 10
US-09-925-442-3
; Sequence 3; Application US/09925442
; Patent No. US20020103346A1
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; BREDEHORST, REINHORST
; KOCK, MICHAEL
; FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/925.442
; FILING DATE: 10-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/017,947
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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;; CURRENT FILING DATE: 2002-05-23  
;; PRIOR APPLICATION NUMBER: PCT/JP01/0469;  
;; PRIOR FILING DATE: 2001-06-04  
;; PRIOR APPLICATION NUMBER: JP 2000-166903  
;; PRIOR FILING DATE: 2000-06-05  
;; PRIOR APPLICATION NUMBER: JP 2001-347340  
;; PRIOR FILING DATE: 2001-11-13  
;; PRIOR APPLICATION NUMBER: JP 2001-347338  
;; PRIOR FILING DATE: 2001-11-13  
;; PRIOR APPLICATION NUMBER: JP 2001-371175  
;; PRIOR FILING DATE: 2001-12-05  
;; PRIOR APPLICATION NUMBER: JP 2001-371366  
;; PRIOR FILING DATE: 2001-12-05  
;; NUMBER OF SEQ ID NOS: 156  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 72  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic Construct  
;; NAME/KEY: VARIANT  
;; LOCATION: 7  
;; OTHER INFORMATION: Xaa - Any Amino Acid  
US 10-155-922-72

Query Match 36.8%; Score 25; DB 11; Length 10;  
Best Local Similarity 80.0%; Pred. No. 4.9e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 CLEGG 5  
DB 6 CXEDG 10

RESULT 15  
US-03-863 049A-77  
; Sequence 77, Application US/09863049A  
; Publication No. US2003032055A1  
; GENERAL INFORMATION:  
; APPLICANT: Kerwick, Sue J.  
; APPLICANT: Nelson, David L.  
; APPLICANT: Aradhyia, Swaroop  
; APPLICANT: D'Urso, Michele  
; APPLICANT: Woffendin, Hayley  
; APPLICANT: Munnich, Arnold  
; APPLICANT: Smahi, Asmae  
; APPLICANT: Israel, Alain  
; APPLICANT: Poustka, Annemarie  
; APPLICANT: Lewis, Richard A  
; APPLICANT: Levy, Moise  
; APPLICANT: Heiss, Nina  
; TITLE OF INVENTION: Diagnosis and Treatment of Medical Conditions Associated with Des  
; FILE REFERENCE: HO-201961US1  
; CURRENT APPLICATION NUMBER: US/09/863,049A  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/206,223  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 77  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human  
US-09-863 049A-77

Query Match 36.8%; Score 25; DB 11; Length 11;  
Best Local Similarity 66.7%; Pred. No. 4.9e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 1 CLEGG 6

Db  
4 CLEGG 9

Search completed: November 5, 2003, 18:11:58  
Job time : 23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

CM protein - protein search, using sw model

Run on: November 5, 2003, 18:30:39 : Search time 14 Seconds  
(without alignments)  
39.289 Million cell updates/sec

Title: US-09-914-088-8

Perfect score: 68

Sequence: 1 CLEGGQVMDVLL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 11:645

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/iaa/6B-COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS-COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	28	41.2	10	2	US-08-662-227-3
5	29	41.2	10	4	US-09-017-947-3
6	28	41.2	13	2	US-08-162-081B-13
7	28	41.2	13	2	US-08-780-872-13
8	28	41.2	13	3	US-09-085-957-13
9	27	39.7	8	4	US-09-057-937-15
10	27	39.7	10	2	US-08-724-548-28
11	27	39.7	10	2	US-08-724-548-23
12	27	39.7	10	3	US-07-978-674B-23
13	27	39.7	10	3	US-07-978-674B-29
14	27	39.7	12	3	US-09-238-448-8
15	27	39.7	13	4	US-09-341-435-57
16	26	38.2	8	1	US-08-571-985-20
17	26	38.2	8	2	US-09-116-766-20
18	26	38.2	11	3	US-07-861-458C-110
19	25.5	37.5	12	3	US-08-888-088A-2
20	25.5	37.5	12	3	US-08-257-781-9
21	25.5	37.5	12	3	US-09-577-027-2
22	25.5	37.5	12	5	PCT-US95-07157-9
23	25	36.8	8	1	US-08-571-985-26
24	25	36.8	8	2	US-09-116-766-26
25	25	36.8	10	4	US-08-398-852B-6
26	25	36.8	12	2	US-08-617-949-32
27	24	35.3	8	4	US-09-127-815D-2

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33	24	35.3	9	3	US-09-371-710-25
34	24	35.3	9	3	US-09-648-386-25
35	24	35.3	11	2	US-08-726-308A-134
36	24	35.3	11	3	US-08-836-480-38
37	24	35.3	11	3	US-09-562-897-38
38	24	35.3	13	1	US-07-842-089E-13
39	24	35.3	13	1	US-07-842-089E-19
40	24	35.3	13	1	US-08-264-485-13
41	24	35.3	13	1	US-08-264-485-19
42	24	35.3	13	2	US-08-580-988A-19
43	23	33.8	8	1	US-08-346-455B-47
44	23	33.8	8	3	US-08-977-221-47
45	23	33.8	8	4	US-09-483-831B-47

ALIGNMENTS

RESULT 1  
US-09-057-897-13  
; Sequence 13, Application US/09057897  
; Patent No. 6300476  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Anthony Y.H.  
; APPLICANT: Wang, Regina W.  
; TITLE OF INVENTION: Anti-Peptide Antibody Against Human  
; TITLE OF INVENTION: Cytochrome P450 3A4  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: US  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,897  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hand, J. Mark  
; REGISTRATION NUMBER: 36,545  
; REFERENCE/DOCKET NUMBER: 19902  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (732)594-3905  
; TELEFAX: (732)594-4720  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-057-897-13

Query Match 45.6%; Score 31; DB 4; Length 11;  
Best Local Similarity 63.6%; Red. No. 14;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CLEGGQVMDV 11  
DB 1 CLEDTQKRV 11

```

RESULT 2
US-09-842-164A-12
; Sequence 12, Application US/09842:164A
; Patent No. 6544754
; GENERAL INFORMATION:
; APPLICANT: INOUE, SATOSHI
; TITLE OF INVENTION: LUCIFERASE AND PHOTOPROTEIN
; FILE REFERENCE: 206497050
; CURRENT APPLICATION NUMBER: US/09/842,164A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: JP 2000 125053
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Opicphorus graciliorostris
US-09-842-164A-12

Query Match 41.2%; Score 28; DB 4; Length 7;
Best Local Similarity 71.4%; Pred. No. 2,56-65;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 5 EDGQMDVDL 11
DB 1 EDGFIADSDI 7

RESULT 3
US-09-447-411-46
; Sequence 46, Application US/08447:411
; Patent No. 5773243
; GENERAL INFORMATION:
; APPLICANT: FRITZINGER, DAVID C.
; APPLICANT: BREDEHORST, REINHARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: DNA ENCODING CBRA C3, CVP1, AND CVP2
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.0.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,411
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/043,747
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5773243mar F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-101-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```

```

; MOLECULE TYPE: peptide
US-08-447-411-46

Query Match 41.2%; Score 28; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CY 3 EDGQMDVDL 12
DB 1 EDGFIADSDI 10

RESULT 4
US-08-662-227-3
; Sequence 3, Application US/08662:227
; Patent No. 5922320
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/662,227
; FILING DATE: 14 JUN-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-662-227-3

Query Match 41.2%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CY 3 EDGQMDVDL 12
DB 1 EDGFIADSDI 10

RESULT 5
US-09-017-947-3
; Sequence 3, Application US/09017:947
; Patent No. 6303754
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL

```

APPLICANT: FRITZINGER, DAVID  
TITLE OF INVENTION: RECOMBINANT PROCVF  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
ADDRESSEE: 1755 S. JEFFERSON DAVIS HIGHWAY  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/017,947  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/662,227  
FILING DATE: 14-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 1126-0107-2X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-017-947-3

Query Match 41.2%; Score 28; DB 4; Length 10;  
Best Local Similarity 50.0%; Pred. No. 44;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 EDGQVMDVDL 12  
DB 1 EDGFIADSDI 10

RESULT 6  
US-08-162-081B-13  
Sequence 13, Application US/08162081B  
Patent No. 5824492  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano; Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/780,872  
FILING DATE: 09-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 839-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids

APPLICATION NUMBER: US/08/162,081B  
FILING DATE: February 7, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-162-081B-13

Query Match 41.2%; Score 28; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 60;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDGQVMDVD 11  
DB 1 DDGQLFHID 9

RESULT 7  
US-08-780-872-13  
Sequence 13, Application US/08780872  
Patent No. 5846824  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano; Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/780,872  
FILING DATE: 09-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 839-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids

? TYPE: amino acid  
? STRANDEDNESS: single  
? TOPOLOGY: linear  
US 08-780-872-13

Query Match 41.2% Score 29; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 60;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDGQWMDVD 11  
      :|:|:|:|  
DB 1 DGGQWMDVD 9

## RESULT 2

US-09-C85-957-13  
? Sequence 13, Application US/09085957

? Patent No. 6274327

? GENERAL INFORMATION:

? APPLICANT: Hales, Ian Donald; Fry, Michael John; Drand, Eric

? APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter

? APPLICANT: Joseph; Otsu, Masayuki; Panayiotou, George; Volinnia,

? APPLICANT: Stefano; Golt, Ivan Tarasovich

? TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,

? TITLE OF INVENTION: THEIR PREPARATION AND USE

? NUMBER OF SEQUENCES: 50

? CORRESPONDENCE ADDRESS:

? ADDRESSEE: Felfe & Lynch

? STREET: 805 Third Avenue

? CITY: New York

? STATE: New York

? CCOUNTRY: USA

? ZIP: 10022

? COMPUTER READABLE FORM:

? MEDIUM TYPE: Diskette, 5.25 inch, 360 kb st

? COMPUTER: IBM PS/2

? OPERATING SYSTEM: PC-DOS

? SOFTWARE: Wordperfect

? CURRENT APPLICATION DATA:

? APPLICATION NUMBER: US/09/085,957

? FILING DATE:

? CLASSIFICATION:

? PRIOR APPLICATION DATA:

? APPLICATION NUMBER: 08/780,872

? FILING DATE: 09-JAN-1997

? APPLICATION NUMBER: 08/152,041

? FILING DATE: February 7, 1994

? APPLICATION NUMBER: PCT/GB93/02961

? FILING DATE: 13 April 1993

? ATTORNEY/AGENT INFORMATION:

? NAME: Pasquardini, Patricia A.

? REGISTRATION NUMBER: 34,894

? REFERENCE/DOCKET NUMBER: LMD 5256

? TELECOMMUNICATION INFORMATION:

? TELEPHONE: (212) 688-9203

? TELEFAX: (212) 838-3884

? INFORMATION FOR SEQ ID NO: 13:

? SEQUENCE CHARACTERISTICS:

? LENGTH: 13 amino acids

? TYPE: amino acid

? STRANDEDNESS: single

? TOPOLOGY: linear

US-09-085 957 13

Query Match 41.2% Score 28; DB 1; Length 13;  
Best Local Similarity 44.4%; Pred. No. 60;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDGQWMDVD 11  
      :|:|:|:|  
DB 1 DGGQWMDVD 9

## RESULT 9

US-09-057-897-15

? Sequence 15, Application US/09057897

? Patent No. 6300476

? GENERAL INFORMATION:

? APPLICANT: Lu, Anthony Y.H.

? APPLICANT: Wang, Regina W.

? TITLE OF INVENTION: Anti-Peptide Antibody Against Human

? TITLE OF INVENTION: Cytochrome P450 3A4

? NUMBER OF SEQUENCES: 36

? CORRESPONDENCE ADDRESS:

? ADDRESSEE: Merck & Co., Inc.

? STREET: P.O. Box 2080

? CITY: Rahway

? STATE: NJ

? COUNTRY: US

? ZIP: 07065-0907

? COMPUTER READABLE FORM:

? MEDIUM TYPE: Floppy disk

? COMPUTER: IBM PC compatible

? OPERATING SYSTEM: PC-DOS/MS-DOS

? SOFTWARE: Patent In Release #1.0, Version #1.30

? CURRENT APPLICATION DATA:

? APPLICATION NUMBER: US/09/057,897

? FILING DATE:

? CLASSIFICATION:

? ATTORNEY/AGENT INFORMATION:

? NAME: Hand, J. Mark

? REGISTRATION NUMBER: 36,545

? REFERENCE/DOCKET NUMBER: 19902

? TELECOMMUNICATION INFORMATION:

? TELEPHONE: (732)594-3905

? TELEFAX: (732)594-4720

? INFORMATION FOR SEQ ID NO: 15:

? SEQUENCE CHARACTERISTICS:

? LENGTH: 8 amino acids

? TYPE: amino acid

? STRANDEDNESS: single

? TOPOLOGY: linear

? MOLECULE TYPE: peptide

US-09-057-897-15

Query Match 39.7% Score 27; DB 4; Length 8;  
Best Local Similarity 53.3%; Pred. No. 2.5e+05;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLEDTQ 6

DB 1 CLEDTQ 6

## RESULT 10

US-08-724-548-28

? Sequence 28, Application US/08724548

? Patent No. 5830637

? GENERAL INFORMATION:

? APPLICANT: Frank, Ronald

? APPLICANT: Guler, Sinan

? TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF

? TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR

? TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL

? TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND

? TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE

? TITLE OF INVENTION: PROCESS

? NUMBER OF SEQUENCES: 54

? CORRESPONDENCE ADDRESS:

? ADDRESSEE: Joseph T. Eisele

? ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,

? ADDRESSEE: Levy, Eisele and Richard

? STREET: 711 Third Avenue

? CITY: New York

? STATE: New York

? COUNTRY: U.S.A.

ZIP: 10017-4059  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3-1/2" DISKETTE  
COMPUTER: IBM-XT COMPATIBLE  
OPERATING SYSTEM: DOS 3.3:  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,548  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/978,674  
FILING DATE: 03/22/93  
ATTORNEY/AGENT INFORMATION:  
NAME: EISELE, JOSEPH T.  
REGISTRATION NUMBER: 25,331  
REFERENCE/DOCKET NUMBER: 2727-68 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 687-6000  
TELEFAX: (212) 682-3485  
TELEX: (212) 426767  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 residues  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: Peptide  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE: internal fragment  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
US-08-724 548 28

Query Match 39.7%; Score 27; DB 2; Length 10;  
Best local Similarity 50.0%; Ref. No. 67;  
Matches 5; Conservative 2; Mismatches 3; Gaps 0;

Cy 3 DDGQVMDVLL 12  
||| :|||  
Db 1 DDGGLDXDL 10

## RESULT 11

US-08-724-548-29

; Sequence 29, Application US/08724548

; Patent No. 5896637

; GENERAL INFORMATION:

; APPLICANT: Frank, Ronald

; TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF

; TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR

; TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL

; TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND

; TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Joseph T. Eisele

; ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,

; ADDRESSEE: Levy, Eisele and Richard

; STREET: 711 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10017-4059

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3-1/2" DISKETTE

; COMPUTER: IBM-XT COMPATIBLE

; OPERATING SYSTEM: DOS 3.3:

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/724,548

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/978,674

; FILING DATE: 03/22/93

; ATTORNEY/AGENT INFORMATION:

; NAME: EISELE, JOSEPH T.

; REGISTRATION NUMBER: 25,331

; REFERENCE/DOCKET NUMBER: 2727-68 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 687-6000

; TELEFAX: (212) 682-3485

; TELEX: (212) 426767

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 residues

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: LINEAR

; MOLECULE TYPE: Peptide

; HYPOTHETICAL:

; ANTI-SENSE:

; FRAGMENT TYPE: internal fragment

; ORIGINAL SOURCE:

; ORGANISM:

; STRAIN:

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE:

; HAPLOTYPE:

; TISSUE TYPE:

; CELL TYPE:

; CELL LINE:

; ORGANELLE:

; IMMEDIATE SOURCE:

; US-08-724 548 29

Query Match 39.7%; Score 27; DB 2; Length 10;

Best local Similarity 50.0%; Ref. No. 67;

Matches 5; Conservative 2; Mismatches 3; Gaps 0;

Cy 3 DDGQVMDVLL 12

||| :|||

Db 1 DDGGLDXDL 10

RESULT 11

US-08-724-548-29

; Sequence 29, Application US/08724548

; Patent No. 5896637

; GENERAL INFORMATION:

; APPLICANT: Frank, Ronald

; TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF

; TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR

; TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL

; TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND

; TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Joseph T. Eisele

; ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,

; ADDRESSEE: Levy, Eisele and Richard

; STREET: 711 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10017-4059

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3-1/2" DISKETTE

; COMPUTER: IBM-XT COMPATIBLE

; OPERATING SYSTEM: DOS 3.3:

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/724,548

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/978,674

; FILING DATE: 03/22/93

; ATTORNEY/AGENT INFORMATION:

; NAME: EISELE, JOSEPH T.

; REGISTRATION NUMBER: 25,331

; REFERENCE/DOCKET NUMBER: 2727-68 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 687-6000

; TELEFAX: (212) 682-3485

; TELEX: (212) 426767

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 residues

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: LINEAR

; MOLECULE TYPE: Peptide

; HYPOTHETICAL:

; ANTI-SENSE:

; FRAGMENT TYPE: internal fragment

; ORIGINAL SOURCE:

; ORGANISM:

; STRAIN:

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE:

; HAPLOTYPE:

; TISSUE TYPE:

; CELL TYPE:

; CELL LINE:

; ORGANELLE:

; IMMEDIATE SOURCE:

; US-08-724 548 30

Query Match 39.7%; Score 27; DB 2; Length 10;

Best local Similarity 50.0%; Ref. No. 67;

Matches 5; Conservative 2; Mismatches 3; Gaps 0;

Cy 3 DDGQVMDVLL 12

||| :|||

Db 1 DDGGLDXDL 10

RESULT 11

US-08-724-548-30

; Sequence 29, Application US/08724548

; Patent No. 5896637

; GENERAL INFORMATION:

; APPLICANT: Frank, Ronald

; TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF

; TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR

; TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL

; TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND

; TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Joseph T. Eisele

; ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,

; ADDRESSEE: Levy, Eisele and Richard

; STREET: 711 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10017-4059

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3-1/2" DISKETTE

; COMPUTER: IBM-XT COMPATIBLE

; OPERATING SYSTEM: DOS 3.3:

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/724,548

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/978,674

; FILING DATE: 03/22/93

; ATTORNEY/AGENT INFORMATION:

; NAME: EISELE, JOSEPH T.

; REGISTRATION NUMBER: 25,331

; REFERENCE/DOCKET NUMBER: 2727-68 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 687-6000

; TELEFAX: (212) 682-3485

; TELEX: (212) 426767

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 residues

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: LINEAR

; MOLECULE TYPE: Peptide

; HYPOTHETICAL:

; ANTI-SENSE:

; FRAGMENT TYPE: internal fragment

; ORIGINAL SOURCE:

; ORGANISM:

; STRAIN:

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE:

; HAPLOTYPE:

; TISSUE TYPE:

; CELL TYPE:

; CELL LINE:

; ORGANELLE:

; IMMEDIATE SOURCE:

; US-08-724 548 31

Query Match 39.7%; Score 27; DB 2; Length 10;

Best local Similarity 50.0%; Ref. No. 67;

Matches 5; Conservative 2; Mismatches 3; Gaps 0;

Cy 3 DDGQVMDVLL 12

||| :|||

Db 1 DDGGLDXDL 10

RESULT 11

US-08-724-548-31

; Sequence 29, Application US/08724548

; Patent No. 5896637

; GENERAL INFORMATION:

; APPLICANT: Frank, Ronald

; TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF

; TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR

; TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL

; TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND

; TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Joseph T. Eisele

; ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,

; ADDRESSEE: Levy, Eisele and Richard

; STREET: 711 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10017-4059

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3-1/2" DISKETTE

; COMPUTER: IBM-XT COMPATIBLE

; OPERATING SYSTEM: DOS 3.3:

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/724,548

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/978,674

; FILING DATE: 03/22/93

; ATTORNEY/AGENT INFORMATION:

; NAME: EISELE, JOSEPH T.

; REGISTRATION NUMBER: 25,331

; REFERENCE/DOCKET NUMBER: 2727-68 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 687-6000

; TELEFAX: (212) 682-3485

; TELEX: (212) 426767

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 residues

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: LINEAR

; MOLECULE TYPE: Peptide

; HYPOTHETICAL:

; ANTI-SENSE:

; FRAGMENT TYPE: internal fragment

; ORIGINAL SOURCE:

; ORGANISM:

; STRAIN:

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE:

; HAPLOTYPE:

; TISSUE TYPE:

; CELL TYPE:

; CELL LINE:

; ORGANELLE:

; IMMEDIATE SOURCE:

; US-08-724 548 32

Query Match 39.7%; Score 27; DB 2; Length 10;

Best local Similarity 50.0%; Ref. No. 67;

Matches 5; Conservative 2; Mismatches 3; Gaps 0;

Cy 3 DDGQVMDVLL 12

||| :|||

Db 1 DDGGLDXDL 10

RESULT 11

US-08-724-548-32

; Sequence 29, Application US/08724548

; Patent No. 5896637

; GENERAL INFORMATION:

; APPLICANT: Frank, Ronald

; TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF

; TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR

; TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL

; TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND

; TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Joseph T. Eisele

; ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,

; ADDRESSEE: Levy, Eisele and Richard

; STREET: 711 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10017-4059

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3-1/2" DISKETTE

STREET: 711 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10017-4059  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3-1/2" DISKETTE  
 COMPUTER: IBM-XT COMPATIBLE  
 OPERATING SYSTEM: DOS 3.3:  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/978,674B  
 FILING DATE: 03/22/93  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: EISELE, JOSEPH T.  
 REGISTRATION NUMBER: 25,331  
 REFERENCE/DOCKET NUMBER: 2727-68 PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 687-6000  
 TELEFAX: (212) 682-3485  
 TELEX: (212) 426767  
 INFORMATION FOR SEQ ID NO: 28:  
 LENGTH: 10 residues  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: LINEAR  
 MOLECULE TYPE: Peptide  
 HYPOCHETICAL:  
 ANTI-SENSE:  
 FRAGMENT TYPE: internal fragment  
 ORIGINAL SOURCE:  
 ORGANISM:  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL TYPE:  
 CELL LINE:  
 ORGANELLER:  
 IMMEDIATE SOURCE:  
 US 07 978 674B-24

Query Match 39.7% Score 27; DB 3; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 67;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 EGGQVMDL 12  
 DE 1 DPGGLXCL 10

RESULT 11  
 US-07 978 674B-24  
 Sequence 29, Application US/07978674B  
 Patent No. 6040423  
 GENERAL INFORMATION:  
 APPLICANT: Frank, Ronald  
 APPLICANT: Guier, Sinan  
 TITLE OF INVENTION: PROCESS FOR THE RAPID DETERMINATION OF  
 SUPPORT-BOUND OF FREE PEPTIDES  
 TITLE OF INVENTION: GLYCOPOLYMERES, A FEAT NUCLEOL  
 TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE IN  
 TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE  
 TITLE OF INVENTION: PROCESS  
 NUMBER OF SEQUENCES: 54  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Joseph T. Eisele

ADDRESSEE: Kane, Balsimer, Sullivan, Kurucz,  
 ADDRESSEE: Levy, Eisele and Richard  
 STREET: 711 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10017-4059  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3-1/2" DISKETTE  
 COMPUTER: IBM-XT COMPATIBLE  
 OPERATING SYSTEM: DOS 3.3:  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/978,674B  
 FILING DATE: 03/22/93  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: EISELE, JOSEPH T.  
 REGISTRATION NUMBER: 25,331  
 REFERENCE/DOCKET NUMBER: 2727-68 PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 687-6000  
 TELEFAX: (212) 682-3485  
 TELEX: (212) 426767  
 INFORMATION FOR SEQ ID NO: 29:  
 LENGTH: 10 residues  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: LINEAR  
 MOLECULE TYPE: Peptide  
 HYPOCHETICAL:  
 ANTI-SENSE:  
 FRAGMENT TYPE: internal fragment  
 ORIGINAL SOURCE:  
 ORGANISM:  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL TYPE:  
 CELL LINE:  
 ORGANELLER:  
 IMMEDIATE SOURCE:  
 US 07 978 674B-25

Query Match 39.7% Score 27; DB 3; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 67;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 DGOVMDVCL 13  
 DE 1 DPGGLXCL 10

RESULT 14  
 US-09-238-448-6  
 Sequence 8, Application US/09238448  
 Patent No. 6238925  
 GENERAL INFORMATION:  
 APPLICANT: Satpou, Hugh A.  
 TITLE OF INVENTION: Method for Determining Likelihood of Developing  
 TITLE OF INVENTION: Immunological Tolerance  
 FILE REFERENCE: HS 100  
 CURRENT APPLICATION NUMBER: US/09/238,448  
 CURRENT FILING DATE: 1999-01-28  
 EARLIER APPLICATION NUMBER: 60/073,171  
 EARLIER FILING DATE: 1998-01-10  
 NUMBER OF SEQ ID NOS: 10



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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-238-448-8

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Query Match          39.7% Score 27; DB 3; Length 12;
Best Local Similarity 83.3% Pred. No. 82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EDGQVM 8
   |||
Db 5 RDGKVM 10

```

```

RESULT 15
US-09-341-435-57
; Sequence 57, Application US/09341435
; Patent No. 651136;
; GENERAL INFORMATION:
; APPLICANT: TAKAHASHI, TOSHIYA
; APPLICANT: SAITO, NOBUO
; APPLICANT: TAKESHIGE, HIDEYUKI
; APPLICANT: TANAKA, TOSHIAKI
; APPLICANT: KAINOH, MIE
; TITLE OF INVENTION: CYCLIC PEPTIDES AND MEDICINAL USE THEREOF
; FILE REFERENCE: 2109-14
; CURRENT APPLICATION NUMBER: US/09/341,435
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: PCT/JP98/05096
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cyclic peptide
US-09-341-435-57

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Query Match          39.7% Score 27; DB 4; Length 13;
Best Local Similarity 40.0% Pred. No. 93;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLDSQVMGV 10
   |||
Db 1 CLDSPEHDSV 10

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Search completed: November 5, 2003, 18:04:57  
Job time : 15 secs

GeoCore version 3.1.2  
Copyright (c) 1993-2003 Compugen Ltd.

QM protein protein search, using sw model

Run on: November 5, 2003, 17:00:59 / Search time is 3 seconds  
without alignment  
56,163 Million cell updates/sec

Title: US-09-914-088 11

Perfect score: 73

Sequence: 1 GLENGQWQVQDLC17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616942 residues

Total number of hits satisfying chosen parameters: 1025

Minimum DB seq length: 6

Maximum DB seq length: 13

Post-processing: Minimum Match of

Maximum Match 100%

Listing first 45 summaries

Database: PIR261\*

1: PIR261\*

2: PIR261\*

3: PIR261\*

4: PIR261\*

Pred. No. is the number of results predicted by name in here 4  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	25	34	2	Q02106	hypothetical 1.4K protein - tomato chloroplast
2	25	34	2	Q02106	hypothetical 1.4K protein - tomato chloroplast
3	22	30	7	P14914	endo-1,4-beta-xylanase
4	21	29	8	A28413	H-hyosphorin
5	21	29	10	G08511	hypothetical prote
6	20	27	4	A60419	T-cell receptor be
7	20	27	10	G08511	T-cell receptor be
8	19	27	11	PS0283	parapara crystal
9	19	26	12	PS0160	NADP-cytochrome P4
10	19	26	13	S01243	hypothetical prote
11	18	24	10	A32295	alpha-macroglobulin
12	18	24	13	A33660	zinc-metallophosph
13	18	24	13	S47357	cardioexcitatory c
14	18	24	13	S66235	neomycin suppressin
15	17	24	12	140665	endo-1,4-beta-xylanase
16	17	23	6	PT0624	H-hyosphorin
17	17	23	6	PT0624	H-hyosphorin
18	17	23	7	PT0624	H-hyosphorin
19	17	23	7	PT0624	H-hyosphorin
20	17	23	10	PC4442	hypothetical 1.4K protein - potato chloroplast
21	17	23	10	PC4442	hypothetical 1.4K protein - potato chloroplast
22	17	23	12	C58502	hypothetical prote
23	17	23	12	C58502	hypothetical prote
24	17	23	12	C58502	hypothetical prote
25	17	23	12	C58502	hypothetical prote
26	17	23	12	C58502	hypothetical prote
27	17	23	12	C58502	hypothetical prote
28	17	23	12	C58502	hypothetical prote
29	16	21	9	A33660	zinc-metallophosph

30	16	21	10	A32543	cardioexcitatory c
31	16	21	10	A32543	cardioexcitatory c
32	16	21	11	S18301	neomycin suppressin
33	16	21	11	A34243	endo-1,4-beta-xylanase
34	16	21	12	A44794	H-hyosphorin
35	16	21	12	PH1172	hypothetical prote
36	16	21	13	PH1172	hypothetical prote
37	16	21	13	PH1172	hypothetical prote
38	15	20	6	R34815	ig heavy chain DJ
39	15	20	10	PH2907	tubulin alpha-chain
40	15	20	10	PH2907	dnaA protein Pse
41	15	20	10	PH2907	T-cell receptor al
42	15	20	11	S14087	T-cell receptor be
43	15	20	11	S18185	parapara crystal
44	15	20	12	H34082	NADP-cytochrome P4
45	15	20	12	S29764	hypothetical prote
			12	S48209	alpha-macroglobulin
			12	S48209	zinc-metallophosph

ALIGNMENTS

RESULT 1

Q02106  
hypothetical 1.4K protein - tomato chloroplast (strain Toko)  
C:Species: chloroplast Lycopersicon esculentum (tomato)  
C>Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 23-Mar-1995  
C:Accession: Q02106  
R:Kawagoe, Y.; Kikuta, Y.  
Theor. Appl. Genet. 91, 13 20, 1991  
A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.)  
A:Reference number: Q02106  
A:Accession: Q02106  
A:Molecule type: DNA  
A:Residues: 1-12 <RAW>  
A:Experimental source: strain Toko  
C:Genetics:  
A:Genome: chloroplast  
C:Keywords: chloroplast

Query Match 34.2% Score 25; DB 2; length 12;  
Best Local Similarity 50.0%; Pied. No. 4.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QV	R	MSVDLC 13
Ec	4	11085-9

RESULT 2

Q02108  
hypothetical 1.4K protein - potato chloroplast  
C:Species: chloroplast Solanum tuberosum (potato)  
C>Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 05-Jan-1996  
C:Accession: Q02108; Q02113  
R:Kawagoe, Y.; Kikuta, Y.  
Theor. Appl. Genet. 91, 13 20, 1991  
A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.)  
A:Reference number: Q02106  
A:Accession: Q02108  
A:Molecule type: DNA  
A:Residues: 1-12 <RW1>  
A:Experimental source: cv. W553-4  
A:Accession: Q02113  
A:Molecule type: DNA  
A:Residues: 1-12 <RW2>  
A:Experimental source: cv. 150  
C:Genetics:  
A:Genome: chloroplast  
C:Keywords: chloroplast

Query Match 4.4% Score 35; DB 2; length 12;  
Best Local Similarity 50.0%; Pied. No. 4.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;



Best Local Similarity 50.0%; Score 18; DB 2; Length 10;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EVGQVM 4  
DB 4 EVGQVM 4

RESULT 9  
PN0160  
Ribosomal protein S16 - fungus (Fusarium sporotrichoides) (fragment)  
C:Species: Fusarium sporotrichoides  
C:Date: 25 Aug 1994 #sequence\_revision 11 Nov 1994  
C:Accession: PN0160  
R:Kukaya, N.; Chow, L.P.; Sugita, A.; Kono, Y.; Tanuchi, K.  
submitted to JGIPD, May 1994  
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichoides  
A:Reference number: PN0160  
A:Accession: PN0160  
A:Molecule type: protein  
A:Residues: 1-12 <PK>  
C:Keywords: protein biosynthesis; ribosome

Query Match 26.0%; Score 19; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 4; Indels 0;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 VMDVD 11  
DB 4 VMDVD 12

RESULT 10  
S01045  
Glutamate ammonia lyase (EC 6.3.1.2) - fungus yeast, Schizosaccharomyces pombe (fragment)  
N:Alternative names: glutamate synthetase  
C:Species: Schizosaccharomyces pombe  
C:Date: 07-Sep-1993 #sequence\_revision 27-Sep-1993 #text\_change 06 Jun 2002  
C:Accession: S01045  
R:Rate, L.; Ridel, G.; Simpson, A.; Mathias, J., Jr.  
Cell. Genet. 23, 487-494, 1988  
A:Title: Isolation of a DNA fragment which complements the in vivo synthetase deficient strain  
A:Reference number: S01045; MIM:298295.2; PMID:315559  
A:Accession: S01045  
A:Molecule type: DNA  
A:Residues: 1-13 <PK>  
A:Cross-references: EMBL:X00978; NID:952745.7; PID:CAAR4750.1; PDB:527452  
C:Keywords: lyase

Query Match 26.0%; Score 19; DB 2; Length 10;  
Best Local Similarity 42.0%; Pred. No. 4; Indels 0;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VMDVD 13  
DB 4 VMDVD 12

RESULT 11  
A02195  
NirXK+ exchanging ATPase (EC 3.6.3.9) alpha chain - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C:Date: 20-Oct-1989 #sequence\_revision 26-Oct-1989 #text\_change 13 Apr 2002  
C:Accession: A02195  
R:Tyson, B.A.; Steinberg, M.; Wallick, B.T.; Kallay, J.C.  
Cell. Biochem. 284, 726-734, 1989  
A:Title: Identification of the 5'-coding strand of the gene for the Na,K ATPase  
A:Reference number: A02195; MIM:289021.1; PMID:249191  
A:Accession: A02195  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-16 <PK>  
C:Keywords: hydrolase

Query Match 24.7%; Score 18; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 5; Indels 0;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 VMD 13  
DB 2 VMD 5

RESULT 12  
A03660  
osteoclast functional antigen alpha chain - green monkey (fragment)  
C:Species: Cercopithecus aethiops (green monkey, grivet)  
C:Date: 30 Mar 1993 #sequence\_revision 30-Mar-1993 #text\_change 23 Mar 1995  
C:Accession: A03660  
R:Davies, C.; Watwick, J.; Torry, N.; Philp, R.; Helfrich, M.; Horton, M.  
Cell Biol. 109, 1817-1824, 1989  
A:Title: The osteoclast functional antigen, implicated in the regulation of bone resorption  
A:Reference number: A03660; MIM:300905.4; PMID:2477382  
A:Accession: A03660  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <PK>  
A:Experimental source: a green monkey kidney Vero cell line

Query Match 24.7%; Score 18; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 7; Indels 0;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 MVD 11  
DB 3 MVD 6

RESULT 13  
S47157  
T-cell antigen receptor VJ junction beta chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05 Nov 1999  
C:Accession: S47157  
R:Lehner, P.C.  
submitted to the EMBL Data Library, August 1994  
A:Description: Human HLA A2.01 restricted recognition of influenza A is dominated by T  
A:Reference number: S47157  
A:Accession: S47157  
A:Status: Preliminary  
A:Molecule type: RNA  
A:Residues: 1-13 <PK>  
A:Cross-references: EMBL:Z15681; NID:952745.7; PID:CAAR4750.1; PDB:527452  
C:Keywords: T-cell receptor

Query Match 24.7%; Score 18; DB 2; Length 13;  
Best Local Similarity 53.3%; Pred. No. 7; Indels 0;  
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CLEGGQMD 9  
DB 1 CASSCRSTD 9

RESULT 14  
S66235  
sperm motility inhibitor protein - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 14 Feb 1997 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S66235  
R:Watanabe, T.; Hiroaki, H.; Furutani, Y.; Wada, K.; Satoh, M.; Osada, T.; Gao  
PDB Lett. 366, 420-424, 1995  
A:Title: Cloning of boar SMI gene which is expressed specifically in seminal vesicle  
A:Reference number: S66235; MIM:361314; PMID:7635190  
A:Accession: S66235  
A:Status: Preliminary

A:Molecule type: Protein  
A:Residues: 133 <LWA>  
A:Note: P126 was also found

Query Match 24.0% Score 10.5; ID: 1; Length: 133.  
Best Local Similarity 50.0%; P126, No. 7, 1999  
Matches 3; Conservative 2; Mismatches 1; Indels 1; Gaps 0.

QY 3 EGGVUM 8  
|||  
Db 7 EGGVUM 12

RESULT 15  
140663  
Bma protein, Clostridium cochlearium filament.  
C:Species: Clostridium cochlearium  
C:Date: 12-Aug-1996 #sequence\_revision 12 Aug 1996 #ext. change 13-Oct-1999  
C:Accession: 140663; S47465  
P:Zeiger, C.; Beatrix, B.; Leutbecher, D.; Buckel, W.  
E:J. Biochem. 226: 577-585, 1994  
A:Title: Characterization of the coenzyme B12-dependent glutamate mutase from Clostridium  
A:Reference number: 140659; X01039504816; F0103949251  
A:Accession: 140663  
A>Status: preliminary; translated from DB/EMBL/DBA  
A:Molecule type: DBA  
A:Residues: 132 <RES>  
A:Cross references: EMBL: X80997; NID: J540256; PDB: 1A55-14; 1A55-15; 1A55-16; 1A55-17  
C:Genetics:  
A:Gene: Bma

Query Match 24.0% Score 10.5; ID: 1; Length: 133.  
Best Local Similarity 50.0%; P126, No. 7, 1999  
Matches 3; Conservative 2; Mismatches 1; Indels 1; Gaps 0.

QY 6 QVNVVLC 13  
|||  
Db 2 KIVV 10 5

Creation completed: November 5, 2003, 18:54:16  
Run time: 1.13 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Computer Ltd.

CM protein: protein search, using sw model

Run on: November 5, 2003, 17:50:33 : Search time for the data  
without alignment  
64,352 Matches, 101 of them/seq

Title: US-09-914-088-11  
Perfect score: 13  
Sequence: 1 MLESGQWMDVCLC 13

Scoring table: BLASTX62  
Gapop 10.0 , Gapext 0.5

Searched: 127563 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 5

Minimum hit seq length: 0  
Maximum hit seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARY:

Result No.	Score	Query Match	Length	ID	Description
1	30	27.4	10	GAJU_HUMAN	P1366 Homo sapien
2	19	24.3	12	V23K_WSSV	P82055 white spot
3	18	24.3	8	ACT_CARMR	P80199 carinatus ma
4	17	23.1	13	UJAI_HUMAN	P36049 Homo sapien
5	16	21.9	8	PLP_EBARR	P14707 translocat na
6	16	21.9	10	FARP_EBARR	P14707 translocat na
7	16	21.9	10	FARP_EBARR	P14707 translocat na
8	16	21.9	10	MALE_KLEIN	P14707 translocat na
9	16	21.9	12	US9A_RAT	P14707 translocat na
10	16	21.9	12	NO4C_SCHEN	P14707 translocat na
11	16	21.9	13	GEA2_HPV1	P14707 translocat na
12	15	20.5	9	D1_NERNG	P14707 translocat na
13	15	20.5	10	PRCK_FASHE	P14707 translocat na
14	15	20.5	10	SPT_BALFO	P14707 translocat na
15	15	20.5	12	LICH_BAWEL	P14707 translocat na
16	15	20.5	13	GER1_HCVU	P14707 translocat na
17	14	19.2	9	PARD_GALVO	P14707 translocat na
18	14	19.2	10	UJAI_HUMAN	P14707 translocat na
19	14	19.2	11	CA41_LITRI	P14707 translocat na
20	14	19.2	11	RR2_TGMAN	P14707 translocat na
21	14	19.2	12	CA41_GCMIM	P14707 translocat na
22	14	19.2	12	PA2B_VIBRO	P14707 translocat na
23	14	19.2	13	ACT7_SCHEN	P14707 translocat na
24	14	19.2	13	ADFB_TERNV	P14707 translocat na
25	14.5	18.5	9	UF02_MUSE	P14707 translocat na
26	13	17.8	9	WPI_PPRAT	P14707 translocat na
27	13	17.8	9	ENFI_LCUM	P14707 translocat na
28	13	17.8	9	UPA6_HUMAN	P14707 translocat na
29	13	17.8	10	AP6_GGAL	P14707 translocat na
30	13	17.8	10	COMC_SAT	P14707 translocat na
31	13	17.8	10	GMZ2_CHEEP	P14707 translocat na
32	13	17.8	10	SP34_PLMC	P14707 translocat na
33	13	17.8	10	UMA6_CHLTR	P14707 translocat na

44	13	17.8	12	1	VEG6_BACSU	P80699 bacillus su
45	13	17.8	11	1	CA21_EITCI	P82087 litoria cit
46	13	17.8	11	1	CAL2_CCMR	P58807 conus marmo
47	13	17.8	11	1	FAP6_PENVO	P83321 penaeus ven
48	13	17.8	11	1	RFP2_CHAV	P13179 chandipura
49	13	17.8	12	1	CD14_LITXA	P56245 litoria xan
50	13	17.8	12	1	CD14_LITXA	P56245 litoria xan
51	13	17.8	12	1	CYL3_CCMR	P58909 conus marmo
52	13	17.8	12	1	K340_SESRO	O24358 sessanta ro
53	13	17.8	12	1	SPS1_DROVI	P17645 drosophila
54	13	17.8	12	1	XYLA_STROV	P14405 streptomyce
55	13	17.8	13	1	CXLA_CCMR	P59810 conus marmo

ALIGNMENTS

RESULT 1  
GAJU\_HUMAN  
ID GACU\_HUMAN STANDARD: PRT: 10 AA.  
AC P01358;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Gastric juice peptide.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN 11;  
RP SEQUENCE.  
RX MEDLINE=75150368; PubMed=5518385;  
RA Heathcote J.G., Washington R.J.;  
RT "Peptides of normal human gastric juice";  
RL Int. J. Protein Res. 2:117-126(1970).  
DR PIR; A01628; GKH11;  
DR MIM; 137230;  
CR GC; GO:0007586; P:digestion; NAS.  
FT PEPTIDE 1 10  
FT PEPTIDE 2 10  
SQ SEQUENCE 10 AA; 1004 MW; CFE6GAB02C3367D CRC64;

Query Match 27.4% Score 20; DB 1; Length 10;

Best Local Similarity 50.0%; Pred. No. 1.1e-03;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OV 1 LENGTH=10  
DB 1; LAGAKVENSEU 10

RESULT 2  
V23K\_WSSV  
ID V23K\_WSSV STANDARD: PRT: 12 AA.  
AC P82055;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 23 kDa structural glycoprotein (Fragment).  
OS White spot syndrome virus (WSSV).  
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.  
OX NCBI\_TaxID=92652;  
RN 11;  
RP SEQUENCE.

STRAIN=South Carolina;  
RX MEDLINE=20114217; PubMed=10752552;  
RA Wang Q., Follis B.T., Lightner D.V.;  
RT "Protein analysis of geographic isolates of shrimp white spot syndrome virus";  
RL Arch. Virol. 145:261-274(2000).  
CR 11;  
FT FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.  
SQ SEQUENCE 12 AA; 1323 MW; 3CF4F1E91D51A724 CRC64;









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SQ SEQUENCE 9 AA: 1028 MW: 60ECT9VA6D9D92VB CFC64;
Query Match 20.5% Score 15; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EDQG 6
DB 2 EDQG 5

RESULT 13
PECK FASHE STANDARD; PRT; 10 AA
AC PRG525;
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.11)
DE (Phosphoenolpyruvate carboxyase) (PEPCK) (Newly expressed juvenile
protein 1) (Fragment)
DE PASCOLA HEPARICA (Liver fluke).
OS Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea
CC Echinostomidae; Echinostomata; Fasciolidae; Fasciolidae; Fasciola
CX NCBI_TaxID=6592;
RN [1]
RP SEQUENCE.
RX MEDLINE=9536698; PubMed=763732;
RA Kraljevic J., Ashman K., Veessen E.J.
PT "Fasciola hepatica: rapid identification of newly expressed juvenile
proteins";
RC Biochem. Biophys. Res. Commun. 233:163-174(1998);
CC 1- CATALYTIC ACTIVITY: GTP + oxaloacetate + H2O + phosphoenolpyruvate
+ CO2
CC 1- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE (GTP)
FAMILY
KW InterPro: IPR003664; PEP carboxykin.
DR PROSITE: PS00505; PEPCK_GTP; PARTIAL
KW Lyase; Decarboxylase; GTP-binding.
FT NKM_TSF 10
SQ SEQUENCE 10 AA: 1069 MW: 819AA619AA978A CFC64;

Query Match 20.5% Score 15; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 INQNM 9
DB 6 DQNAV 10

RESULT 14
SPI BALBC STANDARD; PRT; 10 AA
AC OLQ987;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1996 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (Fragment)
OS Halcystidia corezi (Sea squirt)
CC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia
CX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE.
RX TISSUE: Hemolymph; PubMed=8793295;
RA Shishikura F., Abe T., Ohtake S., Iizuka K.
DE "Purification and characterization of a 59,000 Da proteinase
inhibitor from the hemolymph of a solitary ascidian, Halcystidia
corezi";
RC Corp. Biochem. Biophys. 154B:1-9(1999);
CC 1- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA KINETIN. ACTIVITY
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CC 1- SUBUNIT: MONOMER.
CC 1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro: IPR00215; Serpin.
KW PROSITE: PS00284; SERPIN; PARTIAL.
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.
FT NKM_TSF 10
SQ SEQUENCE 10 AA: 1104 MW: 4225C73B19187AA3 CFC64;

Query Match 20.5% Score 15; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EDQG 6
DB 3 KDGE 6

RESULT 15
LICH BACLI STANDARD; PRT; 12 AA
AC P82907;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lichenus...
OS Bacillus licheniformis.
CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE.
RX STRAIN=26L-10/3RA;
RX MEDLINE=1460732; PubMed=11578302;
RA Pattnaik P., Kaushik J.K., Grover S., Batish V.K.;
PT "Purification and characterization of a bacteriocin-like compound
(Ribocin) produced anaerobically by Bacillus licheniformis isolated
from water buffalo";
RT J. Appl. Microbiol. 91:636-645(2001);
RN [2]
RP SEQUENCE.
RX STRAIN=26L-10/3RA;
RA Pattnaik P.;
PT "Biochemical characterization and molecular genetics of bacteriocin
produced by a selected rumen bacterial isolate";
RC Thesis (1999), National Dairy Research Institute / Karnal, India.
CC 1- FUNCTION: OXGEN LABILE BACTERIOICIN LIKE. HAS ANTIBACTERIAL
ACTIVITY.
CC 1- SUBCELLULAR LOCATION: Secreted.
KW Antibiotic; Bacteriocin.
SQ SEQUENCE 12 AA: 1414 MW: 1C05B56CFC4AEEB0 CFC64;

Query Match 20.5% Score 15; DB 1; Length 12;
Best Local Similarity 16.7%; Pred. No. 9e+03;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 8 NFDVLC 11
DB 1 ISLEIC 6

Search completed: Nov+Dec 5, 2003, 18:02:29
Job time : 3.5 secs
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```
PT C1-OCT-2001 (TIEVBLrel. 22, Last annotation update)
RE Early nodulin endodermis
OS Trifolium repens (Leguminosae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; rosids; Fabaceae;
OC entegale 1; Fabales; Fabaceae; Papilionoideae; Trifolium; Trifolium
CX NCBI TaxID=3899;
RN
RP
SQ SEQUENCE FROM N.A.
RA MEDLINE=22111131; PubMed 12114569;
RA Varkanyi-Basic E., White D.W.;
RT "The White Clover erod4C Gene Family: Expression Patterns of ER Types
RT of Genes Indicate a Role in Vascular Function";
RL Plant Physiol. 129:1107-1118(2002);
DR EMBL AF424440; AAK81037.1;
SC SEQUENCE 12 AA; 1405 MW; 306965857B2A215F34;

Query Match 27.4%; Score 20; DB 16; Length 12;
Best Local Similarity 75.0%; Pred. No. 7.6e-04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 VMDVLC 13
QZ 1 MLC 4

RESULT 3
Q9243 PRELIMINARY; PRT; 12 AA.
AC Q9243;
DT C1-NOV-1996 (TIEVBLrel. 01, Created);
DT C1-NOV-1996 (TIEVBLrel. 01, Last sequence update);
DT C1-OCT-2001 (TIEVBLrel. 18, Last annotation update);
DE Goto protein (fragment);
OS Woodchuck hepatitis B virus;
OC Viruses; Retroviruses; Hepadnaviridae; with replicase;
CX NCBI TaxID=35369;
RN
RP SEQUENCE FROM N.A.
RA STRAIN=64;
RX MEDLINE=8714836; PubMed=3382979;
RA Scheraga J., Morley T., Trepo C., Tishman J., Pomeroy M.B.;
RT "Nucleotide sequence of the woodchuck hepatitis virus surface
RT antigen and the variability of three coding regions";
RL Gene 500:271-284(1991);
LR EMBL Y55044; AAK43576.1;
DR InterPro:IP00046; Hepatitis vir;
DR Pfam:PF00046; Hepatitis core 1;
FT MEN TER 12 12
SC SEQUENCE 12 AA; 1398 MW; 21A9C2E610E91616;

Query Match 27.4%; Score 20; DB 16; Length 12;
Best Local Similarity 75.0%; Pred. No. 7.6e-04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 MVE 11
QZ 1 MLC 4

RESULT 4
Q9243 PRELIMINARY; PRT; 12 AA.
AC Q9243;
DT C1-NOV-1996 (TIEVBLrel. 01, Created);
DT C1-NOV-1996 (TIEVBLrel. 01, Last sequence update);
DT C1-NOV-1996 (TIEVBLrel. 01, Last annotation update);
DE Plus expression protein (fragment);
OS Pseudomonas syringae;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Proteobacteria;
OC Pseudomonadales; Pseudomonas;
CX NCBI TaxID=317;

PT C1-OCT-2001 (TIEVBLrel. 22, Last annotation update)
RE Early nodulin endodermis
OS Trifolium repens (Leguminosae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; rosids; Fabaceae;
OC entegale 1; Fabales; Fabaceae; Papilionoideae; Trifolium; Trifolium
CX NCBI TaxID=3899;
RN
RP
SQ SEQUENCE FROM N.A.
RA MEDLINE=22111131; PubMed 12114569;
RA Varkanyi-Basic E., White D.W.;
RT "The White Clover erod4C Gene Family: Expression Patterns of ER Types
RT of Genes Indicate a Role in Vascular Function";
RL Plant Physiol. 129:1107-1118(2002);
DR EMBL AF424440; AAK81037.1;
SC SEQUENCE 12 AA; 1405 MW; 306965857B2A215F34;

Query Match 27.4%; Score 20; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 8.2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 VMDVLC 13
QZ 7 LGVSLC 13

RESULT 5
Q96P97 PRELIMINARY; PRT; 9 AA.
AC Q96P97;
DT C1-DEC-2001 (TIEVBLrel. 19, Created);
DT C1-DEC-2001 (TIEVBLrel. 19, Last sequence update);
DT C1-DEC-2001 (TIEVBLrel. 19, Last annotation update);
DE Reptin52 protein (fragment);
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
CX NCBI TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RA Kang H.S., Park Y.-J., Jung H.M., Kim D.Y., Huh T.L., Kim Y.H.;
RT "Characterization of tPA responsive genes in U937 cells using ordered
RT differential display PCR";
RL Submitted (JUL 2001) to the EMBL/GenBank/DBJ databases;
DR EMBL AF401216; AAL0172.1;
FT MEN TER 1 1
SC SEQUENCE 9 AA; 981 MW; 5CDDAA681A51873 CRC64;

Query Match 46.0%; Score 19; DB 4; Length 9;
Best Local Similarity 40.0%; Pred. No. 8.3e-05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCMQ 1
QZ 3 GCMQ 7

RESULT 6
Q96P97 PRELIMINARY; PRT; 9 AA.
AC Q96P97;
DT C1-OCT-2001 (TIEVBLrel. 22, Created);
DT C1-OCT-2001 (TIEVBLrel. 22, Last sequence update);
DT C1-OCT-2001 (TIEVBLrel. 22, Last annotation update);
DE Beta-expansin like protein (fragment);
OS Zea mays (Maize);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAU Clade; Pan. 10; Andropogoneae; Zea;
CX NCBI TaxID=4573;
RN
RP SEQUENCE FROM N.A.
RA STRAIN CV-2231;
RA Chung A.S., Gutierrez R.S., Jung M., Dolan M., Smith C.S., Timney S.;
PA "Genomic organization of the beta-expansin gene and linkage disequilibrium in
PA Zea mays inbred lines";
RT Submitted Apr. 2001 to the EMBL/GenBank/DBJ databases;
CX NCBI TaxID=317;
```

DR EMBL: AY094100; AA021836.1; ...  
 FC NON TER  
 SQ SEQUENCE 3 AA; 977 MW; 5055800 POLYMAA; (Frag);  
 Query Match  
 Best Local Similarity 42.9%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CV 3 EDQVMD 9  
 DB 5 KLEUVD 11

RESULT 9  
 ID 076614 PRELIMINARY; PST: 13 AA;  
 AC C05614;  
 DT 01-NOV-1998 (TRENDS)rel. 08, Created;  
 DT 01-NOV-1998 (TRENDS)rel. 04, Last sequence update;  
 DT 01-DEC-2001 (TRENDS)rel. 19, Last annotation update;  
 DE DNA fragment which complements glutamine synthetase deficient strains (Fragment);  
 DE (Fragment);  
 OS Schizosaccharomyces pombe (Fission Yeast);  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes;  
 OC Schizosaccharomycetes;  
 OC NCBI TaxID:4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:86295229; PubMed 2903077;  
 RA Bate, I., Birnle, G., Sirpso, A., Macdonald D.,  
 RT "Isolation of a DNA fragment which complements glutamine synthetase deficient strains of S. pombe";  
 RC Curr. Genet. 13:497-499 (1988);  
 DR EMBL: X0976; CAA3789.1; ...  
 FT NON TER 13  
 SQ SEQUENCE 13 AA; 1454 MW; 49448593433AC57 CRC64;

Query Match  
 Best Local Similarity 42.9%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

CV 7 VMWVDC 13  
 DB 6 LLSADAC 12

RESULT 10  
 ID 041X8 PRELIMINARY; PST: 13 AA;  
 AC 041X8;  
 DT 01-MAY-2000 (TRENDS)rel. 19, Created;  
 DT 01-MAY-2000 (TRENDS)rel. 19, Last sequence update;  
 DT 01-JUN-2000 (TRENDS)rel. 19, Last annotation update;  
 DE 170 kDa DBV pre S region binding protein (Fragment);  
 OS Duck hepatitis B virus (DHBV);  
 OC Viruses; Petoviridae; Hepadnaviridae; Avihepadnavirus;  
 OC NCBI TaxID:12639;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE:9601813; PubMed:1474112;  
 RA Tong S., Li J., Wands J.R.;  
 RT "Interaction between duck hepatitis B virus and a 170-kilodalton cellular protein is mediated through a neutralizing epitope of the pre-S region and occurs during viral infection";  
 RC J. Virol. 69:715-7112 (1995);  
 DR J. Virol. 69:715-7112 (1995);  
 FT NON TER 13  
 SQ SEQUENCE 13 AA; 1197 MW; DC478FE0148CD772 CRC64;

Query Match  
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CV 2 LDCQV 7  
 DB 1 VEEKV 7

RESULT 11

DR EMBL: AY094100; AA021836.1; ...  
 FC NON TER  
 SQ SEQUENCE 3 AA; 977 MW; 5055800 POLYMAA; (Frag);  
 Query Match  
 Best Local Similarity 42.9%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CV 3 EDQVMD 9  
 DB 5 KLEUVD 11

RESULT 9  
 ID 076614 PRELIMINARY; PST: 13 AA;  
 AC C05614;  
 DT 01-NOV-1998 (TRENDS)rel. 08, Created;  
 DT 01-NOV-1998 (TRENDS)rel. 04, Last sequence update;  
 DT 01-DEC-2001 (TRENDS)rel. 19, Last annotation update;  
 DE DNA fragment which complements glutamine synthetase deficient strains (Fragment);  
 DE (Fragment);  
 OS Schizosaccharomyces pombe (Fission Yeast);  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes;  
 OC Schizosaccharomycetes;  
 OC NCBI TaxID:4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:86295229; PubMed 2903077;  
 RA Bate, I., Birnle, G., Sirpso, A., Macdonald D.,  
 RT "Isolation of a DNA fragment which complements glutamine synthetase deficient strains of S. pombe";  
 RC Curr. Genet. 13:497-499 (1988);  
 DR EMBL: X0976; CAA3789.1; ...  
 FT NON TER 13  
 SQ SEQUENCE 13 AA; 1454 MW; 49448593433AC57 CRC64;

Query Match  
 Best Local Similarity 42.9%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

CV 7 VMWVDC 13  
 DB 6 LLSADAC 12

RESULT 10  
 ID 041X8 PRELIMINARY; PST: 13 AA;  
 AC 041X8;  
 DT 01-MAY-2000 (TRENDS)rel. 19, Created;  
 DT 01-MAY-2000 (TRENDS)rel. 19, Last sequence update;  
 DT 01-JUN-2000 (TRENDS)rel. 19, Last annotation update;  
 DE 170 kDa DBV pre S region binding protein (Fragment);  
 OS Duck hepatitis B virus (DHBV);  
 OC Viruses; Petoviridae; Hepadnaviridae; Avihepadnavirus;  
 OC NCBI TaxID:12639;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE:9601813; PubMed:1474112;  
 RA Tong S., Li J., Wands J.R.;  
 RT "Interaction between duck hepatitis B virus and a 170-kilodalton cellular protein is mediated through a neutralizing epitope of the pre-S region and occurs during viral infection";  
 RC J. Virol. 69:715-7112 (1995);  
 DR J. Virol. 69:715-7112 (1995);  
 FT NON TER 13  
 SQ SEQUENCE 13 AA; 1197 MW; DC478FE0148CD772 CRC64;

Query Match  
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CV 2 LDCQV 7  
 DB 1 VEEKV 7

RESULT 11



RN (1)  
 RP SEQUENCE FROM N.A.  
 PA CDS X.1  
 PD Submitted (MAY-2003) to the EMBL/GenBank/DBP databases  
 DR EMBL; Accession: CAB92069.1; 1  
 FT NON TER 12  
 SQ SEQUENCE 12 AA: 1594 MW: 115474.14 DALY 0.0004  
 Query Match 24.74 Score 18.18 43.10000 124  
 Percentical Similarity 60.04 Pred. No. 124  
 Matches 31 Conservative 17 Mismatches 17 Indels 0 Gaps 0  
 CY 2 LDDGQ F  
 DD : MEDGQ S

Search completed: November 5, 2003, 18:01:34  
 Job time : 27.5 secs





19 23-NOV-1999; 9A05 0022699.  
 XX (SMIK : SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT : PEPTIDE THERAPEUTICS LTD.  
 XX  
 XX Dymally M., Friede M., Greenwood J., Hewitt E., Lambert A., Mason S.,  
 P1 Randall R., Turnell W.G., Van Vechelien M.P., Vinals De Bassols YC;  
 XX WPI: 2000-572673/53.  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 XX Claim 14: Page 9; 129pp; English.  
 XX  
 XX The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (E1) of Cεpsilon 2 domain (D) of  
 CC immunoglobulin E (IgE), or its mimotope. Also described are: (II) an  
 CC immunogen (I1) for treating allergy comprising (I1), (I2) a vaccine (I11)  
 CC for treating allergies comprising (I1), (I3) a ligand (I14) capable of  
 CC recognising (I1), (I4) a pharmaceutical composition (I15) comprising (I1),  
 CC (I3), a peptide (I16) capable of being recognised by (I1), (I6) an immunogen  
 CC (I17), comprising (I16); and (I7) producing (I16) by producing (I1), (I1)  
 CC can have antiallergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (I1), (I11) and (I11) are  
 CC useful in medicine and in the manufacture of reagents for treating  
 CC and preventing allergies. (I16) is useful for identifying mimotopes of (I),  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (I1) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (I1), (I11) and (I16) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (I16) is also useful in diagnosing allergy. AAD5903 or AAD5903 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX  
 XX Sequence 13 AA:  
 QY 1 CLEGGQWMDVLC 13  
 DB 1 CLEGGQWMDVLC 13  
 1 1 1 1 1 1 1 1 1 1 1 1 1  
 1 CLEGGQWMDVLC 13  
 RESULT 2  
 AAD5643  
 CC AAD5643 standard; Peptide; 13 AA.  
 XX  
 XX AAD5643  
 CC 02-SEP-2002 (first entry)  
 XX  
 XX Peptide P14 derived as mimotope of Cεpsilon 2 domain of human IgE  
 XX Human linkage technology; conjugated compound; Part of molecule.  
 XX epitope; Cεpsilon2; Cεpsilon2; Cεpsilon2; Cεpsilon2; Cεpsilon2; Cεpsilon2;  
 XX IgE mediated disease; antibody response.  
 XX  
 XX Homo sapiens.  
 XX Synthetic.  
 XX  
 XX W0203145745 A2  
 XX 28-JUN-2003  
 XX  
 XX 21-SEP-2003; 2003WO-0020707.  
 XX  
 XX 21-SEP-1999; 1999-0030243.  
 XX 20-SEP-2003; 2003WO-004096.  
 XX 23-AUG-2000; 2000GP-0020707.

BR 22-AUG-2000; 2000GB-0020708.  
 XX  
 XX (ACAM : ACAMBI RES LTD.  
 PA (SMIK : SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 XX Flint N., Johnson T;  
 XX WPI: 2001-521963/57  
 XX  
 XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
 PT mediated diseases  
 XX  
 XX Example 4; Page 21; 48pp; English.  
 XX  
 XX The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC Cεpsilon2, Cεpsilon3 or Cεpsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAD5642-AAD5643 represent peptides derived from or mimotopes of:  
 CC the Cεpsilon2/Cεpsilon3/Cεpsilon4 region of human IgE.  
 XX  
 XX Sequence 13 AA:  
 QY 1 CLEGGQWMDVLC 13  
 DB 1 CLEGGQWMDVLC 13  
 1 1 1 1 1 1 1 1 1 1 1 1 1  
 1 CLEGGQWMDVLC 13  
 RESULT 2  
 AAD5643  
 CC AAD5643 standard; Peptide; 13 AA.  
 XX  
 XX AAD5643  
 CC 02-SEP-2002 (first entry)  
 XX  
 XX Human IgE cyclic immunogenic peptide SEQ ID NO: 96.  
 XX Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 XX vaccine; antiallergic; cyclic.  
 XX  
 XX Homo sapiens.  
 XX  
 XX W0203146409 A2.  
 XX 26-FEB-2002.  
 XX  
 XX 17-AUG-2001; 2001WO-EP09576.  
 XX  
 XX 22-AUG-2000; 2000GB-0020717.  
 XX  
 XX (SMIK : SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT : PEPTIDE THERAPEUTICS LTD.  
 XX  
 XX Friede M., Mason S., Turnell W.G., Vinals De Bassols YC;  
 XX WPI: 2000-499647/52.  
 XX  
 XX Conjugate for use in vaccine for treatment of allergy, comprises

PT disulfide bridge cyclized peptide and immunogenic carrier  
 PS Claim 4, Page 11, 45pp; English.  
 CC The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a cyclic peptide derived  
 CC from human immunoglobulin E (IgE) suitable for use in the invention  
 XX  
 SQ Sequence 13 AA;  
 Query Match 87.73; Score 64; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CLEGGQWMDVLC 13  
 Db 1 CLEGGQWMDVLC 13  
 RESULT 4  
 AAB25914  
 ID AAB25914 standard; peptide; 13 AA  
 XX  
 AC AAB25914  
 XX  
 DT 03 JAN 2001 (first entry)  
 XX  
 DE Antiallergy peptide mimotope SEQ ID NO:11  
 KW Immunoglobulin E, IgE; immunogenic; immunogen; Protein E; carrier;  
 KW prostate cancer; haemophilus influenzae; vaccine; infectious disease;  
 KW malaria; cytotoxic; antiallergic; nocturnal; neurodegenerative;  
 KW proinflammatory; Alzheimer's disease; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2002050403 A1.  
 XX  
 PD 31 AUG 2002  
 XX  
 PF 22 FEB 2003; 2002WO-EP01455.  
 XX  
 PS 25-FEB 1999; 99GB 0004405.  
 PS 29-MAR 1999; 99GB 0002752.  
 PS 07-MAY 1999; 99GB 0005370.  
 PS 07-MAY 1999; 99GB 0005380.  
 PS 07-AUG 1999; 99GB 0016594.  
 PS 07-AUG 1999; 99GB 0016621.  
 PS 07-SEP 1999; 99GB 0021046.  
 PS 07-SEP 1999; 99GB 0021047.  
 PS 29-OCT-1999; 99GB 0025619.  
 PS 23-NOV 1999; 99GB 0027698.  
 XX  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;  
 PI Ramsdell P, Turnell WG, Van Neechelen WP, Vinals De Bassols YC;  
 XX  
 DR WPI: 2002 57207/53.  
 XX  
 PT Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 PS Claim 10, Page 18; 53pp; English.  
 CC The present invention describes an immunogen comprising a peptide  
 CC (Ia) and a carrier (Ib) derived from protein E of hemophilus influenzae  
 CC or its fragments. Also described are (II) a vaccine comprising (I) and  
 CC an adjuvant; (2) preparation of (I), comprising (I) and a fragment  
 CC to prevent (I) or its fragment; and (3) preparation of a vaccine (I) and  
 CC containing formulation (I) with an excipient, and (4) a starting  
 CC antiallergic, noctropic, neuroprotective and flat of the immunogen  
 CC (I) and the vaccine are useful for the treatment of allergy and for

CC preventing and treating infectious diseases such as malaria or chronic  
 CC disease such as cancer, Alzheimer's disease or allergy in a patient.  
 CC Unlike prior art immunogens, (I) induces high levels of antipeptide  
 CC immune responses while inducing a moderate humoral response against the  
 CC carrier. The present sequence represents a specifically claimed  
 CC mimotope peptide sequence, which can be used in an immunogen of the  
 CC present invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 87.73; Score 64; DB 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CLEGGQWMDVLC 12  
 Db 1 CLEGGQWMDVLC 12  
 RESULT 5  
 AAB25914  
 ID AAB25914 standard; peptide; 13 AA  
 XX  
 AC AAB25914  
 XX  
 DT 03 JAN 2001 (first entry)  
 XX  
 DE PI mimotope peptide PT15 SEQ ID NO:8.  
 KW Epitope; mimotope; human; immunoglobulin E, IgE; C-epsilon-2 domain;  
 KW allergic disease; immunoprophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2002050403 A1.  
 XX  
 PD 31 AUG 2002  
 XX  
 PF 22 FEB 2003; 2002WO-EP01455.  
 XX  
 PS 25-FEB 1999; 99GB 0004405.  
 PS 29-MAR 1999; 99GB 0002752.  
 PS 07-MAY 1999; 99GB 0005370.  
 PS 07-MAY 1999; 99GB 0005380.  
 PS 07-AUG 1999; 99GB 0016594.  
 PS 07-AUG 1999; 99GB 0016621.  
 PS 07-SEP 1999; 99GB 0021046.  
 PS 07-SEP 1999; 99GB 0021047.  
 PS 29-OCT-1999; 99GB 0025619.  
 PS 23-NOV 1999; 99GB 0027698.  
 XX  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;  
 PI Ramsdell P, Turnell WG, Van Neechelen WP, Vinals De Bassols YC;  
 XX  
 DR WPI: 2002 57207/53.  
 XX  
 PT Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 PS Claim 14, Page 9, 129pp; English.  
 CC The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed epitope (E1) of C-epsilon-2 domain (D) of  
 CC immunoglobulin E (IgE), or its mimotope. Also described are: (i) an  
 CC immunogen comprising (I) and an adjuvant; (ii) a vaccine (I) and  
 CC containing formulation (I) with an excipient; (iii) a starting  
 CC antiallergic, noctropic, neuroprotective and flat of the immunogen  
 CC (I) and the vaccine are useful for the treatment of allergy and for

CC (5) a peptide that capable of being recognised by (IV); (6) an immunogen  
 CC (III) comprising (Ia); and (7) producing (III) by producing (II); (I)  
 CC can have anti-allergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor; (II), (III) and (IV) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies; (IV) is useful for identifying mimotopes of PI,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies; (7) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood; (II), (III) and (IV) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AAR25907 to AAR26009 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.

XX Sequence 13 AA;  
 CC Query Match 87.0%; Score 64; DB 21; Length 13;  
 CC Best Local Similarity 100.0%; Pred. NC 0.5015;  
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : CLEDGQWMDVLC 12  
 ID : CLEDGQWMDVLC 12

RESULT 6  
 AAR25916  
 ID AAR25916 standard; Peptide; 13 AA;  
 AC AAR25916;  
 XX AC

XX XX  
 DT 05 JAN 2001 (first entry)  
 DE PI mimotope peptide P1sp SEQ ID NO: 10;

XX XX  
 DE Epitope; mimotope; human; immunoglobulin E (IgE); C-epitope 2 domain  
 FW allergic disease; immunophylaxis; immunotherapy; anti-allergy  
 FW immunosuppressive; vaccine; histamine release inhibitor; immunogen  
 FW allergy; atopy.

XX XX  
 OS Home sapiens.  
 OS Synthesis  
 XX XX  
 PN W020001465 A1  
 XX XX  
 DT 31 AUG 2000  
 DE 22 FEB 2001 (first entry); EP014441

XX XX  
 DT 25 FEB 1999; 99JP-0034405;  
 DT 29 MAR 1999; 99JP-0037151;  
 DT 07 MAY 1999; 99JP-0010517;  
 DT 07 MAY 1999; 99JP-0010516;  
 DT 07 AUG 1999; 99JP-0018594;  
 DT 07 AUG 1999; 99JP-0018603;  
 DT 07 SEP 1999; 99GB-0021046;  
 DT 07 SEP 1999; 99GB-0021047;  
 DT 29 OCT 1999; 99GB-0025619;  
 DT 21 NOV 1999; 99GB-0027698.

XX XX  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS  
 PA (SEPT) SEPTIDE THERAPEUTICS LTD.

XX XX  
 PI Dyson M, Fride M, Greenwood J, Hewitt E, Jarrett A, Mason G,  
 PI Randall E, Turnell WG, Van Mechelen MJ, Vignali P, Wood J, Yr

XX XX  
 DT 01 MAR 2003/53;  
 XX Reported useful for treating, preventing and ameliorating allergic  
 DT diseases, comprising an isolated surface epitope of IgE C-epitope 2  
 DT domain from immunoglobulin E  
 XX XX  
 DT (invention, Seq ID: 12) (first entry)

CC The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group; epitope (II) of C-epitope 2 domain (5) of  
 CC immunoglobulin E (IgE) or its mimotope. Also described are: (1) an  
 CC immunogen (II) for treating allergy comprising (II); (2) a vaccine (III)  
 CC for treating allergies comprising (III); (3) a ligand (IV) capable of  
 CC recognising (II); (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
 CC (IIa) comprising (Ia) and (7) producing (III) by producing (II); (II)  
 CC can have anti-allergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor; (II), (III) and (IV) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies; (IV) is useful for identifying mimotopes of PI,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies; (II) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood; (I), (III) and (IV) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AAR25907 to AAR26009 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.

XX Sequence 13 AA;  
 CC Query Match 87.0%; Score 64; DB 21; Length 13;  
 CC Best Local Similarity 100.0%; Pred. NC 0.5015;  
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : CLEDGQWMDVLC 13  
 ID : CLEDGQWMDVLC 13

RESULT 7  
 AAR16639  
 ID AAR16639 standard; Peptide; 13 AA;  
 AC AAR16639;  
 XX AC

XX XX  
 DT 07 NOV 2001 (first entry)  
 DE Peptide file derived as mimotope of C-epitope 2 region of human IgE.

XX XX  
 KW Human, linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; C-epitope 2; C-epitope 3; C-epitope 4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.

XX XX  
 OS Homo sapiens.  
 OS Synthesis

XX XX  
 PN W020014615 A2  
 XX XX  
 DT 28 JUN 2001;  
 DT 21 FEB 2000; 2000W-0504935;  
 DT 21 FEB 1999; 99GB-0030233;  
 DT 22 FEB 2000; 2000GB-0004096;  
 DT 22 AUG 2000; 2000GB-0023707;  
 DT 22 AUG 2000; 2000GB-0020708.

XX XX  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS  
 PA (SEPT) SEPTIDE THERAPEUTICS LTD.

XX XX  
 PI Farnes K, Johnson T;  
 XX XX  
 DT 01 MAR 2003/521967/53;

XX XX  
 DT A linkage comprising an immunogenic conjugate useful treatment of IgE  
 DT mediated diseases  
 XX XX  
 DT (first entry, Seq ID: 13) (first entry)  
 XX The present invention relates to a method for use in the  
 DT diagnosis and treatment of allergic diseases using mimotopes

(e.g. macromolecules, polymers, dendrimers, proteins) to provide biological and immunological constructs. The invention provides a method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition or a vaccine. The invention describes peptides derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E (IgE), which are used to produce conjugated compounds. The compounds or compositions of the invention are useful in the manufacture of a medicament for the treatment of IgE mediated diseases. The invention allows for controlled conjugation of a peptide epitope (antigen) to a protein so as to form an immunogenic conjugate which may be able to raise a protective antibody response in an animal or human patient. AAU16612-AAU16913 represent peptides derived from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.

XX Sequence 13 AA;  
SQ

Query Match 87.7%; Score 64; DB 22; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEGGQWMDVLC 12  
1 |||||  
DB 1 CEEGGQWMDVLC 12

RESULT 9  
AAU16641  
ID AAU16641 standard; Peptide, 13 AA  
XX AAU16641  
XX 07-JUN-2000 (first entry)  
XX Peptide R15p derived as mimotope of Cepsilon2 region of human IgE.  
XX Human linkage technology; conjugated compounds, carrier vaccines;  
KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
KW IgE mediated disease; antibody response.  
XX Humo sapiens.  
XX Synthetic.  
XX WC200149245-A2.  
XX 28-JUN-2000  
XX 21-FEB-2000; 2000WG GB04345  
XX 21-DEC-1999; 99JA-CC30243.  
XX 23-FEB-2000; 2000GB-0004096.  
XX 22-JUL-2000; 2000GB-0020707.  
XX 22-JUL-2000; 2000GB-0020708.  
XX (ACAM); ACAM215 RES LTD.  
XX (SMK); SMITHKLINE BEECHAM BIOLOGICALS.  
XX Flynn N. Johnson T;  
XX WPI; 2001-521967/53.  
XX A linkage comprising an immunogenic conjugate useful treatment of IgE mediated diseases -  
XX Example 4; Page 21; 48pp; English.  
XX The present invention relates to linkage methodology for use in the conjugation of compounds (e.g. peptides) to carrier vehicles (e.g. macromolecules, polymers, dendrimers, proteins) to provide biological and immunological constructs. The invention provides a method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition or a vaccine. The invention describes peptides derived from or mimotopes of the

Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E (IgE) which are used to produce conjugated compounds. The compounds or compositions of the invention are useful in the manufacture of a medicament for the treatment of IgE mediated diseases. The invention allows for controlled conjugation of a peptide epitope (antigen) to a protein so as to form an immunogenic conjugate which may be able to raise a protective antibody response in an animal or human patient. AAU16612-AAU16913 represent peptides derived from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.

XX Sequence 13 AA;  
SQ

Query Match 87.7%; Score 64; DB 22; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EECGGQWMDVLC 13  
1 |||||  
DB 2 EECGGQWMDVLC 13

RESULT 9  
AAB51028  
ID AAB51028 standard; Peptide, 13 AA  
XX AAB51028  
XX 21-MAR-2001 (first entry)  
XX IgE peptide #6.  
XX Vaccine; immunoglobulin E; IgE; anti-allergy.  
XX Mammalia.  
XX WC200047716-A2.  
XX 14-DEC-2000  
XX 06-JUN-2000; 2000WG EP05164.  
XX 08-JUN-1999; 99GR-001121.  
XX (SMK); SMITHKLINE BEECHAM BIOLOGICALS.  
XX Primels A;  
XX WPI; 2001-541150/100.  
XX New vaccine comprising allergy peptides linked by an inert carrier, useful for boosting an anti-allergy immune response in an individual susceptible to an allergic response -  
XX Claim 5; Page 23; 26pp; English.  
XX The present invention relates to a composition comprising allergy peptides linked by an inert carrier. The allergy peptides are derived from Immunoglobulin E (IgE) or IgE receptor. The present peptide is one such peptide from IgE. The composition is useful as a vaccine or for manufacturing a medicament for the prophylaxis or treatment of allergy. In particular, for boosting an anti-allergy immune response in an individual susceptible to an allergic response.  
XX Sequence 13 AA;  
SQ

Query Match 87.7%; Score 64; DB 22; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEEGGQWMDVLC 12  
1 |||||  
DB 1 EEEGGQWMDVLC 12

```

RESULT 10
AB000224
ID AR000224 standard; Peptide: 13 AA.
AC
XX AB000224
XX
XX 02 SEP 2000 (first entry)
XX
XX Human IgE immunogenic peptide SEQ ID NO: 10.
XX
XX Immunogen; human; IgE; immunoglobulin E; allergy; anti-allergic;
XX vaccine; anti-allergic.
XX
XX Homo sapiens.
XX
XX WO200216403 A2
XX
XX 28 FEB 2000.
XX
XX 17-AUG-2000; 2001WO-EP09576.
XX
XX 22-AUG-2000; 2000GB-0020717.
XX
XX (SMIX) SMITHKLINE BEECHAM BIOLOGICALS
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Friede M, Mason S, Turnell WG, Vinals Bassols YC.
XX
XX WPI: 2002-483648/52.
XX
XX Conjugate for use in vaccine for treatment of allergy; comprises
XX disulfide bridge cyclized peptide and immunogenic carrier.
XX
XX Claim 4; Page 9; 45pp; English.
XX
XX The present invention relates to conjugates suitable for use in vaccines,
XX where the conjugate comprises a disulfide bridge cyclized peptide and an
XX immunogenic carrier. The vaccines can be used in the treatment of
XX allergies. The present sequence is a peptide immunogen derived from human
XX immunoglobulin E (IgE) suitable to be cyclised and used in the invention.
XX
XX Sequence 13 AA:
XX
XX Query Match 97.7%; Score 64; D5 23; Length 13.
XX Best Local Similarity 100.0%; Pred. No. 0.0015;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0;
XX
XX QY 1 CLEGGQWMDVL 13
XX I 1 CLEGGQWMDVL 12
XX
XX RESULT 11
AB000226
ID AR000226 standard; Peptide: 13 AA.
AC
XX AB000226
XX
XX 02 SEP 2000 (first entry)
XX
XX Human IgE immunogenic peptide SEQ ID NO: 10.
XX
XX Immunogen; human; IgE; immunoglobulin E; allergy; anti-allergic;
XX vaccine; anti-allergic.
XX
XX Homo sapiens.
XX
XX WO200216403 A2
XX
XX 28 FEB 2000.
XX
XX 17-AUG-2000; 2001WO-EP09576.
XX
XX 22-AUG-2000; 2000GB-0020717.
XX
XX (SMIX) SMITHKLINE BEECHAM BIOLOGICALS
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Friede M, Mason S, Turnell WG, Vinals Bassols YC.
XX
XX WPI: 2002-483648/52.
XX
XX Conjugate for use in vaccine for treatment of allergy; comprises
XX disulfide bridge cyclized peptide and immunogenic carrier.
XX
XX Claim 4; Page 9; 45pp; English.
XX
XX The present invention relates to conjugates suitable for use in vaccines,
XX where the conjugate comprises a disulfide bridge cyclized peptide and an
XX immunogenic carrier. The vaccines can be used in the treatment of
XX allergies. The present sequence is a peptide immunogen derived from human
XX immunoglobulin E (IgE) suitable to be cyclised and used in the invention.
XX
XX Sequence 13 AA:
XX
XX Query Match 97.7%; Score 64; D5 23; Length 13.
XX Best Local Similarity 100.0%; Pred. No. 0.0015;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0;
XX
XX QY 1 CLEGGQWMDVL 13
XX I 1 CLEGGQWMDVL 12
XX
XX RESULT 12
AB000229
ID AAR05929 standard; Peptide: 10 AA.
AC
XX AAR05929
XX
XX 05 JAN-2001 (first entry)
XX
XX PI mimotope peptide P1st SEQ ID NO:23.
XX
XX Epitope: mimotope; human; immunoglobulin E; IgE; C-peptide-2 domain;
XX allergic disease; immunophy; axis; immunotherapy; anti-allergic;
XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;
XX anti-IgY; atopy.
XX
XX Homo sapiens.
XX
XX WO2000050400 A1
XX
XX 31-AUG-2000.
XX
XX 22-FEB-2000; 2000WO-EP01455.
XX
XX 25-FEB-1999; 99GB-0004405.
XX
XX 29-MAR-1999; 99GB-0007151.
XX
XX 07-MAY-1999; 99GB-0010537.
XX
XX 07-MAY-1999; 99GB-0010538.
XX
XX 07-AUG-1999; 99GB-0018594.
XX
XX 07-AUG-1999; 99GB-0018603.
XX
XX 07-SEP-1999; 99GB-0021046.
XX
XX 07-SEP-1999; 99GB-0021047.
XX
XX 29-OCT-1999; 99GB-0025619.
XX
XX 23 NOV-1999; 99GB-0027699.
XX
XX (SMIX) SMITHKLINE BEECHAM BIOLOGICALS.
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Dwyer M, Filmer M, Greenwood C, Hewitt E, Lamont A, Mason S,
XX Sandall R, Turnell WG, Van Mechelen MP, Vinals De Bassols YC.
XX
XX WPI: 2000-520000/52.

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XX
XX 22-AUG-2000; 2000GB-0020717.
XX
XX (SMIX) SMITHKLINE BEECHAM BIOLOGICALS.
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Friede M, Mason S, Turnell WG, Vinals Bassols YC.
XX
XX WPI: 2002-483648/52.
XX
XX Conjugate for use in vaccine for treatment of allergy; comprises
XX disulfide bridge cyclized peptide and immunogenic carrier.
XX
XX Claim 4; Page 9; 45pp; English.
XX
XX The present invention relates to conjugates suitable for use in vaccines,
XX where the conjugate comprises a disulfide bridge cyclized peptide and an
XX immunogenic carrier. The vaccines can be used in the treatment of
XX allergies. The present sequence is a peptide immunogen derived from human
XX immunoglobulin E (IgE) suitable to be cyclised and used in the invention.
XX
XX Sequence 13 AA:
XX
XX Query Match 87.7%; Score 64; D5 23; Length 13.
XX Best Local Similarity 100.0%; Pred. No. 0.0015;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0;
XX
XX QY 2 LEDGGQWMDVL 13
XX I 2 LEDGGQWMDVL 13
XX
XX RESULT 13
AAR05929
ID AAR05929 standard; Peptide: 10 AA.
AC
XX AAR05929
XX
XX 05 JAN-2001 (first entry)
XX
XX PI mimotope peptide P1st SEQ ID NO:23.
XX
XX Epitope: mimotope; human; immunoglobulin E; IgE; C-peptide-2 domain;
XX allergic disease; immunophy; axis; immunotherapy; anti-allergic;
XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;
XX anti-IgY; atopy.
XX
XX Homo sapiens.
XX
XX WO2000050400 A1
XX
XX 31-AUG-2000.
XX
XX 22-FEB-2000; 2000WO-EP01455.
XX
XX 25-FEB-1999; 99GB-0004405.
XX
XX 29-MAR-1999; 99GB-0007151.
XX
XX 07-MAY-1999; 99GB-0010537.
XX
XX 07-MAY-1999; 99GB-0010538.
XX
XX 07-AUG-1999; 99GB-0018594.
XX
XX 07-AUG-1999; 99GB-0018603.
XX
XX 07-SEP-1999; 99GB-0021046.
XX
XX 07-SEP-1999; 99GB-0021047.
XX
XX 29-OCT-1999; 99GB-0025619.
XX
XX 23 NOV-1999; 99GB-0027699.
XX
XX (SMIX) SMITHKLINE BEECHAM BIOLOGICALS.
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Dwyer M, Filmer M, Greenwood C, Hewitt E, Lamont A, Mason S,
XX Sandall R, Turnell WG, Van Mechelen MP, Vinals De Bassols YC.
XX
XX WPI: 2000-520000/52.

```

XX Peptides useful for treating, preventing and ameliorating allergic  
PT diseases, comprising an isolated surface exposed group of a specific  
PT domain from immunoglobulin E.  
XX  
XX Disclosure: Page 9; 129pp; English.  
XX  
XX The present invention describes a peptide (I) comprising an isolated  
XX surface exposed group/epitope (II) of C epsilon-2 domain (I) of  
XX immunoglobulin E (IgE), or its mimotope. Also described are (I) an  
XX immunogen (II) for treating allergy comprising (II) as a vaccine (III)  
XX for treating allergies comprising (II), (I) a brand (IV) capable of  
XX recognising E1; (4) a pharmaceutical composition (V) comprising (IV);  
XX (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
XX (IIa) comprising (Ia); and (7) producing (IIa) by producing (II), (I)  
XX can have anti-allergic and immunosuppressive activities, and can be used  
XX as a vaccine and histamine release inhibitor. (I), (II) and (III) are  
XX useful in medicine and in the manufacture of medicaments for treating  
XX and preventing allergies. (IV) is useful for identifying mimotopes of E1,  
XX in medicine and also in manufacturing medicaments for treating  
XX allergies. (I) is useful in diagnostics and in the affinity purification  
XX of circulating anti-IgE antibodies from blood. (I), (II) and (Ic) are  
XX useful for treating a patient susceptible to or suffering from allergies.  
XX (IV) is also useful in diagnosing atopy. AAS2997 to AAS2699 represent  
XX peptide sequences which are used in the exemplification of the present  
XX invention.  
XX  
XX Sequence 10 AA;

Query Match 69.9%; Score 51; DB 21; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEDGQWVVD 11  
DB 1 LEDGQWVVD 10  
RESULT 13  
AAS2654  
ID AAS2654 standard; Peptide; 10 AA.  
XX AAS2654  
XX  
XX CV N/A-2001 (first entry).  
XX Peptide P58 derived as epitope of C epsilon-2 domain from IgE.  
XX  
XX Human; linkage technology; conjugated compounds; carrier vehicles;  
XX epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
XX IgE mediated disease; antibody response.  
XX  
XX Homo sapiens.  
XX Synthesis.  
XX  
XX WC000145745-A2.  
XX  
XX 28 JUN 2001.  
XX  
XX 21-DEC-2000; 2000WO-GB04915.  
XX  
XX 21-DEC-1999; 99GB-0030233.  
XX 22-FEB-2000; 2000GB-0034096.  
XX 22-AUG-2000; 2000GB-0020707.  
XX 22-AUG-2000; 2000GB-0020708.  
XX  
XX JACAY J ACAMBIS RES LTD.  
XX (SMIX) SMITHKLINE BEECHAM BIOLOGICALS  
XX  
XX Eliam N, Johnson T;  
XX WPI; 2001 501967/57.

PT A linkage comprising an immunogenic conjugate useful treatment of IgE  
PT mediated diseases.  
XX  
XX Example 4; Page 21; 48pp; English.  
XX  
XX The present invention relates to linkage methodology for use in the  
XX conjugation of compounds (e.g. peptides) to carrier vehicles  
XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
XX biological and immunological constructs. The invention provides a  
XX method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
XX protein) for use in a pharmaceutical composition or a vaccine. The  
XX invention describes peptides derived from or mimotopes of the  
XX Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
XX (IgE) which are used to produce conjugated compounds. The compounds or  
XX compositions of the invention are useful in the manufacture of a  
XX medicament for the treatment of IgE mediated diseases. The invention  
XX allows for controlled conjugation of a peptide epitope (antigen) to a  
XX protein so as to form an immunogenic conjugate which may be able to  
XX raise a protective antibody response in an animal or human patient.  
XX AAS2632-AAS1691 represent peptides derived from or mimotopes of  
XX the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.

XX Sequence 10 AA.

Query Match 69.9%; Score 51; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEDGQWVVD 11  
DB 1 LEDGQWVVD 10  
RESULT 14  
AAS26226  
ID AAS26226 standard; Peptide; 10 AA.  
XX AAS26226  
XX  
XX AB200228;  
XX  
XX 02-SEP-2002 (first entry)  
XX  
XX Human IgE immunogenic peptide SEQ ID NO: 12.  
XX  
XX Immunogen; Human IgE, immunoglobulin E; allergy; thio-ether linkage;  
XX vaccine; antiallergic  
XX  
XX Homo sapiens.  
XX  
XX WC200216479-A2.  
XX  
XX 29-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-EF09576.  
XX  
XX 22-AUG-2000; 2000GB-0020717.  
XX  
XX (SMIX) SMITHKLINE BEECHAM BIOLOGICALS.  
XX (PEPT), PEPTIDE THERAPEUTICS LTD.  
XX  
XX Friede N, Mason S, Turnell WG, Vinals Bassols YC;  
XX  
XX WPI; 2002-489645/52.  
XX  
XX  
XX Conjugate for use in vaccine for treatment of allergy, comprises  
XX disulfide bridge cyclized peptide and immunogenic carrier.  
XX  
XX  
XX Claim 4; Page 9; 4pp; English.  
XX  
XX The present invention relates to conjugates suitable for use in vaccines,  
XX where the conjugate comprises a disulphide bridge cyclised peptide and an  
XX immunogenic carrier. The vaccines can be used in the treatment of  
XX allergies. The present sequence is a peptide immunogen derived from human  
XX immunoglobulin E (IgE) suitable to be cyclised and used in the invention.

XX  
SQ Sequence 10 AA:  
Query Match 69.8%, Score 51, 15 AA, Identical  
Best Local Similarity 100.0%; Pct Ident 100.0%;  
Matches 10; Conservative 0; Mismatches 0; Gaps 0;

QY 1 LAGDQVNDV 11  
DB 1 LAGDQVNDV 10

RESULT 15  
ABJ0054:  
10 AR00541 standard; Peptide; 13 AA.  
XX  
AC AR00541:  
XX  
DT 02 SEP 2002 (first entry)  
XX  
DE Human IgE cyclic immunogen.c peptide SEQ ID NO: 101.  
XX  
KW Immunogen; human; IgE; immunoglobulin; B; allergy; non-covalent linkage;  
XX  
KW vaccine; antitubercular; cyclic  
XX  
ES Homo sapiens.  
XX  
FN K026016409-A1.  
XX  
PD 28 FEB 2002.  
XX  
PF 17-JUN 2001; 2001W-EP05516.  
XX  
PP 22 AUG 2001; 2000GR-0020712.  
XX  
QA LUMIR; SMITHKLINE BEECHAM BIOLOGICALS  
QA (SEPT); PEPTIDE THERAPEUTICS LTD  
XX  
PI Friesse, M., Mason, S., Turbell, W.G., Vaccines Research Yb.  
XX  
PE WPI; 2002-043449/52.  
XX  
PT Candidate for use in vaccine for treatment of allergy in humans  
PT Disulfide bridge cyclized peptide and immunogen  
XX  
PS Claim 4; Page 16; 45pp; English.  
XX

XX The present invention relates to a vaccine and to a method of vaccines.  
XX where the vaccine comprises a humanized protein, a short peptide and an  
XX immunogenic carrier. The vaccine can be used for the treatment of  
XX allergies. The present sequence is a cyclic peptide derived  
XX from human immunoglobulin E (IgE) variable region. The invention.

XX  
SQ Sequence 13 AA:  
Query Match 68.8%, Score 50, 15 AA, Identical  
Best Local Similarity 100.0%; Pct Ident 100.0%;  
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 1 LAGDQVNDV 9  
DB 1 LAGDQVNDV 9

OnCore version 3.1.6  
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QV protein - protein search, using sw model

Run on: November 5, 2003, 18:03:44, search time 20 seconds  
without alignment  
101,486 Million pairs of residues

Title: US-09-914-088-11  
Perfect score: 73  
Sequence: MEDGOWMVDLC 13

Scoring table: BLOSUM62  
Gap: 10.0, Gapext: 0.5

Sequences: 444079 seqs, 17149292 residues

Total number of hits satisfying chosen parameters: 3029

Minimum DB seq length: 0  
Maximum DB seq length: 13

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications AA:  
1: /cgn2\_6/prodata/2/pbpa/US09\_PBCOXB.fpr  
2: /cgn2\_6/prodata/2/pbpa/PER\_NEW\_PBC.fpr  
3: /cgn2\_6/prodata/2/pbpa/US06\_NEW\_PBC.fpr  
4: /cgn2\_6/prodata/2/pbpa/US06\_PBCOXB.fpr  
5: /cgn2\_6/prodata/2/pbpa/US09\_NEW\_PBC.fpr  
6: /cgn2\_6/prodata/2/pbpa/US09\_PBCOXB.fpr  
7: /cgn2\_6/prodata/2/pbpa/US09\_NEW\_PBC.fpr  
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12: /cgn2\_6/prodata/2/pbpa/US09\_PBCOXB.fpr  
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14: /cgn2\_6/prodata/2/pbpa/US09\_PBCOXB.fpr  
15: /cgn2\_6/prodata/2/pbpa/US09\_PBCOXB.fpr  
16: /cgn2\_6/prodata/2/pbpa/US09\_PBCOXB.fpr  
17: /cgn2\_6/prodata/2/pbpa/US09\_PBCOXB.fpr  
18: /cgn2\_6/prodata/2/pbpa/US09\_PBCOXB.fpr

Pred. No. is the number of results predicted by the search.  
Score greater than or equal to the score of the relevant printed,  
and is derived by analysis of the total score data table

SEQUENCES

Result	Seq	Score	Match	Length	DB	ID	Description
1	49	67.1	10	12	US-10-092-014-282	US-10-092-014-282	Sequence 252, App
2	49	67.1	10	12	US-10-092-014-282	US-10-092-014-282	Sequence 135, App
3	47	64.4	9	12	US-10-092-014-282	US-10-092-014-282	Sequence 273, App
4	47	64.4	9	12	US-10-092-014-282	US-10-092-014-282	Sequence 127, App
5	45	61.6	10	12	US-10-092-014-282	US-10-092-014-282	Sequence 55, App
6	74	46.6	10	12	US-10-092-014-282	US-10-092-014-282	Sequence 1084, App
7	39	39.7	10	12	US-10-092-014-282	US-10-092-014-282	Sequence 1286, App
8	28	38.4	10	12	US-10-092-014-282	US-10-092-014-282	Sequence 12, App
9	28	38.4	10	12	US-10-092-014-282	US-10-092-014-282	Sequence 1, App
10	28	38.4	10	12	US-10-092-014-282	US-10-092-014-282	Sequence 1, App
11	27	37.6	10	11	US-10-092-014-282	US-10-092-014-282	Sequence 1983, App
12	26	36.6	10	11	US-10-092-014-282	US-10-092-014-282	Sequence 12, App
13	25	34.2	10	11	US-10-092-014-282	US-10-092-014-282	Sequence 12, App
14	25	34.2	10	11	US-10-092-014-282	US-10-092-014-282	Sequence 12, App
15	25	34.2	10	11	US-10-092-014-282	US-10-092-014-282	Sequence 12, App

16	25	34.2	13	11	US-09-829-884-34	Sequence 34, Appl
17	24	32.9	8	14	US-10-095-450-2	Sequence 2, Appl
18	24	32.9	8	14	US-10-095-450-6	Sequence 6, Appl
19	24	32.9	8	14	US-10-095-450-10	Sequence 10, Appl
20	24	32.9	8	14	US-10-095-450-14	Sequence 14, Appl
21	24	32.9	8	14	US-10-095-450-18	Sequence 18, Appl
22	24	32.9	8	14	US-10-095-450-22	Sequence 22, Appl
23	24	32.9	9	10	US-09-780-053-434	Sequence 434, Appl
24	24	32.9	9	10	US-09-780-053-556	Sequence 556, Appl
25	24	32.9	12	12	US-09-766-353A-8	Sequence 8, Appl
26	24	32.9	13	12	US-10-345-764-22	Sequence 22, Appl
27	24	32.9	16	15	US-10-006-869-2346	Sequence 2346, App
28	24	32.9	16	15	US-09-932-165-1419	Sequence 1419, App
29	23	31.5	9	12	US-10-147-140-47	Sequence 47, Appl
30	23	31.5	9	8	US-05-464-363-55	Sequence 55, Appl
31	23	31.5	9	12	US-09-332-165-20	Sequence 20, Appl
32	23	31.5	9	12	US-09-332-165-1569	Sequence 1569, App
33	23	31.5	9	12	US-09-335-384-535	Sequence 535, App
34	23	31.5	9	12	US-09-335-384-533	Sequence 533, App
35	23	31.5	9	12	US-10-277-292-458	Sequence 458, App
36	23	31.5	10	12	US-09-932-165-102	Sequence 591, App
37	23	31.5	10	12	US-09-932-165-102	Sequence 102, App
38	23	31.5	12	12	US-09-932-165-196	Sequence 196, App
39	23	31.5	12	12	US-09-932-165-504	Sequence 504, App
40	23	31.5	12	12	US-09-935-384-163	Sequence 163, App
41	23	31.5	12	12	US-09-935-384-289	Sequence 289, App
42	23	31.5	10	12	US-09-935-384-587	Sequence 587, App
43	23	31.5	10	12	US-10-353-929-174	Sequence 174, App
44	23	31.5	10	12	US-09-755-630A-23	Sequence 23, Appl
45	23	31.5	10	12	US-10-277-292-64	Sequence 64, Appl

# ALIGNMENTS

RESULT 1  
US-10-092-014-282  
Sequence 352, Application US/10092014  
Publication No. US2003185859A  
APPLICANT: Birkett, Ashley J.  
TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL C  
FILE REFERENCE: US/10-04564/85124  
CURRENT APPLICATION NUMBER: US/10/082,014  
CURRENT FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 07/910,915  
PRIOR FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 290  
SOFTWARE: Patent version 3.1  
SEQ ID NO: 282  
LENGTH: 10  
TYPE: PST  
ORGANISM: Homo sapiens  
US-10-092-014-282

Query Match: 67.1%, Score 43; DB 12; Length 10;  
Best local similarity: 90.0%; Pred. No. 0.051; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 1; Mismatches 0;

QY 2 MEDGOWMVD 11  
DB MEDGOWMVD 10

RESULT 2  
US-10-372-036-116  
Sequence 135, Application US/10372016  
Publication No. US/03198645A1  
GENERAL INFORMATION  
APPLICANT: Pfizer, Inc.  
TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
HUMAN BRUCELLOSIS





ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide antigen  
US-10-144 186-60

Query Match 46.6%; Score 34; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GQVMDV 12  
DB 1 GQVMDV 7

## RESULT 7

US-09-572-270A-1084

Sequence 1084; Application US/09572270A

Publication No. US2003014836A1

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Inter-complementary peptide (1084)

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/572,270A

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 1144

SOFTWARE: ProPatent version 1.0

SEQ ID NO 1084

LENGTH: 10

TYPE: PRT

ORGANISM: Arabidopsis Thaliana

OTHER INFORMATION: Sequence located in (AVA-P) OR TABLE 1001 AND AVA-P2

US-09-572-270A-1084

Query Match 39.7%; Score 29; DB 12; Length 10;

Best Local Similarity 71.4%; Pred. No. 1; 2;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GQVMDV 11  
DB 2 GQVMDV 8

## RESULT 8

US-09-572-270A-1086

Sequence 1086; Application US/09572270A

Publication No. US2003014836A1

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Inter-complementary peptide (1086)

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/572,270A

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 1144

SOFTWARE: ProPatent version 1.0

SEQ ID NO 1086

LENGTH: 10

TYPE: PRT

ORGANISM: Arabidopsis Thaliana

OTHER INFORMATION: Sequence located in (AVA-P) OR TABLE 1001 AND AVA-P2

US-09-572-270A-1086

Query Match 39.7%; Score 29; DB 12; Length 10;

Best Local Similarity 71.4%; Pred. No. 1; 2;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GQVMDV 11  
DB 3 GQVMDV 9

## RESULT 9

US-09-842-164-12

Sequence 12; Application US/09842164

Patent No. US20020102697A)  
GENERAL INFORMATION:  
APPLICANT: INCOVE, Satoshi  
TITLE OF INVENTION: Luciferase and Photoprotein  
FILE REFERENCE: 206497US9  
CURRENT APPLICATION NUMBER: US/09/842,164  
CURRENT FILING DATE: 2001-04-26  
PRIOR APPLICATION NUMBER: JAPAN 2000 125053  
PRIOR FILING DATE: 2000 04 26  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Oplophorus gracilirostris  
NAME/KEY: MISC FEATURE  
LOCATION: 113-173  
OTHER INFORMATION: PRT, 35 kDa protein, partial  
US-09-842-164-12

Query Match 39.4%; Score 28; DB 10; Length 7;  
Best Local Similarity 71.4%; Pred. No. 5; 8e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GQVMDV 11  
DB 1 GQVMDV 7

## RESULT 10

US-09-925 442-3

Sequence 3; Application US/09925442

Patent No. US20020103346A1

GENERAL INFORMATION:

APPLICANT: VOGEL, CARL WILHELM

BRODERHOFST, REINHOLD

KOCK, MICHAEL

FRITZINGER, DAVID

TITLE OF INVENTION: RECOMBINANT PROCVF

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDICAL TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/925,442

FILING DATE: 10-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/017,947

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 1126-0107-CX

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDNESS: single

```

1  TOPOLOGY: linear
2  SCHEDULE TYPE: peptide
3  SEQUENCE DESCRIPTION: SEQ ID NOS: 3
4  US 09-925-442 3
5
6  Query Match: 38.4%; Score 28; DB ID: 1000110
7  Best Local Similarity: 50.0%; Pred. No. 1000110
8  Matches: 4; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0
9
10 QY 3 EAGQGMVDC 12
11 1111111
12 1 EAGQGMVDC 10
13
14 RESULT 11
15 US-09-925-442 3
16 1 Sequence 1; Application US/09962151
17 2 Publication No. US2003092746A1
18 3 GENERAL INFORMATION:
19 4 APPLICANT: Hagmann, William K.
20 5 APPLICANT: Delasalle, Stephen E.
21 6 APPLICANT: Kameoka, Theodore
22 7 APPLICANT: MacCoss, Malcolm
23 8 TITLE OF INVENTION: SUBSTITUTED AMIDINE DERIVATIVES AND
24 9 FILE REFERENCE: 20698
25 10 CURRENT APPLICATION NUMBER: US/09/642,151
26 11 PRIOR FILING DATE: 2002-11-14
27 12 PRIOR FILING DATE: 2000-05-22
28 13 NUMBER OF SEQ ID NOS: 4
29 14 SOFTWARE: FASTSEQ for Windows Version 4.0
30 15 SEQ ID NO 1
31 16 LENGTH: 12
32 17 TYPE: PRT
33 18 ORGANISM: Homo sapiens
34 19 862-1511
35
36 Query Match: 37.0%; Score 27; DB ID: 1000110
37 Best Local Similarity: 40.0%; Pred. No. 1000110
38 Matches: 4; Conservative: 3; Mismatches: 1; Indels: 0; Gaps: 0
39
40 QY 1 EAGQGMVDC 10
41 1111111
42 1 EAGQGMVDC 10
43
44 RESULT 12
45 US-09-925-442 3
46 1 Sequence 1; Application US/09962151
47 2 Publication No. US2003092746A1
48 3 GENERAL INFORMATION:
49 4 APPLICANT: Hagmann, William K.
50 5 APPLICANT: Delasalle, Stephen E.
51 6 APPLICANT: Kameoka, Theodore
52 7 APPLICANT: MacCoss, Malcolm
53 8 TITLE OF INVENTION: SUBSTITUTED AMIDINE DERIVATIVES AND
54 9 FILE REFERENCE: 20698
55 10 CURRENT APPLICATION NUMBER: US/09/642,151
56 11 PRIOR FILING DATE: 2002-11-14
57 12 PRIOR FILING DATE: 2000-05-22
58 13 NUMBER OF SEQ ID NOS: 4
59 14 SOFTWARE: FASTSEQ for Windows Version 4.0
60 15 SEQ ID NO 1
61 16 LENGTH: 12
62 17 TYPE: PRT
63 18 ORGANISM: Homo sapiens
64 19 862-1511
65
66 Query Match: 35.6%; Score 26; DB ID: 1000110
67 Best Local Similarity: 44.4%; Pred. No. 1000110
68 Matches: 4; Conservative: 2; Mismatches: 3; Indels: 0; Gaps: 0
69
70 QY 1 EAGQGMVDC 9

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```

1  DB 2 CPSEGSVD 10
2
3 RESULT 13
4 US-10-155-922-72
5 1 Sequence 77; Application US/10/155922
6 2 Publication No. US2001008689A1
7 3 GENERAL INFORMATION:
8 4 APPLICANT: Hata, Yutaro
9 5 APPLICANT: Oka, Yutiko
10 6 APPLICANT: Takeba, Kyoko
11 7 APPLICANT: Tsuda, Eikari
12 8 APPLICANT: Teshigi, Keiko
13 9 APPLICANT: Shinagawa, Toko
14 10 APPLICANT: Kurakami, Kayoko
15 11 APPLICANT: Koshida, Shogo
16 12 TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
17 13 FILE REFERENCE: 4679200220
18 14 CURRENT APPLICATION NUMBER: US/10/155,922
19 15 CURRENT FILING DATE: 2002-05-23
20 16 PRIOR APPLICATION NUMBER: PCT/JP01/04691
21 17 PRIOR FILING DATE: 2001-06-14
22 18 PRIOR APPLICATION NUMBER: JP 2000-166903
23 19 PRIOR FILING DATE: 2000-06-05
24 20 PRIOR APPLICATION NUMBER: JP 2001-347340
25 21 PRIOR FILING DATE: 2001-11-13
26 22 PRIOR APPLICATION NUMBER: JP 2001-347338
27 23 PRIOR FILING DATE: 2001-11-13
28 24 PRIOR APPLICATION NUMBER: JP 2001-371175
29 25 PRIOR FILING DATE: 2001-12-25
30 26 PRIOR APPLICATION NUMBER: JP 2001-371166
31 27 PRIOR FILING DATE: 2001-12-25
32 28 NUMBER OF SEQ ID NOS: 156
33 29 SOFTWARE: FASTSEQ for Windows Version 4.0
34 30 SEQ ID NO 72
35 31 LENGTH: 10
36 32 TYPE: PRT
37 33 ORGANISM: Artificial Sequence
38 34 FEATURE:
39 35 OTHER INFORMATION: Synthetic Construct
40 36 FEATURE:
41 37 NAME/KEY: VARIANT
42 38 LOCATION: 7
43 39 OTHER INFORMATION: Xaa = Any Amino Acid
44 40 US-10-155-922-72
45
46 Query Match: 34.2%; Score 26; DB ID: 1000110
47 Best Local Similarity: 80.0%; Pred. No. 5.6e-07
48 Matches: 4; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0
49
50 QY 1 QLEDS 9
51 1111111
52 1 QLEDS 10
53
54 RESULT 14
55 US-09-863-043A-77
56 1 Sequence 77; Application US/09963049A
57 2 Publication No. US2001033205A1
58 3 GENERAL INFORMATION:
59 4 APPLICANT: Kenwick, Sue J.
60 5 APPLICANT: Nelson, David L.
61 6 APPLICANT: Aradhye, Swaroop
62 7 APPLICANT: D'Urso, Michele
63 8 APPLICANT: Wofford, Hayley
64 9 APPLICANT: Murnick, Arnold
65 10 APPLICANT: Smith, As-ae
66 11 APPLICANT: Israel, Alain
67 12 APPLICANT: Foustka, Annette
68 13 APPLICANT: Lewis, Richard A.
69 14 APPLICANT: Levy, Wase
70 15 APPLICANT: Heiss, Nina

```

1 TITLE OF INVENTION: Diagnosis and Treatment of Medial and Lateral Ankle Associated with Def

2 TITLE OF INVENTION: NFKAPPA B (NF- $\kappa$ B) Activation  
 3 FILE REFERENCE: HQ-PC196/US1  
 4 CURRENT APPLICATION NUMBER: US/09/963,042A  
 5 PRIOR APPLICATION NUMBER: US 60/266,223  
 6 PRIOR FILING DATE: 2003-05-22  
 7 NUMBER OF SEQ ID NOS: 77  
 8 SOFTWARE: Patent in version 3.1  
 9 SEQ ID NO 77  
 10 LENGTH: 11  
 11 TYPE: PRT  
 12 ORGANISM: Human  
 13 (S-09-914-088-11)

Query Match: 14.2% Score 25; DB 11; Length 11.  
 Best local similarity: 56.3%; Pred. No. 6.5e+02;  
 Matches: 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 1 CLEGG 6  
 11 11  
 12 4 CLEGG 9

RESULT 15  
 1 US-09-914-088-11  
 2 Sequence 34; Application US/99/9854  
 3 Patent No. US2002076739A1  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Abersold, Rudolf; H.  
 6 APPLICANT: Gelb, Michael H.  
 7 APPLICANT: Gysi, Steven  
 8 APPLICANT: Turcsek, Frantisek  
 9 APPLICANT: Gerber, Scott A.  
 10 APPLICANT: Riss, Beate  
 11 TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins  
 12 FILE REFERENCE: 98A  
 13 CURRENT APPLICATION NUMBER: US/99/9854  
 14 CURRENT FILING DATE: 2001-04-20  
 15 PRIOR APPLICATION NUMBER: 93/383,052  
 16 PRIOR FILING DATE: 1999-08-25  
 17 PRIOR APPLICATION NUMBER: 60/097,328  
 18 PRIOR FILING DATE: 1998-08-26  
 19 NUMBER OF SEQ ID NOS: 64  
 20 SOFTWARE: Patent in Ver. 2.0  
 21 SEQ ID NO 34  
 22 LENGTH: 11  
 23 TYPE: PRT  
 24 ORGANISM: Yeast  
 25 FEATURES:  
 26 NAME/KEY: VARIANT  
 27 LOCATION: (1)  
 28 OTHER INFORMATION: C at position 11 is not coded (see seq 34)  
 29 OTHER INFORMATION: residue  
 30 (S-09-914-088-11)

Query Match: 14.2% Score 25; DB 11; Length 11.  
 Best local similarity: 56.3%; Pred. No. 6.5e+02;  
 Matches: 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 9 DVSIC 13  
 11 11  
 12 7 EVSIC 11

Search completed: November 5, 2003, 14:11:14  
 Job time: 122 secs





```

12 1 11111111
1 1 EDGFIADSCI 10

RESULT 6
US-08-162-227 3
Sequence 3, Application US/0866227
Patent No. 5924492
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUBAUER,
ADDRESS: P.O.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,227
FILING DATE: 14-JUN-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/662,227
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107 CX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-017-947.3

Query Match 38.4%; Score 28; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 78;
Matches 5; Conservative 2; Mismatches 3; Gaps 0;

QY 3 EDGQMVQVL 12
1 1 1 1 1
Db 1 EDGFIADSCI 10

RESULT 7
US-08-162-227 3
Sequence 3, Application US/0866227
Patent No. 5924492
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUBAUER,
ADDRESS: P.O.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualucci, Patricia A.

```

REGISTRATION NUMBER: 34,894  
 REFERENCE/DOCKET NUMBER: LUD 5256  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 688-3884  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US 08-162-081B 13

Query Match 38.4% Score 28; DB 2; Length 13;  
 Best Local Similarity 44.4% Pred. No. Left 2;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDGQWMDL 11  
 DB : DDGQLEHD 9

RESULT 9  
 US-09-085-957-13

Sequence 13, Application US/05780872  
 Patent No. 646824  
 GENERAL INFORMATION:  
 APPLICANT: Hiles, Ian Donald; Fyfe, Michael John; Chard, Ritu  
 APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter;  
 APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,  
 APPLICANT: Strefano, Gout, Ivac Parasovitch  
 TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
 TITLE OF INVENTION: THEIR PREPARATION AND USE  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Felfe & Lynch  
 STREET: 205 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10022

COMPUTER READABLE FORM:  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: Wordperfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/05780872  
 FILING DATE: 09 JAN 1997  
 CLASSIFICATION: 425  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/162,081  
 FILING DATE: February 7, 1994  
 APPLICATION NUMBER: PCT/GB93/00761  
 FILING DATE: 13 April 1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Pasqualini, Patricia A.  
 REGISTRATION NUMBER: 34,894  
 REFERENCE/DOCKET NUMBER: LUD 5256  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 688-3884  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US 08-162-081B 13

Query Match 38.4% Score 28; DB 2; Length 13;  
 Best Local Similarity 44.4% Pred. No. Left 2;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDGQWMDL 11  
 DB : DDGQLEHD 9

RESULT 11  
 US-09-057-897-15

Sequence 15, Application US/05057897  
 Patent No. 6360476  
 GENERAL INFORMATION:  
 APPLICANT: L. Ashbury Y.H.  
 APPLICANT: Wada, Reina W.  
 TITLE OF INVENTION: Anti-Influenza Antibody Against Human

QY 3 EDGQWMDL 11  
 DB : DDGQLEHD 9

RESULT 10  
 US-09-085-957-13  
 Sequence 13, Application US/05057897  
 Patent No. 6274127  
 GENERAL INFORMATION:  
 APPLICANT: Hiles, Ian Donald; Fyfe, Michael John; Chard, Ritu  
 APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter;  
 APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,  
 APPLICANT: Strefano, Gout, Ivac Parasovitch  
 TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
 TITLE OF INVENTION: THEIR PREPARATION AND USE  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Felfe & Lynch  
 STREET: 205 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10022

COMPUTER READABLE FORM:  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: Wordperfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/05780872  
 FILING DATE: 09 JAN 1997  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/162,081  
 FILING DATE: February 7, 1994  
 APPLICATION NUMBER: PCT/GB93/00761  
 FILING DATE: 13 April 1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Pasqualini, Patricia A.  
 REGISTRATION NUMBER: 34,894  
 REFERENCE/DOCKET NUMBER: LUD 5256  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 688-3884  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-085-957-13

Query Match 38.4% Score 28; DB 3; Length 13;  
 Best Local Similarity 44.4% Pred. No. Left 2;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EDGQWMDL 11  
 DB : DDGQLEHD 9

RESULT 11  
 US-09-057-897-15

Sequence 15, Application US/05057897  
 Patent No. 6360476  
 GENERAL INFORMATION:  
 APPLICANT: L. Ashbury Y.H.  
 APPLICANT: Wada, Reina W.  
 TITLE OF INVENTION: Anti-Influenza Antibody Against Human



TITLE OF INVENTION: Cytochrome P450 3A4  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: NJ  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS DOS  
SOFTWARE: Patent in Release #1, Version #1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,877  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hurd, C. Mark  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 19902  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (732)594-3305  
TELEFAX: (732)594-4720  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-057-877-15

Query Match: 37.0% Score 27 DB 47 Length 47  
Best Local Similarity: 81.3% Pref No: 2 Seqs: 1  
Matches: 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : CLEOTQ 6  
DB : CLEOTQ 6

RESULT 12  
US-09-914-088-24  
Sequence ID: Application US/78724544  
Patent No: 583530  
GENERAL INFORMATION:  
APPLICANT: Frank, Ronald  
TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF  
TITLE OF INVENTION: SUPPORT BOUND OR FREE PEPTIDES OR  
TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL  
TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND  
TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joseph T. Eisele  
ADDRESSEE: Kane, Daisner, Sullivan, Kurucz,  
ADDRESSEE: Levy, Eisele and Richard  
STREET: 711 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10017-4259  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3-1/2" DISKETTE  
COMPUTER: IBM-XT COMPATIBLE  
OPERATING SYSTEM: DOS 5.1  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,544

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/928,674  
FILING DATE: 04/22/93  
ATTORNEY/AGENT INFORMATION:  
NAME: EISELE, JOSEPH T.  
REGISTRATION NUMBER: 25,311  
REFERENCE/DOCKET NUMBER: 2727 68 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 487-6800  
TELEFAX: (212) 482-3485  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 residues  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE: Internal fragment  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLER:  
IMMEDIATE SOURCE:  
US-08-724-544-26

Query Match: 37.0% Score 27 DB 24 Length 13;  
Best Local Similarity: 50.0% Pref No: 116-02;  
Matches: 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY : EDGQVNVKL 12  
DB : DDGICLXKL 13

RESULT 13  
US-09-928-674-24  
Sequence ID: Application US/979286744  
Patent No: 6045421  
GENERAL INFORMATION:  
APPLICANT: Frank, Ronald  
TITLE OF INVENTION: SUPPORT BOUND OR FREE PEPTIDES OR  
TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL  
TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND  
TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joseph T. Eisele  
ADDRESSEE: Kane, Daisner, Sullivan, Kurucz,  
ADDRESSEE: Levy, Eisele and Richard  
STREET: 711 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10017-4259  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3-1/2" DISKETTE  
COMPUTER: IBM-XT COMPATIBLE  
OPERATING SYSTEM: DOS 5.1  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,544

1 CURRENT APPLICATION DATA:  
2 APPLICATION NUMBER: US/07/978,634B  
3 FILING DATE: 03/22/93  
4 CLASSIFICATION: 435  
5 EPIC APPLICATION DATA:  
6 APPLICATION NUMBER:  
7 FILING DATE:  
8 ATTORNEY/AGENT INFORMATION:  
9 NAME: BISELE, JOSEPH T.  
10 REGISTRATION NUMBER: 25,332  
11 REFERENCE/DOCKET NUMBER: 2727 FR 907  
12 TELECOMMUNICATION INFORMATION:  
13 TELEPHONE: (212) 687-6600  
14 TELEFAX: (212) 682-3485  
15 TELEX: (212) 426767  
16 INFORMATION FOR SEQ ID NO: 28:  
17 SEQUENCE CHARACTERISTICS:  
18 LENGTH: 10 residues  
19 TYPE: amino acid  
20 STRANDEDNESS:  
21 TOPOLOGY: LINEAR  
22 MOLECULE TYPE: Peptide  
23 HYPOTHEetical:  
24 ANTI-SENSE:  
25 FRAGMENT TYPE: Internal fragment  
26 ORIGINAL SOURCE:  
27 ORGANISM:  
28 STRAIN:  
29 INDIVIDUAL ISOLATE:  
30 DEVELOPMENTAL STAGE:  
31 HAPLOTYPE:  
32 TISSUE TYPE:  
33 CELL TYPE:  
34 CELL LINE:  
35 ORGANELLER:  
36 IMMEDIATE SOURCE:  
37 US-09-914-088-11

Query Match 37.03; Score 27; DB 4; Length 13;  
Best Local Similarity 50.03; Pred No. 1,5e-02;  
Matches 5; Conservative 2; Mismatches 1; Gaps 0;

CY ? EDGQVY 12  
|||  
DB 1 EDGQVY 10

RESULT 14  
US-09-914-448-B  
1 Sequence No. Application US/09/38448  
2 Patent No. 6218945  
3 GENERAL INFORMATION:  
4 APPLICANT: Simpson, Hugh A.  
5 TITLE OF INVENTION: Method for Determining Likelihood of Immunogenicity  
6 FILE REFERENCE: US 100  
7 CURRENT APPLICATION NUMBER: US/09/384,448  
8 CURRENT FILING DATE: 1999-01-28  
9 EARLIER APPLICATION NUMBER: 60/021,331  
10 EARLIER FILING DATE: 1998-01-30  
11 NUMBER OF SEQ ID NOS: 10  
12 SOFTWARE: Patent In Ver. 2.1  
13 SEQ ID NO: 8  
14 LENGTH: 12  
15 TYPE: PRT  
16 ORGANISM: Artificial Sequence  
17 FEATURES:  
18 OTHER INFORMATION: Description of Artificial Sequence: peptide  
19 US-09-914-448-B

Query Match 37.03; Score 27; DB 4; Length 13;  
Best Local Similarity 50.03; Pred No. 1,5e-02;  
Matches 5; Conservative 2; Mismatches 1; Gaps 0;

CY 3 EDGQVY 8  
|||  
DB 5 EDGQVY 10  
RESULT 15  
US-09-341-435-57  
1 Sequence 57; Application US/09/341,435  
2 Patent No. 6311961  
3 GENERAL INFORMATION:  
4 APPLICANT: TAKAHASHI, TOSHIYA  
5 APPLICANT: SAITO, NARIQ  
6 APPLICANT: TAKESHIGE, HIDEYUKI  
7 APPLICANT: TANAKA, TOSHIAKI  
8 APPLICANT: KAINOH, NAIE  
9 TITLE OF INVENTION: CYCLIC PEPTIDES AND MEDICINAL USE THEREOF  
10 FILE REFERENCE: 210914  
11 CURRENT APPLICATION NUMBER: US/09/341,435  
12 CURRENT FILING DATE: 1999-07-09  
13 PRIOR APPLICATION NUMBER: PCT/JP98/05096  
14 PRIOR FILING DATE: 1998-11-12  
15 NUMBER OF SEQ ID NOS: 57  
16 SOFTWARE: Patent In Ver. 2.1  
17 SEQ ID NO: 57  
18 LENGTH: 13  
19 TYPE: PRT  
20 ORGANISM: Artificial Sequence  
21 FEATURES:  
22 OTHER INFORMATION: Description of Artificial Sequence: Cyclic peptide  
23 US-09-341-435-57

Query Match 37.03; Score 27; DB 4; Length 13;  
Best Local Similarity 40.03; Pred No. 1,5e-02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
CY 1 CLEDSQVYMN 10  
|||  
DB 1 CLEDSQVYMN 10

Search completed: November 5, 2003, 16:04:57  
Job time: 14 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2001 Compaq Inc

OM Protein - protein search, using sw model

Run on: November 5, 2003, 18:11:55 / Search time 30 seconds  
(without alignment)  
76,935 Million cell updates/sec

Title: US-09-914-088-13

Perfect score: 89  
Sequence: 1 CFMKQLADLELCPR 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 2.5

Searched: 283308 seqs, 96168692 residues

Total number of hits satisfying chosen parameters: 2793

Minimum DP seq length: 0  
Maximum DP seq length: 16

Post-processing: Minimum Match 38  
Maximum Match 100  
Listing first 45 summaries

Database: PIR 76\*

1: PIR1\*  
2: PIR2\*  
3: PIR3\*  
4: PIR4\*

Field No. is the number of results predicted by chosen to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	27.0	12	2	S7044	140K protein, Sal
2	23	25.8	10	2	S7048	Glycine reductase
3	22	24.9	9	2	S5639	transmembrane protein
4	22	24.7	9	2	B4194	putative protein
5	22	24.3	10	2	A3121	protein, bullfro
6	22	24.2	12	2	A3360	protein, African
7	22	24.7	15	2	PAC342	protein, GEMK001
8	21	23.6	9	2	B28495	compressin S - co
9	21	23.6	9	2	A29477	transmembrane protein
10	21	23.6	15	2	S6261	protein, human sy
11	20.5	23.0	9	2	A26495	compressin G - co
12	20.5	23.0	9	2	S3902	lysine-transportin
13	20	22.5	10	2	A2195	Na <sup>+</sup> /K <sup>+</sup> exchanging
14	20	22.5	12	2	G9215	arabinose 5C-3,5,6
15	20	22.5	14	2	A35377	77 binding protein
16	20	22.5	14	2	I49514	B44 protein A m
17	20	22.5	15	2	S10891	cholesterol thiole
18	20	22.5	15	2	P70093	protein, thiole
19	19	21.3	8	2	A32573	protein, thiole
20	19	21.3	9	2	PIC119	transmembrane p
21	19	21.3	9	2	I52974	seminal vesicle pr
22	19	21.3	12	2	J02308	hypothetical 1.4K
23	19	21.3	15	2	G2318	hypothetical 1.4K
24	19	21.3	15	2	S3690	transmembrane p
25	19	21.3	16	2	S99631	transmembrane p
26	18.5	20.8	9	2	PC2021	oxyluciferin relat
27	18	20.2	11	2	B39504	octamer-binding pr
28	18	20.2	9	2	S66656	transmembrane p
29	18	20.2	12	2	S23148	protein, guinea

ALIGNMENTS

RESULT 1

S71034  
potB protein - Salmonella typhimurium (fragment)  
C:Species: Salmonella typhimurium  
C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 08-Oct-1999  
C:Accession: S71034  
R:Stein, M.A.; Leung, K.Y.; Zwick, M.; Garcia-del Portillo, F.; Finlay, B.B.  
Mol. Microbiol. 20, 151-164, 1996  
A:Title: Identification of a Salmonella virulence gene required for formation of filamentous structures  
A:Reference number: S71034; MIM:97014378; PMID:8861213  
A:Accession: S71034  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-12 <ST>  
A:Cross-references: EMBL:U51867; NID:91272352; PIDN:AAA97466.1; PID:91272353  
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, March 1996  
C:Genetics:  
A:Gene: potB

Query Match 27.0% Score 24; DB 2; Length 12;  
Best Local Similarity 37.5% Pred. No. 9,8e-02;  
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 6 MKKQLADLELCPR  
DB 3 MKKQLADLELCPR

RESULT 2

B39308  
glycine reductase (EC 1.4.99.1) sulphydryl protein C, beta chain - Clostridium sticklandii  
C:Species: Clostridium sticklandii  
C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 15-Aug-1997  
C:Accession: B39308  
R:Stadman, T.C.; Davis, J.N.  
J. Biol. Chem. 266, 22147-22153, 1991  
A:Title: Glycine reductase protein C: Properties and characterization of its role in the  
A:Reference number: A39308; MIM:92324241; PMID:1939235  
A:Accession: B39308  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <ST>  
C:Function:  
A:Description: glycine reductase complex catalyzes the reductive deamination of glycine  
C:Keywords: ATP, oxidoreductase

Query Match 25.8% Score 23; DB 2; Length 10;  
Best Local Similarity 57.1% Pred. No. 1.2e-03;  
Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 6 MKKQLADLELCPR  
DB 3 MKKQLADLELCPR

```

Db          3  MNKVIAD 9

RESULT 3
Sat75
Arginine vasotocin sea lamprey
C:Species: Petromyzon marinus [sea lamprey]
C:Date: 29-Feb-1993 #sequence_revision 29-Feb-1993 #text_change 31-Mar-1993
C:Accession: S06175
P:Lang, T.F.; Sower, S.A.; Kawachi, H.
Gen. Comp. Endocrinol. 70, 152-157, 1994
A:Title: Arginine vasotocin from the pituitary gland of the lamprey (Petromyzon marinus)
A:Reference number: S06175; MUID:98225256; PMID:1319449
A:Accession: S06175
A:Molecule type: protein
A:Residues: 1-9 <LAN>
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pituitary
F:1-6/Disulfide bonds: #status experimental
F:9/Modified site: amidated carboxyl end (Gly); #status experimental

Query Match      24.7% Score 22; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Gaps 0;

CY          10  LKQCFR 15
DB          3  LKQCFR 8

RESULT 4
H61364
vasotocin common carp
C:Species: Cyprinus carpio (common carp)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 23-Jun-2000
C:Accession: B61364
A:Chauvet, J.; Chauvet, M.T.; Chauvet, J.; Acher, R.
Comp. Biochem. Physiol. A 14, 245-254, 1983
A:Title: Characterization des hormones neurohypophysiales chez le poisson osseux d'eau douce
A:Reference number: A61364
A:Accession: B61364
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <AB>
C:Keywords: amidated carboxyl end; neuropeptide; posterior pituitary

Query Match      24.7% Score 22; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Gaps 0;

CY          10  LKQCFR 15
DB          3  LKQCFR 8

RESULT 5
A61131
Hydrotin 2 bullfrog
N:Alternate names: AVT-related peptide
N:Compains: Arg-vasotocin
C:Species: Rana catesbeiana (bullfrog)
C:Date: 12-Mar-1994 #sequence_revision 23-Mar-1994 #text_change 11-Jul-1997
C:Accession: A61131
P:Ikawano, S.; Hayashi, H.; Yatabuchi, K.; Kikuyama, S.
Gen. Comp. Endocrinol. 84, 412-418, 1991
A:Title: Arginine vasotocin (AVT) and AVT related peptide from the pituitary gland of the American bullfrog (Rana catesbeiana)
A:Reference number: A61131; MUID:92224111; PMID:1836420
A:Accession: A61131
A:Molecule type: protein
A:Residues: 1-10 <AW>
C:Comment: With the decapeptide hydrotin 20 and the undecapeptide neurophysin
C:Superfamily: oxytocin-neurophysin
C:Keywords: amidated carboxyl end; neuropeptide; pituitary
F:1-9/Product: Arg vasotocin #status experimental <AWAS>

F:9/Modified site: amidated carboxyl end (Gly); #status experimental

Query Match      24.7% Score 22; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 1; Gaps 0;

CY          10  LKQCFR 15
DB          3  LKQCFR 8

RESULT 6
A33900
Hydrotin 1 African clawed frog
N:Alternate names: arginine-vasotocin-related peptide; vasotocinyl-Gly Lys
C:Species: Xenopus laevis (African clawed frog)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 31-Mar-1997
C:Accession: A33900; S06176
P:Rouille, Y.; Michel, G.; Chauvet, M.T.; Chauvet, J.; Acher, R.
Proc. Natl. Acad. Sci. U.S.A. 86, 5272-5275, 1989
A:Title: Hydrotin, hydrocorticot neurohypophysial peptides: osmoregulatory adaptation in
A:Reference number: A33900; MUID:59151579; PMID:2787509
A:Accession: A33900
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <RCC>
P:Ikawano, S.; Hayashi, H.; Kikuyama, S.
Biochim. Biophys. Acta 1176, 143-147, 1993
A:Title: An additional arginine-vasotocin-related peptide, vasotocinyl-Gly Lys, in Xenopus
A:Reference number: S06176; MUID:93200145; PMID:84552872
A:Accession: S06176
A:Molecule type: protein
A:Residues: 1-12 <AWA>
C:Keywords: neuropeptide

Query Match      24.7% Score 22; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY          10  LKQCFR 18
DB          3  LKQCFR 8

RESULT 7
PA0092
Protein Oricin-1 fusaria (Fusarium sporotrichoides) (fragment)
C:Species: Fusarium sporotrichoides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0092
P:Chow, L.F.; Fukaya, N.; Sugura, Y.; Jeno, Y.; Tabuchi, K.; Tsugita, A.
Submitted to JBC, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichoides
A:Reference number: PA0092
A:Accession: PA0092
A:Molecule type: protein
A:Residues: 1-15 <CHG>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental

Query Match      24.7% Score 22; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 2.7e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

CY          3  MNKQIADLQCP 14
DB          2  MNVLFDMKCHP 13

RESULT 8
B28495
compressin S cone shell (Conus striatus)
N:Alternate names: Arg vasopressin

```

C:Species: Conus striatus (striated cone)  
 C:Date: 30 Jun-1989 #sequence\_revision 10 Jun-1989 #text\_change 20 Apr-1997  
 C:Accession: B28495  
 R:Cruz, L.J., de Santos, V., Zafaralla, G.C., Ramilo, C.A., Zeikus, R., Gray, W.R., Oliv  
 J. Biol. Chem. 262, 15821-15824, 1987  
 A:Title: Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from C  
 A:Reference number: A28417; MUID:88059932; PMID:3490424  
 A:Accession: B28495  
 A:Molecule type: protein  
 A:Residues: 1-9 <CPU>  
 C:Superfamily: oxytocin/neurophysin  
 C:Keywords: amidated carboxyl end; venom  
 F:6/Disulfide bonds: #status experimental  
 F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 23.6%, Score 20.5, DB 2, Length 9;  
 Best Local Similarity 100.0%, Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CPR 15  
 Db 5 CPR 8

RESULT 9  
 A29477  
 C:Species: Locusta migratoria (migratory locust)  
 C:Date: 31 Dec-1988 #sequence\_revision 1 Dec-1988 #text\_change 31-Dec-1993  
 C:Accession: A29477  
 R:Proulx, J.P., Miller, C.A., Jr., J.P., Curney, P., Le Garrec, A., Delage, M., Schooley  
 Biochem. Biophys. Res. Commun. 149, 148-156, 1987  
 A:Title: Identification of an arginine vasopressin like diuretic hormone from Locusta mi  
 A:Reference number: A29477; MUID:88079077; PMID:3488410  
 A:Accession: A29477  
 A:Molecule type: protein  
 A:Residues: 1-9 <PEO>  
 A:Note: two neuropeptides, P1 and P2, were identified. P2 is an antiparallel dimer of P1  
 C:Keywords: neuropeptide

Query Match 23.6%, Score 20.5, DB 2, Length 9;  
 Best Local Similarity 100.0%, Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CPR 15  
 Db 5 CPR 8

RESULT 10  
 S62641  
 C:Species: Drosophila melanogaster (fruit fly)  
 A:Title: Purification, metal cofactor, N-terminal sequence and subunit composition of a  
 A:Reference number: S62641; MUID:96195600; PMID:8810164  
 A:Accession: S62641  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <STO>  
 C:Keywords: carbon-oxygen lyase; hydrolase

Query Match 23.6%, Score 20.5, DB 2, Length 9;  
 Best Local Similarity 100.0%, Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CPR 15  
 Db 5 CPR 8

RESULT 11  
 A28495  
 C:Species: Conus geographus (geography cone)  
 C:Date: 30 Jun-1989 #sequence\_revision 10 Jun-1989 #text\_change 25-Apr-1997  
 C:Accession: A28495  
 R:Cruz, L.J., de Santos, V., Zafaralla, G.C., Ramilo, C.A., Zeikus, R., Gray, W.R., Oliv  
 J. Biol. Chem. 262, 15821-15824, 1987  
 A:Title: Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from C  
 A:Reference number: A28417; MUID:88059932; PMID:3490424  
 A:Accession: A28495  
 A:Molecule type: protein  
 A:Residues: 1-9 <CPU>  
 C:Superfamily: oxytocin/neurophysin  
 C:Keywords: amidated carboxyl end; venom  
 F:6/Disulfide bonds: #status experimental  
 F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 23.6%, Score 20.5, DB 2, Length 9;  
 Best Local Similarity 100.0%, Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CPR 15  
 Db 5 CPR 8

RESULT 12  
 S39040  
 C:Species: Epibobdella octoculata  
 C:Date: 19 Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 17-Mar-1999  
 C:Accession: S39040  
 R:Salzer, M., Biele, P., van Dorsselaer, A., Maechler, S.  
 Eur. J. Biochem. 247, 897-903, 1999  
 A:Title: Isolation, structural characterization and biological function of a lysine-cont  
 A:Reference number: S39040; MUID:94039146; PMID:18223646  
 A:Accession: S39040  
 A:Molecule type: protein  
 A:Residues: 1-9 <SA>

Query Match 23.6%, Score 20.5, DB 2, Length 9;  
 Best Local Similarity 100.0%, Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CPR 15  
 Db 5 CPR 8

RESULT 13  
 A32195  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 20 Oct-1989 #sequence\_revision 20 Oct-1989 #text\_change 19-Apr-2002  
 C:Accession: A32195  
 R:Tyson, P.A., Steinberg, M., Wallack, E.T., Kirley, T.J.  
 J. Biol. Chem. 264, 726-734, 1989  
 A:Title: Identification of the 5-iodoacetamidofluorescein reporter site on the Na,K-ATP  
 A:Reference number: A32195; MUID:89093137; PMID:2536022  
 A:Accession: A32195  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <TVS>  
 C:Keywords: hydrolase

Query Match 22.5%, Score 20.5, DB 2, Length 10;  
 Best Local Similarity 75.0%, Pred. No. 3.9e+03;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 CPR 15  
 Db 5 CPR 8

[illegible]

# Shi

• 100 •

G49215  
Enzyme EC 4.5.1.13; small subunit UroA; H-1 of enter toxin; Enterotoxin  
Species: Helicobacter felis  
C.Dat.: 19-Dec-1993 #sequence revision to Rev 1994 #EXT date: 1 May 1994  
C.Accession: G49215  
Ritterbett, G.R.; Ho, P.B.; Horne, R.T.; Voss, P.O.  
Infect. Immun. 60, 5259-5266, 1992  
Abstract: Purification and characterization of the mouse anti-toxin 1 Helicobacter species  
A.Reference number: A49215; MIMD:93084194; PMID:14542159  
A.Accession: G49215  
A.Status: preliminary  
A.Molecule type: protein  
A.Residues: 1-12 <tr>  
A.Experimental source: ATCC 49219  
A.Note: sequence extracted from NCBI database (NCBI:P01154-9)  
A.Keywords: hydrolase

Query March	22.5%	Score 10	38.2%	Temp 120
Post March Similarity	42.9%	Pref. No 4,70,000		
Matches	37	Conservative	37	Mismatches 17
				Gap 0

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99	1	1
100	1	1

2011-2012

10  
11  
12  
13  
14  
15  
16

A33377  
 GTP binding protein G alpha-12 chain, rat, brain  
 Species: Rattus norvegicus (McNwy 14)  
 Date: 17 Aug 1993 #sequence\_revision 1 Add 1000 extra amino acids 1997  
 Date: 17 Aug 1993 #sequence\_revision 1 Add 1000 extra amino acids 1997  
 GIAccession: A33377  
 Emitter: M.E.V. Kwaal, D.A. Miller, P. J. Gilman, A. G. J. Biol. Chem. 265, 8243-8251, 1990  
 Abstract: Purification and characterization of G proteins and their types of G alpha after  
 Affiliation: University of California, San Diego, CA 92094  
 Reference number: A33377, PMID:9024370, PMID:267474  
 AAccession: A33377  
 AStatus: preliminary  
 AMolecule type: protein  
 APeptides: 1-14 aa's  
 ASpecificity: GTP binding relatively to GTP and GDP

Only Match	2018	Score	Home Team	Away Team
First Goal Scorer	2018	Goal	Home Team	Away Team
Match	4	Conservative	1	Conservative

QY 1 FNNKLA B  
1 1 1 1  
CB 3 FNNKLA B

— 28 —

Search completed: November 5, 2003, 14:14:11.  
Job time: 20 secs

GenCore version 5.1.6  
Copyright (c) 1993 2003 CompuGen Ltd

OX protein protein search, using sw model

Run on: November 5, 2003, 18:05:00 / Search time: 11 seconds  
without alignments  
68,472 Million cell updates/sec

Title: US-09-914-088-13

Perfect score: 89

Sequence: 1 CFMNRQADLETPRE 16

Scoring table: BLOSUM62

Gapop 10.0, Supext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 632

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	24.7	9	1	OXVT_CYP6A
2	21.5	24.2	9	1	OXYA_SAVCA
3	21.5	24.2	9	1	OXYA_SQAC
4	21	23.6	9	1	CONC_CKST
5	21	23.6	9	1	DNF1_DNFV
6	20.5	23.0	9	1	CONC_SREP
7	20.5	23.0	9	1	OXYF_SVTA
8	20	22.5	12	1	LICH_PABT
9	20	22.5	12	1	KACI_SQAC
10	20	22.5	15	1	UBLI_XRSE
11	19	21.3	15	1	OXIA_CKST
12	18.5	20.8	9	1	OXYT_EBFC
13	18	20.2	9	1	OXYT_BURE
14	18	20.2	11	1	O2CA_CWTE
15	18	20.2	15	1	ALLS_MAXSE
16	18	20.2	16	1	KTRC_ASZYA
17	18	20.2	16	1	LEES_PICLO
18	17.5	19.7	9	1	OXYT_PABT
19	17	19.1	9	1	OXYT_PABT
20	17	19.1	9	1	OXYV_SQAC
21	17	19.1	13	1	SAP_STVA
22	17	19.1	13	1	UREP_MBYOC
23	17	19.1	15	1	COX1_HUOB
24	17	19.1	16	1	OXA1_CKST
25	17	19.1	16	1	UVSX_RPT5
26	16.5	18.5	9	1	ISOT_CYP7A
27	16	18.0	7	1	LANC_CKST
28	16	18.0	9	1	CCW_CWVE
29	16	18.0	9	1	OXYT_CWVE
30	16	18.0	10	1	XTNR_PTP4
31	16	18.0	11	1	OX5A_CKAL
32	16	18.0	11	1	OX5B_CKAL
33	16	18.0	12	1	N040_G0550

34	16	18.0	12	1	PR16_GINBI
35	16	18.0	13	1	ACT7_SOYBN
36	16	18.0	14	1	ATP6_SPIOL
37	16	18.0	15	1	CKX_WHEAT
38	16	18.0	15	1	CK38_CONOU
39	16	18.0	15	1	CIJAN_DIDMA
40	16	18.0	15	1	KLCM_LUYTE
41	16	18.0	15	1	ONCI_OROWY
42	16	18.0	15	1	PH2_PPRAY
43	16	18.0	15	1	UC28_MAIZE
44	16	18.0	16	1	DBH3_RRIZE
45	16	16.9	9	1	UJAH_HUMAN

## ALIGNMENTS

### RESULT 1

OXVT\_CYP6A STANDARD; PRT; 9 AA.  
AC P23879;  
DT 01-NOV-1991 (Rel. 20, Created;  
DT 01-NOV-1991 (Rel. 20, Last sequence update;  
DT 01-NOV-1995 (Rel. 12, Last annotation update;  
DE Vasotocin.  
OS Cyprinus carpio (Common carp), and  
OS Petromyzon marinus (Sea lamprey);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
OC Cyprinidae; Cyprinus  
CX NCBI\_TaxID:7962, 7757;  
RN 1;  
RP SPECIES: Cyprinus carpio, TISSUE: Pituitary;  
RA Acher R., Chalvet J., Chalvet M., Crepy D.;  
RT "Characterization of neurohypophyseal hormones from a fresh water bony  
RT fish, the carp, Cyprinus carpio"; Comparison with hormones from sea  
RT water: bony fishes;  
RC Comp. Biochem. Physiol. 14:245-254(1965);  
RN 2;  
RP SPECIES: Petromyzon marinus, TISSUE: Pituitary;  
RX MEDLINE:88225976, PubMed:3371648;  
RA Kane T.F., Sower S.A., Kawachi H.;  
RT "Arginine vasotocin from the pituitary gland of the lamprey  
RT (Petromyzon marinus): isolation and amino acid sequence";  
RC Gen. Comp. Endocrinol. 70:152-157(1989);  
CC 1- FUNCTION: ANTI-DIURETIC HORMONE.  
CC 1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR: S61364; 86164;  
DR PIR: S61375; S06375;  
DR InterPro: IPR000981; Neurohyp\_horm.  
DR Pfam: PFC0220; Hormone4.1;  
DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1;  
KW Hormone, Amidation.  
FT DISULFID  
FT MOD\_RES 1 9  
SQ SEQUENCE 9 AA; 10-13 WW; 17EB176B5456D045 CRC64;  
AMIDATION

Query Match: 24.7; Score 22; DB 1; Length 9;  
Best Local Similarity: 50.0; Pred. No. 1.3e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 10 LEICPR 15  
DB 3 TONCFR 6

### RESULT 2

OXYA\_SQAC STANDARD; PRT; 9 AA.  
ID OXYA\_SQAC  
AC P42946;  
DT 01-NOV-1991 (Rel. 20, Created;





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RX MEDLINE=85077077; PubMed=3699410;
RA Proulx C.P., Miller C.A., Li J.P., Carney R.J., Girardie A.,
RA Dellaage M., Schooley D.A.;
BT "Identification of an arginine vasopressin-like diuretic hormone from
BT Locusta migratoria";
RL Biochem Biophys Res Commun 249:142-146(1998);
CC -1- FUNCTION: DIURETIC HORMONE.
CC -1- SYNOPSIS: P2 IS AN ANTI-PARALFET DISULFIDE LINKED DIMER OF P1.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
CR PIR: A28477; A28477.
CR InterPro: IPR005981; Neutryp horm.
DR Pfam: PF02220; hormones; 1.
DR PROSITE: PS02264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Neuropeptide; Amidation.
PE DISULFID 1 6 IN P1.
PE DISULFID 1 1 INTERCHAIN (WITH C-6) IN P1.
PE DISULFID 6 6 INTERCHAIN (WITH C-1) IN P2.
FT MCD.RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 976 MW; 56EB176EH451A057 UNQ64;

Query Match 23.0%; Score 20.5; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1; 1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CPR 15
DB 6 CPR 8

RESULT 4
CN CGC RANGE STANDARD: PRT: 4 AA.
AC P0486;
DT 01-NOV-1993 (Rel. 39, Created)
DT 01-NOV-1993 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lys-compressin G.
OS Genus neogriphus (Geography core):
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthostomopoda;
OC Apogastropoda; Caenogastropoda; Siphonophora; Hypsimeristoida;
OC Neogastropoda; Conoidea; Conidae; Conus.
CX NCHI_TaxID=6491;
CX 11.
RN 11.
RP REVIEW.
RX MEDLINE=85058932; PubMed=3680226;
RA Cruz W.P., de Santos V., Zafaralla L.J., Ramirez A., Peris R.;
RA Gray W.R., Oliveira B.M.;
BT "Peptide toxins from venomous Conus snails";
RL Annu Rev Biochem 57:665-700(1988);
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
CR PIR: A28495; A28495.
CR InterPro: IPR000581; Neutryp horm.
DR Pfam: PF02220; hormones; 1.
DR PROSITE: PS02264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
PE DISULFID 1 6
FT MCD.RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1037 MW; D4FC26EB4542B59 UNQ64;

Query Match 23.0%; Score 20.5; DB 1; Length 9;
Best Local Similarity 26.7%; Pred.No. 1; 1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 1;

QY 1 CPMKQQLAC:ELCP 15
DB 1;

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DB 1 CPMK... -CPK 8

RESULT 7
CN CGC RANGE STANDARD: PRT: 9 AA.
AC P42957;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Phasvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchia; Galeomorphi; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
CX NCB_TaxID=7810;
CX 11.
RN 11.
RP SEQUENCE.
RX TISSUE=Plutitary; PubMed=7972045;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauvet M.-T., Acher R.;
BT "Special evolution of neurohypophysial hormones in cartilaginous
BT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
BT isolated from the spotted dogfish (Scyliorhinus canicula)";
RL Proc Natl Acad Sci U S A 91:11266-11270(1994);
CC -1- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
CR InterPro: IPR003981; Neutryp horm.
DR Pfam: PF02220; hormones; 1.
DR PROSITE: PS02264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
PE DISULFID 1 6
FT MCD.RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1016 MW; 17EDD765B4449DB UNQ65;

Query Match 23.0%; Score 20.5; DB 1; Length 9;
Best Local Similarity 28.6%; Pred.No. 1; 1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 1 CPMKQQLAC:ELCP 14
DB 1;
DB 1 CPMK...-CP 7

RESULT 8
CN CGC RANGE STANDARD: PRT: 12 AA.
AC P83307;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lichenin.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCB_TaxID=1402;
CX 11.
RN 11.
RP SEQUENCE.
RX STRAIN=25L 10/3RA; PubMed=21576300;
RX MEDLINE=21460732; PubMed=21576300;
RA Pattnaik P., Kaushik J.K., Grover S., Batish V.K.;
BT "Purification and characterization of a bacteriocin-like compound
BT (lichenin) produced anaerobically by Bacillus licheniformis isolated
BT from water Buffalo";
RL J Appl Microbiol 91:636-645(2001);
RN 12.
RP SEQUENCE.
RX STRAIN=26L-10/3RA;
RA Pattnaik P.;
BT "Biochemical characterization and molecular genetics of bacteriocin
BT produced by a selected pure bacterial isolate";
RL Thesis (1999), National Dairy Research Institute / Karnal, India.
CC -1- FUNCTION: OXYGEN LABILE BACTERIOCIN-LIKE. HAS ANTIBACTERIAL
CC ACTIVITY.

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REASON 15
ID ALLS MANSE STANDARD; PRT: 15 AA.
AC 242559.
BT 01 NOV 1996 Rel. 32. Created.
DT 01 NOV 1996 Rel. 32. Last sequence update.
DE 28 FEB 2003 Rel. 41. Last annotation update.
DE Allotostatin (Mas-AS).
OS Manduca sexta (Tobacco hawkmoth) silkworm, lepidoptera
OC Eukaryota; Metazoa; Arthropoda; Insecta; Lepidoptera
OC Neoptera; Euclypteroptera; Lepidoptera; Glossata; Polyphaga; Apicomplexa
OC Spinnidae; Spinningidae; Manduca.
CX NCBI TaxID=7130;
RN 11.
RP SEQUENCE.
AC TISSUE Head.
EX MEDLINE 92050112; PubMed=1946153.
RA Kravitz S.D., Toschi A., Miller C.A., Karsaka H., Quistad G.B.,
RA Li J.P., Carney R.L., Schooley D.A.
RT "Identification of an allatostatin from the tobacco hornworm Manduca
RT sexta."
R1 Proc. Natl. Acad. Sci. U.S.A. 86:9438-9442(1989)
CC 1 FUNCTION: STRONGLY INHIBITS JUVENILE HORMONE BIOSYNTHESIS IN VITRO
CC BY THE CORPORA ALLATA FROM FIFTH STADIUM LARVAE AND ADULT FEMALES.
CC 1 SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DE PIP, A6162; A6162.
KW Neuropeptide; Pyroglutamate carboxyl; acid.
FT MAP RES 1 1 PYR-GLUTONE CARBOXYLIC ACID.
SO SEQUENCE 15 AA; 1909 MW; 1634PDCDDEHRE CPCR4.

Query Match 20.2%; Score 15; EB 1; Length 15;
Post. local Similarity 50.0%; Prob. No. 40.0%;
MATCHES 2; Conservative 1; Mismatch 1; 100.0% 1; gaps 0;

CY 1 CPM 4
DL 2 CYP 10

Search completed: November 5, 2003, 14:13:16
Job time: 12 secs

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GenCore version: 5.1.6  
Copyright (c) 1993-2003 CompuGen Ltd.

GV protein protein search, using sw model

Run on: November 5, 2003, 18:10:25 ; Search time: 13 Seconds

Without alignment

125,116 Multiple Cell updates

Title: US 09-914-088-13

Perfect score: 89

Sequence: 1 CHMKQLADLECHRE 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 810525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 4 22

Minimum CB seq length: 3

Maximum CB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREML: 23.4

1: sp archaea:

2: sp bacteria:

3: sp fungi:

4: sp human:

5: sp invertebrate:

6: sp mammal:

7: sp mhc:

8: sp organelle:

9: sp phage:

10: sp plant:

11: sp rodent:

12: sp virus:

13: sp vertebrate:

14: sp unclassified:

15: sp rvirus:

16: sp bacteriaph:

17: sp archaeap:

18: sp archaeap:

19: sp archaeap:

20: sp archaeap:

SUMMARIES

Pred. No. is the number of results identified by the search engine  
score greater than or equal to the score of the best hit found,  
and is derived by analysis of the total number of hits found.

Result No.	Score	Query	Match	Length	OR	ID
1	27	30.3	15	5	Q9TW99	1
2	25	28.1	14	4	O15222	1
3	24	22.0	15	2	O9R407	1
4	23	25.8	13	6	Q9TUB1	1
5	23	25.8	15	10	Q8WAX4	1
6	23	25.8	15	11	O91XV9	1
7	23	25.8	16	2	O937M1	1
8	22	24.7	11	4	O75811	1
9	22	24.7	11	4	O9H3V7	1
10	22	24.7	11	13	Q9R524	1
11	22	24.7	14	4	Q81C09	1
12	22	24.7	15	4	Q9UCB1	1
13	22	24.7	15	4	Q9XQ00	1
14	21	23.6	11	7	O76131	1
15	21	23.6	15	13	Q8R265	1
16	21	23.6	14	1	Q81C09	1

17	21.6	21	21.6	14	6	Q9V131	Q8R101 sus scrofa
18	21.6	21	21.6	15	2	Q47832	Q47832 tremyella d
19	21.6	21	21.6	13	10	Q9S631	Q9S631 scenedesmus
20	21.6	21	21.6	16	3	P79014	P79014 emericella
21	22.5	20	22.5	10	2	Q9RSU1	Q9RSU1 helicobacte
22	22.5	20	22.5	10	9	Q37103	Q37103 saccharomyc
23	22.5	20	22.5	11	10	Q9T029	Q9T029 brassica oi
24	22.5	20	22.5	12	2	Q935F7	Q935F7 helicobacte
25	22.5	20	22.5	12	2	Q9R5F5	Q9R5F5 helicobacte
26	22.5	20	22.5	13	4	Q9H4C1	Q9H4C1 homo sapien
27	22.5	20	22.5	14	11	Q921H4	Q921H4 mus musculu
28	22.5	20	22.5	14	5	Q9PYL3	Q9PYL3 human t cell
29	22.5	20	22.5	15	9	Q80277	Q80277 lactococcus
30	22.5	20	22.5	16	4	Q36731	Q36731 homo sapien
31	22.5	20	22.5	12	4	Q9H4F4	Q9H4F4 homo sapien
32	22.5	20	22.5	12	12	Q88577	Q88577 theiler's e
33	22.5	20	22.5	12	12	Q88578	Q88578 theiler's e
34	22.5	20	22.5	12	12	Q88579	Q88579 theiler's e
35	22.5	20	22.5	12	12	Q88575	Q88575 theiler's e
36	22.5	20	22.5	12	12	Q88580	Q88580 theiler's e
37	22.5	20	22.5	12	12	Q88582	Q88582 theiler's e
38	22.5	20	22.5	12	12	Q88581	Q88581 theiler's e
39	22.5	20	22.5	12	12	Q88576	Q88576 theiler's e
40	22.5	20	22.5	13	2	Q9XBYC	Q9XBYC nitrogen-fi
41	22.5	20	22.5	15	2	Q9R542	Q9R542 mycobacteri
42	22.5	20	22.5	15	4	P78482	P78482 homo sapien
43	22.5	20	22.5	15	6	P82665	P82665 bos taurus
44	22.5	20	22.5	16	4	Q9DP51	Q9DP51 homo sapien
45	22.5	20	22.5	9	4	Q16276	Q16276 homo sapien

ALIGNMENTS

RESULT 1

Q9TW99 PRELIMINARY; PR: 15 AA.

AC Q9TW99  
CT 01-MAY 2003 (TREMPEL: 13, Created)  
DT 01-MAY 2003 (TREMPEL: 13, Last sequence update)  
DT 01-JUN 2003 (TREMPEL: 14, Last annotation update)  
DE G39 antigen (fragment)  
OS Hirudo medicinalis (medicinal leech)  
CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudini  
OC Ancyrodermatida; Hirudiniiformes; Hirudiniidae; Hirudo.  
OX NCBI TaxID:6421.  
BN 111  
RN 111  
RS 111  
RA MEDLINE 04195315 (PubMed:5113784)  
RT Identification of a 15 kD protein with sequence homology to squid  
RT neurofilament protein in glial cells of the leech CNS.  
RL 01 Neurobiol. 25:75-82 (1994).  
SQ SEQUENCE 15 AA: 1717 MW: 153584884A11C95E CRC64;

Query Match 30.3% Score 27; DB 5; Length 15;  
Best Local Similarity 62.5%; Pred.No. 7.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 NCQLADLE 11

DB 2 NCQLADVE 9

RESULT 2

O15222 PRELIMINARY; PR: 14 AA.

AC O15222  
CT 01-JAN 1998 (TREMPEL: 05, Created)  
DT 01-JAN 1998 (TREMPEL: 05, Last sequence update)  
DE G39 antigen (fragment)  
OS Hirudo medicinalis (medicinal leech)  
CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudini  
OC Ancyrodermatida; Hirudiniiformes; Hirudiniidae; Hirudo.  
OX NCBI TaxID:6421.  
BN 111  
RN 111  
RS 111  
RA MEDLINE 04195315 (PubMed:5113784)  
RT Identification of a 15 kD protein with sequence homology to squid  
RT neurofilament protein in glial cells of the leech CNS.  
RL 01 Neurobiol. 25:75-82 (1994).  
SQ SEQUENCE 14 AA: 1717 MW: 153584884A11C95E CRC64;

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CC Homo sapiens (Human);
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX XREF:98019011; PubMed:9357979;
YA Flagello C., Gibaud A., Dutrillaux R., Poupin M.P., Mailly P.,
RT "Distinct patterns of alkaline phosphatase expression of
RT the HX3 and HXC homologues in human embryonal and amniotic lung
RT carcinoma cell lines";
PL FERS Lett. 415:263-267(1997);
DR EXEL: X99CF2; CAA67998.1;
DR TRANSFAC; T03327;
FT NON TER
SQ SEQUENCE 14 AA: 1725 MW; 6C5D7220549A1B CRC64;

Query Match 28.11; Score 25; DB 4; Length 14;
Best Local Similarity 55.61; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MKKQADLE 11
DB 4 MKKQADLE 12

RESULT 3
QY 3 MKKQADLE 11
DB 4 MKKQADLE 12

AC Q94U77 PRELIMINARY; PRT; 15 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
FE Malonate decarboxylase gamma subunit (Fragment)
LS Acinetobacter calcoaceticus
CC Bacteria; Proteobacteria; Gammaproteobacteria; Betaproteobacteria;
CX Miftheriaceae; Acinetobacter;
CX NCBI_TaxID=471;
FT NON TER
RP SEQUENCE
RX MEDLINE=95040612; PubMed=7961952;
RA Kiny S., Ryan H.S.;
RT "Purification and properties of a novel type of alkaline phosphatase
RT from Acinetobacter calcoaceticus";
FE J. Biol. Chem. 269:29636-29641(1994);
SQ SEQUENCE 15 AA: 1816 MW; 4E24F1E46F0F0A CRC64;

Query Match 29.23; Score 26; DB 4; Length 15;
Best Local Similarity 56.74; Pred. No. 1.5e+03;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 MKKQADLE 11
DB 4 MKKQADLE 12

RESULT 4
QY 3 MKKQADLE 11
DB 4 MKKQADLE 12

AC Q94U77 PRELIMINARY; PRT; 15 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Tle-2/tek receptor tyrosine kinase (Fragment)
CS Bos taurus (Bovine)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovinae; Bovidae;
CC Bovidae; Bovinae; Bos;
CX NCBI_TaxID=9913;
FT NON TER
RP SEQUENCE FROM N.A.
RX HOWELL F.W., Catt E.L., Murray G.;
RT Tissue Lymphocytes;

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RT "Cloning and characterization of human tle-2/tek promoter.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF077857; AAF01566.1;
KW Kinase; Receptor;
FT NON TER
SQ SEQUENCE 13 AA: 1295 MW; 9AF9F2F5BCBC735 CRC64;

Query Match 25.81; Score 23; DB 6; Length 13;
Best Local Similarity 71.41; Pred. No. 3.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 LADLELC 13
DB 4 LADLELC 10

RESULT 5
QY 7 LADLELC 13
DB 4 LADLELC 10

AC Q84X5 PRELIMINARY; PRT; 15 AA.
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE CH13/nitrate reductase structural protein (Fragment)
GN NIA2
CC Arabidopsis thaliana (House-cat cress);
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eurosids 1; Brassicales; Brassicaceae; Arabidopsids;
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93005711; PubMed=840322;
RA Wilkinson J.Q., Crawford N.M.;
RT "Identification of the Arabidopsis CH13 gene as the nitrate reductase
RT structural gene NIA2";
RA Plant Cell 3:461-471(1991);
DR EMBL; S45394; AAJ3272.1;
FT NON TER
SQ SEQUENCE 15 AA: 1721 MW; 71C91FC829E1CFD CRC64;

Query Match 25.81; Score 23; DB 10; Length 15;
Best Local Similarity 62.51; Pred. No. 3.7e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MKKQADLE 11
DB 3 MKKQADLE 14

RESULT 6
QY 4 MKKQADLE 11
DB 3 MKKQADLE 14

AC Q91XV4 PRELIMINARY; PRT; 15 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 20alpha hydroxysteroid dehydrogenase (Fragment)
OS Rattus norvegicus (Rat)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus;
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE: Liver;
RA Nakamura T., Yasuda K., Okada H., Sanezumi M., Osaki T., Kanzaki H.,
RA Nishizawa Y., Ito S.;
RT "Expression of 20alpha-HSD (hydroxysteroid dehydrogenase) in
RT endometrium";
PL J. Fertilization and Implantation 17:186-197(2001);
DR EMBL; AB025564; BAB2013.1;
FT NON TER
SQ SEQUENCE 15 AA: 1732 MW; 9452E70F45C4622F CRC64;

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Query Match 25.8%; Score 23; DB 11; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 3; 7e+03;  
 Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 MKKQADLEL 12  
 | | | | |  
 DB 1 MNSKIQKVEL 10

RESULT 9  
 Q95811 PRELIMINARY; PRT: 11 AA  
 AC Q95811  
 DT 01-DEC-2001 (TrEMBLrel. 10, Created;  
 DT 01-DEC-2001 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 23, Last annotation update)  
 DE Putative meucuric reductase (Fragment)  
 GN MEPA  
 OS Escherichia coli  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae  
 CC Enterobacteriaceae; Escherichia  
 OX NCBI\_TaxID=562  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HE16; TRANSPOSON-TN5057;  
 EX MEDLINE=21694134; PubMed=11763247  
 RA Mindlin S.Z., Khochbil G.V., Gorienko Z.M., Vinadkina S.V.,  
 RA Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petiova M.A.,  
 RA Yurlova O.V., Nikiforov V.G.  
 RT "Vesicular resistance transposons of Gram-negative environmental  
 RT bacteria and their classification."  
 RL Res. Microbiol. 152:811-822(2001)  
 DE EMBL: AJ162764; CAC83555.1; -  
 FT NON TER 1  
 SQ SEQUENCE 16 AA; 1713 MW; 5AD7D64652956E12364;

Query Match 25.8%; Score 23; DB 21; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 3; 9e+03;  
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 NKQLADLEL 13  
 | | | | |  
 DB 5 NKDVKQLSCC 14

RESULT 9  
 Q95811 PRELIMINARY; PRT: 11 AA  
 AC Q95811  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 09, Last annotation update)  
 DE FHB3\_1; R2 (Fragment)  
 GN C-ERBB-3  
 OS Homo sapiens (Human)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo  
 OX NCBI\_TaxID=9606  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovarian carcinoma;  
 RX MEDLINE=99345147; PubMed=9681822;  
 RA Lee H., Mathis N.J.,  
 RT "Isolation and characterization of four alternative 5'UTR? transcripts  
 RT expressed in ovarian carcinoma-derived cell lines and normal human  
 RT tissues."  
 RL Oncogene 16:3243-3252(1998)  
 DE EMBL: U88358; AAC39858.1; -  
 FT NON TER 1  
 SQ SEQUENCE 11 AA; 1017 MW; 21823466E871979 97647

Query Match 24.7%; Score 22; DB 4; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 4; 7e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 75.0%; Pred. No. 4; 1e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LCPRE 15  
 | | | | |  
 DB 6 LCPK 9

RESULT 9  
 Q9H3V7 PRELIMINARY; PRT: 11 AA  
 AC Q9H3V7  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Aquaporin-4 (Fragment)  
 GN AQP4  
 OS Homo sapiens (Human)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo  
 OX NCBI\_TaxID=9606  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=97008105; PubMed=8855241;  
 RA Lu M., Lee M.D., Smith B.L., Jung J.S., Agre P., Verkijk M.A.J.,  
 RA Merks G., Ripps J.P.L., Beier P.M.,  
 RT "The human AQP4 gene: definition of the locus encoding two water  
 RT channel polypeptides in brain."  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:15908-15912(1996)  
 DE EMBL: J63613; AAG17964.1; -  
 KW Porin  
 FT NON TER 1  
 FT NON TER 1  
 SQ SEQUENCE 11 AA; 1233 MW; 379C9CA111AER737 CRC64;

Query Match 24.7%; Score 22; DB 4; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 4; 1e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 LCPRE 16  
 | | | | |  
 DB 5 LCPRE 9

RESULT 10  
 Q9PS22 PRELIMINARY; PRT: 11 AA  
 AC Q9PS22  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hydrin 1; VASOTOCINYL GAY-LYS  
 OS Xenopus laevis (African Clawed Frog)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 CC Xenopodidae; Xenopus  
 OX NCBI\_TaxID=8355  
 RN 11  
 RP SEQUENCE  
 RX MEDLINE=91200145; PubMed=8452872;  
 RA Iwamuro S., Hayashi H., Kikuyama S.,  
 RT "An additional arginine-vasotocin-related peptide, vasotocinyl-Gly-  
 RT Lys, in Xenopus neurohypophysis."  
 RL Biochem. Biophys. Acta 1176:143-147(1993)  
 DR InterPro: IPR000991; Neutryp\_horm  
 DR Pfam: PF00220; hormone4.1  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1  
 SQ SEQUENCE 11 AA; 1238 MW; CC5B57EB176B9456 CRC64;

Query Match 24.7%; Score 22; DB 13; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 4; 7e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 10 CLOPS 15
CB 1 CLOPS 8

RESULT 11
QBXCO0
ID QBXCO0 PRELIMINARY: PRT: 15 AA
AC QBXCO0
DT 01-JUN-2003 (TRENBERG) 17, Created
DT 01-JUN-2003 (TRENBERG) 17, Last sequence update
DT 01-MAR-2002 (TRENBERG) 20, Last annotation update
DE Tissue transglutaminase (EC 2.3.2.13) (Fragment)
GN TGM2
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
CX NCBI_TaxID:9606
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE:Brain
RA Citron B.A., Santa Cruz K.S., Davies P.J.A., Pestoff R.W.
RT Intron-exon swapping of transglutaminase mRNA and neuronal tau
RT aggregation in Alzheimer's disease
RJ J. Biol. Chem. 276:32001
DR EMBL: AF311286, AAK15272.1
KW ACyltransferase; Transferase
FT NON_TER
SQ SEQUENCE 15 AA: 164 MW; 2345982AFBF851 CRC64;

Query Match 24.7%; Score 22; DB 4; Length 15;
Best Local Similarity 33.3%; Pred. No. 5.6e+03;
Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 FYNKQADLELC 13
DB 4 FSKACCSWIC 15

RESULT 14
Q78121
ID Q78121 PRELIMINARY: PRT: 11 AA
AC Q78121
DT 01-NOV-1998 (TRENBERG) 18, Created
DT 01-NOV-1998 (TRENBERG) 18, Last sequence update
DT 01-DEC-2001 (TRENBERG) 19, Last annotation update
DE MHC class II B locus 12 (Fragment)
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC Acanthopterygii; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
CC Cichlidae; Oreochromis
CX NCBI_TaxID:4128
RN 1
RP SEQUENCE FROM N.A.
RX YEDJIN8581311; PubMed:9649339;
RA Valdega-Trillo E., Mareska-Rutzyńska Z., McAndrew H., Vincek V.,
RA Figueroa F., Sultmann H., Klein G.
RT "Linkage relationships and haplotype polymorphism among cichlid the
RT class II B loci"
RJ Genetics 149:1527-1537(1998)
DR EMBL: AF050527, AAC41866.1
FT NON_TER
SQ SEQUENCE 11 AA: 1262 MW; 03C12C8EB7341B54 CRC64;

Query Match 23.6%; Score 21; DB 7; Length 11;
Best Local Similarity 57.1%; Pred. No. 6.2e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FYNKQCLA 8
DB 2 FYNFELS 8

RESULT 16
QBXCO0
ID QBXCO0 PRELIMINARY: PRT: 15 AA
AC QBXCO0
DT 01-JUN-2003 (TRENBERG) 17, Created
DT 01-JUN-2003 (TRENBERG) 17, Last sequence update
DT 01-MAR-2002 (TRENBERG) 20, Last annotation update
DE Tissue transglutaminase (EC 2.3.2.13) (Fragment)
GN TGM2
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
CX NCBI_TaxID:9606
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE:Brain
RA Citron B.A., Santa Cruz K.S., Davies P.J.A., Pestoff R.W.
RT Intron-exon swapping of transglutaminase mRNA and neuronal tau
RT aggregation in Alzheimer's disease
RJ J. Biol. Chem. 276:32001
DR EMBL: AF311286, AAK15272.1
KW ACyltransferase; Transferase
FT NON_TER
SQ SEQUENCE 15 AA: 164 MW; 2345982AFBF851 CRC64;

Query Match 24.7%; Score 22; DB 4; Length 15;
Best Local Similarity 33.3%; Pred. No. 5.6e+03;
Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 6 QADLELCBP 15
DB 1 QADLELCBP 15

RESULT 12
QBXCO0
ID QBXCO0 PRELIMINARY: PRT: 15 AA
AC QBXCO0
DT 01-MAY-2003 (TRENBERG) 14, Created
DT 01-MAY-2003 (TRENBERG) 14, Last sequence update
DT 01-JUN-2000 (TRENBERG) 14, Last annotation update
DE Insulin like growth factor receptor alpha subunit (Fragment)
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
CX NCBI_TaxID:9606
RN 1
RP SEQUENCE
RX MEDLINE 94079595; PubMed:9257688;
RA Kasuya J., Paz I.B., Maddux B.A., Substone L.F., Bell G.A.,
RA Fujita Y., Yaguchi Y.
RT "Characterization of human placental insulin like growth factor
RT I/insulin hybrid receptors by protein microsequencing and
RT purification"
RJ Biochemistry 42:13531-13536(1993)
DR Biochemistry 42:13531-13536(1993)
SQ SEQUENCE 15 AA: 1761 MW; 856F444F8F470A7504;

Query Match 24.7%; Score 22; DB 4; Length 15;
Best Local Similarity 75.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 ELOP 14
DB 4 ELOP 9

RESULT 13

```

```

QY 10 CLOPS 15
CB 1 CLOPS 8

RESULT 11
QBXCO0
ID QBXCO0 PRELIMINARY: PRT: 15 AA
AC QBXCO0
DT 01-JUN-2003 (TRENBERG) 17, Created
DT 01-JUN-2003 (TRENBERG) 17, Last sequence update
DT 01-MAR-2002 (TRENBERG) 20, Last annotation update
DE Tissue transglutaminase (EC 2.3.2.13) (Fragment)
GN TGM2
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
CX NCBI_TaxID:9606
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE:Brain
RA Citron B.A., Santa Cruz K.S., Davies P.J.A., Pestoff R.W.
RT Intron-exon swapping of transglutaminase mRNA and neuronal tau
RT aggregation in Alzheimer's disease
RJ J. Biol. Chem. 276:32001
DR EMBL: AF311286, AAK15272.1
KW ACyltransferase; Transferase
FT NON_TER
SQ SEQUENCE 15 AA: 164 MW; 2345982AFBF851 CRC64;

Query Match 24.7%; Score 22; DB 4; Length 15;
Best Local Similarity 33.3%; Pred. No. 5.6e+03;
Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 FYNKQADLELC 13
DB 4 FSKACCSWIC 15

RESULT 14
Q78121
ID Q78121 PRELIMINARY: PRT: 11 AA
AC Q78121
DT 01-NOV-1998 (TRENBERG) 18, Created
DT 01-NOV-1998 (TRENBERG) 18, Last sequence update
DT 01-DEC-2001 (TRENBERG) 19, Last annotation update
DE MHC class II B locus 12 (Fragment)
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC Acanthopterygii; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
CC Cichlidae; Oreochromis
CX NCBI_TaxID:4128
RN 1
RP SEQUENCE FROM N.A.
RX YEDJIN8581311; PubMed:9649339;
RA Valdega-Trillo E., Mareska-Rutzyńska Z., McAndrew H., Vincek V.,
RA Figueroa F., Sultmann H., Klein G.
RT "Linkage relationships and haplotype polymorphism among cichlid the
RT class II B loci"
RJ Genetics 149:1527-1537(1998)
DR EMBL: AF050527, AAC41866.1
FT NON_TER
SQ SEQUENCE 11 AA: 1262 MW; 03C12C8EB7341B54 CRC64;

Query Match 23.6%; Score 21; DB 7; Length 11;
Best Local Similarity 57.1%; Pred. No. 6.2e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FYNKQCLA 8
DB 2 FYNFELS 8

RESULT 16
QBXCO0
ID QBXCO0 PRELIMINARY: PRT: 15 AA
AC QBXCO0
DT 01-JUN-2003 (TRENBERG) 17, Created
DT 01-JUN-2003 (TRENBERG) 17, Last sequence update
DT 01-MAR-2002 (TRENBERG) 20, Last annotation update
DE Tissue transglutaminase (EC 2.3.2.13) (Fragment)
GN TGM2
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
CX NCBI_TaxID:9606
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE:Brain
RA Citron B.A., Santa Cruz K.S., Davies P.J.A., Pestoff R.W.
RT Intron-exon swapping of transglutaminase mRNA and neuronal tau
RT aggregation in Alzheimer's disease
RJ J. Biol. Chem. 276:32001
DR EMBL: AF311286, AAK15272.1
KW ACyltransferase; Transferase
FT NON_TER
SQ SEQUENCE 15 AA: 164 MW; 2345982AFBF851 CRC64;

Query Match 24.7%; Score 22; DB 4; Length 15;
Best Local Similarity 33.3%; Pred. No. 5.6e+03;
Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 6 QADLELCBP 15
DB 1 QADLELCBP 15

RESULT 12
QBXCO0
ID QBXCO0 PRELIMINARY: PRT: 15 AA
AC QBXCO0
DT 01-MAY-2003 (TRENBERG) 14, Created
DT 01-MAY-2003 (TRENBERG) 14, Last sequence update
DT 01-JUN-2000 (TRENBERG) 14, Last annotation update
DE Insulin like growth factor receptor alpha subunit (Fragment)
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
CX NCBI_TaxID:9606
RN 1
RP SEQUENCE
RX MEDLINE 94079595; PubMed:9257688;
RA Kasuya J., Paz I.B., Maddux B.A., Substone L.F., Bell G.A.,
RA Fujita Y., Yaguchi Y.
RT "Characterization of human placental insulin like growth factor
RT I/insulin hybrid receptors by protein microsequencing and
RT purification"
RJ Biochemistry 42:13531-13536(1993)
DR Biochemistry 42:13531-13536(1993)
SQ SEQUENCE 15 AA: 1761 MW; 856F444F8F470A7504;

Query Match 24.7%; Score 22; DB 4; Length 15;
Best Local Similarity 75.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 ELOP 14
DB 4 ELOP 9

RESULT 13

```



DT C1-MAR-2003 (TREMBSrel. 23, Created)  
 DT C1-MAR-2003 (TREMBSrel. 23, Last sequence update)  
 DT C1-MAR-2003 (TREMBSrel. 23, Last annotation update)  
 DE Gall urea transporter (Fragment)  
 CN EUT.  
 OS Anguilla japonica (Japanese eel)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Atherinomorpha; Atherinidae;  
 CC Anguilla.  
 OX NCBI\_TaxID:7547;  
 GN 11  
 EN SEQUENCE FROM E.A.  
 EC TISSUE: Liver.  
 RA Hirose S., Mistry A.C.  
 RI Gall urea transporter (EUT) gene.  
 RI Submitted (Oct 2000) to the EMBL/GenBank/CCDC databases.  
 DR EMBL: AB049727; BAC51977.1; -.  
 FT NCN\_TSS 11  
 FT NCN\_TSS 13  
 SC SEQUENCE 13 AA; 1536 MW; 4F367864188AA07 CRC64.

Query Match 23.6% Score 117 CR 13, Length 197  
 Best local Similarity 33.3% Pred. No 7,16+03  
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CPXNKQLAD 9  
 |||  
 Sb 4 CPDDEWPD 12

Search completed: November 5, 2003, 18:14:00  
 Job time : 45 secs

GenCore version: 5.1.6  
Copyright (c) 1993 - 2003 CompuLink Ltd

OM mode:n protein search, using sw model

Run on: November 5, 2003, 18:04:19 : Search time 41 seconds  
Without alignments  
61,942 Million cell updates/sec

Title: US 09-914 088-13

Perfect score: 89

Sequence: 1 CFMKKQACIELOPRE 16

Scoring table: BLASTN62

Gapop 10.0 , Gapext 0.5

Searched: 1107803 seqs, 158726571 residues

Total number of hits satisfying chosen parameters: 16014

Minimum DB seq length: 0

Maximum DB seq length: 16

Fast-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by cluster to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	16	21	AA1961
2	89	100.0	16	22	AA1961
3	89	100.0	16	23	AA1961
4	81	93.3	16	21	AA1961
5	81	93.3	16	22	AA1961
6	81	93.3	16	23	AA1961
7	72	80.9	13	21	AA1961
8	72	80.9	13	22	AA1961
9	72	80.9	13	23	AA1961

10	66	74.2	13	21	AA1961	P1 mimotope SEQ ID
11	66	74.2	13	22	AA1961	Peptide #1 derived
12	66	74.2	13	23	AA1961	Human IgE cyclic
13	33	37.1	13	21	AA1961	P1 mimotope Peptide
14	33	37.1	13	22	AA1961	Peptide P15q deriv
15	33	37.1	13	23	AA1961	Human IgE cyclic
16	33	37.1	16	23	AA1961	Human IgE cyclic
17	32	36.0	15	23	AA1961	Human Fc10.01 N to
18	31	34.8	9	23	AA1961	Human bone marrow
19	31	34.8	15	24	AA1961	Human dioxigenase
20	30	33.7	9	22	AA1961	HIV A24 super moti
21	30	33.7	9	22	AA1961	HIV A24 motif tat
22	30	33.7	11	22	AA1961	HIV A24 super moti
23	30	33.7	11	22	AA1961	HIV A03 motif tat
24	30	33.7	11	22	AA1961	HIV A11 motif tat
25	30	33.7	14	22	AA1961	Human peptide #37
26	30	33.7	15	22	AA1961	HIV DR super motif
27	29	32.6	9	22	AA1961	PRAME derived HLA-
28	29	32.6	10	23	AA1961	CTL epitope HLA pe
29	29	32.6	10	23	AA1961	CTL epitope HLA pe
30	29	32.6	10	23	AA1961	CTL epitope HLA pe
31	29	32.6	10	23	AA1961	CTL epitope HLA pe
32	29	32.6	12	14	AA1961	Synthetic sequence
33	29	32.6	12	14	AA1961	Synthetic sequence
34	29	32.6	12	14	AA1961	Human glycoalbumin
35	29	32.6	12	22	AA1961	Human peptide #132
36	28	31.5	10	24	AA1961	Human cancer-relat
37	28	31.5	10	24	AA1961	Human cancer-relat
38	28	31.5	10	24	AA1961	Human cancer-relat
39	28	31.5	10	24	AA1961	Human cancer-relat
40	28	31.5	10	24	AA1961	Human cancer-relat
41	28	31.5	11	23	AA1961	Sequence of glycop
42	28	31.5	13	19	AA1961	Cyclic-UPA peptide
43	28	31.5	13	19	AA1961	Cyclic-UPA peptide
44	28	31.5	13	23	AA1961	Selective target in
45	28	31.5	14	23	AA1961	Human Hsp90xxx asp

# ALIGNMENTS

RESULT 1  
AAB25919 standard: Peptide; 16 AA

```
XX AAB25919:
XX AC AAB25919:
XX DT 05-JAN-2001 (first entry)
XX PE mimotope peptide P1009 SEQ ID NO:13.
XX KW Epitope/ mimotope/ human; immunoglobulin E; IgE; C-epsilon-2 domain;
XX KW allergic disease; immunophy-axis; immunotherapy; antiallergic;
XX KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;
XX KW allergy; atopy.
XX OS Homo sapiens.
XX PN W0000050460-A1.
XX PD 31-AUG-2000.
XX PF 22 FEB 2003; 2003W-EP01455.
XX PR 25-FEB-1999; 99GB 0004405.
XX PR 23-MAR 1999; 99GB 0007151.
XX PR 07-MAY 1999; 99GB 0010537.
XX PR 07-MAY 1999; 99GB 0010538.
XX PR 07-AUG 1999; 99GB 0015594.
XX PR 07-AUG 1999; 99GB 0015603.
XX PR 07-SEP 1999; 99GB 0021046.
XX PR 07-SEP 1999; 99GB 0021047.
XX PR 09-OCT 1999; 99GB 0026619.
```



PT disulfide bridge cyclized peptide and immunogenic carrier -  
 PS Claim 4: Page 11: 45pp; English.  
 XX  
 CC The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclised peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a cyclic peptide immunogen derived  
 CC from human immunoglobulin E (IgE) suitable for use in the invention.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 83; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CFYKQKQADLELCPE 16  
 DB 1 CFYKQKQADLELCPE 16  
 AC AAR25118;  
 D7 05 JAN 2001 (first entry)  
 DE P1 mimotope peptide C67/8 SEQ ID No:12.  
 XX Epitope mimotope: human; immunoglobulin E (IgE); Cepsilon2 domain;  
 XX allergic disease; immunotherapy; immunotherapy; antiallergic;  
 XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 XX allergy; atopy.  
 OS Homo sapiens.  
 XX  
 XX WQ2000050462 A1.  
 XX 31-AUG 2000.  
 XX 22 FEB 2000; 2000WQ-EP01455.  
 XX 25 FEB 1999; 99GB-0024405.  
 XX 29 MAR 1999; 99GB-0022152.  
 XX 07 MAY 1999; 99GB-0010537.  
 XX 07 MAY 1999; 99GB-0010544.  
 XX 07 AUG 1999; 99GB-0018594.  
 XX 07 AUG 1999; 99GB-0018603.  
 XX 07-SEP 1999; 99GB-C021046.  
 XX 07-SEP 1999; 99GB-C021047.  
 XX 29-OCT 1999; 99GB-C025619.  
 XX 23-NOV-1999; 99GB-C027699.  
 XX  
 XX (SMK) : SMITHKLINE BEECHAM BIOLOGICALS.  
 XX (PEPT) : PEPTIDE THERAPEUTICS LTD.  
 XX  
 XX Cyson N, Friede M, Greenwood J, Hewitt B, Lambert A, Mason J,  
 XX Randall P, Turner WG, Van Mechelen WP, Vanhille P, Bussell R;  
 XX WPI; 2001-521973/53.  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 XX diseases, comprising an isolated surface exposed group of a specific  
 XX domain from immunoglobulin E -  
 XX Example 6: Page 11: 129pp; English  
 XX The present invention describes a peptide containing an isolated  
 XX surface exposed group/epitope (E1) of Cepsilon2 domain of an  
 XX immunoglobulin E (IgE), or its mimotope. Also described is an  
 XX immunogen (II) for treating allergy comprising (a) a vaccine (III)

CC for treating allergies comprising (II); (3) a ligand (IV) capable of  
 CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
 CC (Iia) comprising (Ia); and (7) producing (II) by producing (II); (II)  
 CC can have anti-allergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (II), (III) and (IV) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (IV) is useful for identifying mimotopes of E1,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (II) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (II), (III) and (IV) are  
 CC useful for treating a patient susceptible to it suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AAR25907 to AAR26099 represent  
 CC peptide sequences which are used in the exemplification of the present  
 XX invention.  
 SQ Sequence 16 AA;  
 Query Match 93.3%; Score 83; DB 21; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 1.2e-06;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CFYKQKQADLELCPE 16  
 DB 1 CFYKQKQADLELCPE 16  
 AC AAU16643;  
 DT 07-NOV 2001 (first entry)  
 XX Peptide C67/8 derived as mimotope of Cepsilon2 region of human IgE.  
 XX Human; linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
 KW IgE mediated disease; antibody response.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WQ20014574- A2.  
 XX 28-JUN 2001.  
 XX 21-FEB 2000; 2000WQ-0404935.  
 XX 21-DEC 1999; 99GB-0030233.  
 XX 22-FEB 2000; 2000GB-0004396.  
 XX 22-AUG-2000; 2000GB-0025707.  
 XX 22-AUG 2000; 2000GB-0020708.  
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 XX (ACAM) : ACAMRIS RES LTD.  
 XX (SMK) : SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 XX Flynn N, Johnson T;  
 XX WPI; 2001-521967/57.  
 XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
 XX mediated diseases  
 XX Example 4: Page 21: 46pp; English.  
 XX The present invention relates to linkage methodology for use in the  
 XX conjugation of compounds (e.g. peptides) to carrier vehicles  
 XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 XX biological and immunological constructs. The invention provides a  
 XX method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 XX protein) for use in a pharmaceutical composition or a vaccine. The





FD 41-AUG-2000;  
 XX  
 PF 21-FEB-2000; 2000MC-RP01455;  
 XX  
 XX 25-FEB-1999; 99GB-0004405;  
 PR 23-MAR-1999; 99GB-0007151;  
 PR 02-MAY-1999; 99GB-0010537;  
 PR 03-MAY-1999; 99GB-0010538;  
 PR 07-AUG-1999; 99GB-0018594;  
 PR 07-AUG-1999; 99GB-0018603;  
 PR 07-SEP-1999; 99GB-0021346;  
 PR 07-SEP-1999; 99GB-0021647;  
 PR 24-OCT-1999; 99GB-0025619;  
 PR 21-NOV-1999; 99GB-0027658;  
 XX  
 PA (SMK) : SYNTHELINE BEECHAM BIOLOGICALS;  
 PA (SEPT) : PEPTIDE THERAPEUTICS LTD;  
 XX  
 PI Dymov M, Friede M, Greenwood J, Hewitt E, Jackson A, Mason S;  
 PI Randall R, Turner WG, Van Mechelen VL, Vinakis De Bassotis Y;  
 XX  
 XX WPI: 2000-02071/53;  
 XX  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group, in a specific  
 PT domain from immunoglobulin E;  
 XX  
 XX Disclosures: Page 11; 12pp; English;  
 XX  
 XX The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (E) of Cepsilon2 domain of an  
 CC immunoglobulin E (IgE), or its mimope. Also described are (II) an  
 CC immunogen (II) for treating allergic comprising (I); (I) A vaccine (III)  
 CC for treating allergies comprising (I); (I) A ligand (IV) capable of  
 CC recognising E; (I) A pharmaceutical composition (V) comprising (I);  
 CC (I) A peptide (I), capable of being recognised by (I); (I) An immunogen  
 CC that comprising (I); and (I) producing (I) by producing (I); (I)  
 CC can have anti-allergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor; (I); (I) and (I) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies; (I) is useful for identifying mimotopes of (I),  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies; (I) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood; (I); (I) and (I) are  
 CC useful for treating a patient susceptible to or suffering from allergies;  
 CC (I) is also useful in diagnosing a patient; AA0269154, AA0269155, AA0269156  
 CC peptide sequences which are used in the experiments of the present  
 CC invention;  
 XX  
 XX SQ Sequence 13 AA;  
 Query Match 74.23; Score 66; E-Value 1.0e-13;  
 Best Local Similarity 74.23; E-Value 1.0e-13;  
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CEMVQKQAPLELC 13  
 DE 1 CEMVQKQAPLELC 13  
 RESULT 11  
 AA0269154  
 ID AA0269154 standard; Peptide; 13 AA  
 AC AA0269154  
 XX  
 XX 07-SEP-2000 (first entry)  
 XX  
 XX Peptide #1 derived from Cepsilon2 region of human IgE  
 DE  
 XX Human linkage technology; conjugated epitope; anti-allergic  
 XX epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
 XX IgE-related disease; antibody ref 0001

XX  
 CS Homo sapiens;  
 CS Synthetic;  
 XX  
 XX WC200145745 A2;  
 XX  
 XX 28 JUN-2001;  
 XX  
 XX 21-DEC-2000; 2000MC-RB04935;  
 XX  
 XX 21-DEC-1999; 99GB-0010233;  
 PR 22-FEB-2000; 2000GB-0004036;  
 PR 22-AUG-2000; 2000GB-0020707;  
 PR 22-AUG-2000; 2000GB-0020708;  
 XX  
 PA (ACAM) : ACAM'S RES LTD;  
 PA (SMK) : SMITHKLINE BEECHAM BIOLOGICALS;  
 XX  
 PI Flinn N, Johnson T;  
 XX  
 XX WPI: 2001-521967/57;  
 XX  
 XX A linkage comprising an immunogenic conjugate useful treatment of IgE  
 PT mediated diseases;  
 XX  
 XX Example 4; Page 21; 4pp; English;  
 XX  
 XX The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC reagent for the treatment of IgE-mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AA016612; AA016613 represent peptides derived from or mimotopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE;  
 XX  
 XX SQ Sequence 13 AA;  
 Query Match 74.23; Score 66; E-Value 1.0e-13;  
 Best Local Similarity 74.23; E-Value 1.0e-13;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CEMVQKQAPLELC 13  
 DE 1 CEMVQKQAPLELC 13  
 RESULT 12  
 AB000323  
 ID AB000323 standard; Peptide; 13 AA  
 XX  
 XX AC AB000323;  
 XX  
 XX 02-SEP-2000 (first entry)  
 XX  
 XX Human IgE cyclic immunogenic peptide SEQ ID NO: 107;  
 DE  
 XX Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
 KW vaccine; anti-allergic; cyclic  
 XX  
 XX Homo sapiens;  
 CS  
 XX WC200145745 A2  
 XX  
 XX 28 JUN-2001;  
 XX

XX 17-AUG-2001; 2001WO-EP09576.  
 XX  
 XX  
 PR 22-AUG-2000; 2000GP-0020717.  
 XX  
 XX  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD  
 XX  
 PI Friede M, Mason S, Turrell WG, Vidal's Bassols VC.  
 XX  
 DR WPI; 2002-48964a/50.  
 XX  
 XX Conjugate for use in vaccine for treatment of allergy; comprising  
 PT disulfide bridge cyclized peptide and immunogenic carrier  
 XX  
 PS (Claim 4; Page 11; 45pp; English.  
 XX  
 CC The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclised peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a cyclic peptide immunogen derived  
 CC from human immunoglobulin E (Ige) suitable for use in the invention.  
 XX  
 SQ Sequence 13 AA:  
 Query Match 74.2% Score 66; DB 23; Length 13;  
 Best Local Similarity 84.6% Pred. No. 0.00034;  
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CFMKKQLADLELC 13  
 Db : CFMKKQLADLELC 13  
 RESULT 13  
 AAB25917  
 ID AAB25917 standard; Peptide; 13 AA.  
 AC AAB25917;  
 XX  
 XX 05 JAN 2001 (first entry)  
 XX  
 XX P1 minotope peptide P15q SEQ ID NO:111.  
 XX  
 XX Epitope; minotope; human; immunoglobulin E (Ige); Cepsilon2 domain;  
 KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO20000460-A1.  
 XX  
 XX 31 AUG-2000.  
 XX  
 XX 22 FEB 2000; 2000WO-EP01455.  
 XX  
 XX 25-FEB-1999; 99GB-0004405.  
 PR 23 MAR 1999; 99GB-0007151.  
 PR 03-MAY-1999; 99GB-0010537.  
 PR 04-MAY-1999; 99GB-0010538.  
 PR 07 AUG 1999; 99GB-0018594.  
 PR 07 AUG 1999; 99GB-0018601.  
 PR 07-SEP 1999; 99GB-0021046.  
 PR 07-SEP 1999; 99GB-0021047.  
 PR 23-OCT 1999; 99GB-0025619.  
 PR 23-NOV 1999; 99GB-0027698.  
 XX  
 XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
 XX  
 XX Dyson M, Friede M, Greenwood M, Hewitt E, Gordon A, Vanden  
 PI Randall N, Turrell WG, Van Mechelen MP, Vindels G, Randall N.

XX WPI; 2000-592073/53.  
 XX  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX  
 PS Claim 14; Page 9; 129pp; English.  
 XX  
 CC The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (E1) of Cepsilon2 domain (D) of  
 CC immunoglobulin E (Ige), or its minotope. Also described are: (i) an  
 CC immunogen (II) for treating allergy comprising (i); (2) a vaccine (III)  
 CC for treating allergies comprising (i); (3) a ligand (IV) capable of  
 CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
 CC (IIa) comprising (Ia); and (7) producing (III) by producing (i); (i)  
 CC can have antiallergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (i); (ii) and (iii) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (IV) is useful for identifying mimotopes of E1,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (i) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-Ige antibodies from blood. (i); (iii) and PC are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
 CC peptide sequences which are used in the exemplification of the present  
 XX invention.  
 XX  
 SQ Sequence 13 AA:  
 Query Match 37.1% Score 33; DB 23; Length 13;  
 Best Local Similarity 38.5% Pred. No. 0.02402;  
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 CFMKKQLADLELC 13  
 Db : CFMKKQLADLELC 13  
 RESULT 14  
 AAU16642  
 ID AAU16642 standard; Peptide; 13 AA.  
 XX  
 XX AAU16642;  
 XX  
 XX 07-NOV 2001 (first entry)  
 XX  
 XX Peptide (I); derived as minotope of Cepsilon2 region of human Ige.  
 XX  
 XX Human; linkage technology; conjugated compound; carrier vehicle;  
 KW epitope; Cepsilon2; Cepsilon1; Cepsilon4; immunoglobulin E;  
 KW Ige mediated disease; antibody response.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200145745 A2.  
 XX  
 XX 28-JUN 2001.  
 XX  
 XX 21-DEC-2000; 2000WO-GR04935.  
 XX  
 XX 21-DEC 1999; 99GB-0030233.  
 PR 22-FEB-2000; 2000GB-0034096.  
 PR 22-AUG-2000; 2000GB-002707.  
 PR 22-AUG-2000; 2000GB-002708.  
 XX  
 XX (ACAM) ACAMBIOS RES LTD.  
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 XX Flinn N, Johnson T.





Result No.	Score	Query Match	Length	DB ID	... (truncated)
1	29	32.6	10	12	US-8 11 384 48
2	29	32.6	10	12	US-8 11 384 48
3	29	32.6	10	12	US-8 11 384 48
4	29	32.6	10	12	US-8 11 384 48
5	28	31.5	14	11	US-8 11 384 48
6	28	31.5	14	11	US-8 11 384 48
7	28	31.5	16	10	US-8 11 384 48
8	28	31.5	16	10	US-8 11 384 48
9	27	30.3	14	11	US-8 11 384 48
10	27	30.3	14	12	US-8 11 384 48
11	26	29.2	4	15	US-8 11 384 48
12	26	29.2	4	15	US-8 11 384 48
13	26	29.2	8	15	US-8 11 384 48
14	26	29.2	8	15	US-8 11 384 48
15	26	29.2	10	15	US-8 11 384 48

## RESULT 2

US-09-935-384-485  
 ? Sequence 494, Application US/0993384  
 ? Publication No. US20030166526A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: CHALLITA-BID, PIA  
 ? APPLICANT: HUBERT, RENE  
 ? APPLICANT: RAITANO, ARTHUR  
 ? APPLICANT: AFAR, DANIEL  
 ? APPLICANT: LEVIN, ELANA  
 ? APPLICANT: FARIS, MARY  
 ? APPLICANT: GE, WANMOW  
 ? APPLICANT: JAKROVITZ, AVA  
 ? TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PEPTIDE NAMED 158P1H4  
 ? TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 ? TITLE OF INVENTION: OTHER CANCERS  
 ? FILE REFERENCE: 51158-20033-CC  
 ? CURRENT APPLICATION NUMBER: US/09/935,384  
 ? PRIOR FILING DATE: 2001-08-22  
 ? PRIOR FILING DATE: 2002-08-22  
 ? NUMBER OF SEQ ID NOS: 783  
 ? SOFTWARE: Patent in Ver. 2.1  
 ? SEQ ID NO 488  
 ? LENGTH: 10  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 US-09-935-384-485

Query Match 32.6%, Score 29; DB 12; Length 10;  
 Best Local Similarity 75.0%; Pref. No. 2.2e+02;  
 Matches 6; Conservative 1; Mismatches 1; Gaps 0;

QY 5 KKLAFEL 12  
 ||| ||  
 DB 5 KKLAFEL 10

## RESULT 3

US-09-935-384-500  
 ? Sequence 509, Application US/099335181  
 ? Publication No. US20030166526A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: CHALLITA-BID, PIA  
 ? APPLICANT: HUBERT, RENE  
 ? APPLICANT: RAITANO, ARTHUR  
 ? APPLICANT: AFAR, DANIEL  
 ? APPLICANT: LEVIN, ELANA  
 ? APPLICANT: FARIS, MARY  
 ? APPLICANT: GE, WANMOW  
 ? APPLICANT: JAKROVITZ, AVA  
 ? TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PEPTIDE NAMED 158P1H4  
 ? TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 ? TITLE OF INVENTION: OTHER CANCERS  
 ? FILE REFERENCE: 51158-20033-CC  
 ? CURRENT APPLICATION NUMBER: US/09/935,384  
 ? PRIOR FILING DATE: 2001-08-22  
 ? PRIOR FILING DATE: 2002-08-22  
 ? NUMBER OF SEQ ID NOS: 783  
 ? SOFTWARE: Patent in Ver. 2.1  
 ? SEQ ID NO 509  
 ? LENGTH: 10  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 US-09-935-384-500

Query Match 32.6%, Score 29; DB 12; Length 10;  
 Best Local Similarity 75.0%; Pref. No. 2.2e+02;  
 Matches 6; Conservative 1; Mismatches 1; Gaps 0;

QY 5 KKLAFEL 12  
 ||| ||  
 DB 5 KKLAFEL 10

## DB

3 KKLAFEL 10

## RESULT 4

US-09-935-384-674  
 ? Sequence 674, Application US/09935364  
 ? Publication No. US20030166526A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: CHALLITA-BID, PIA  
 ? APPLICANT: HUBERT, RENE  
 ? APPLICANT: RAITANO, ARTHUR  
 ? APPLICANT: AFAR, DANIEL  
 ? APPLICANT: LEVIN, ELANA  
 ? APPLICANT: FARIS, MARY  
 ? APPLICANT: GE, WANMOW  
 ? APPLICANT: JAKROVITZ, AVA  
 ? TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
 ? TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 ? TITLE OF INVENTION: OTHER CANCERS  
 ? FILE REFERENCE: 51158-20033-CC  
 ? CURRENT APPLICATION NUMBER: US/09/935,384  
 ? PRIOR FILING DATE: 2001-08-22  
 ? PRIOR FILING DATE: 2002-08-22  
 ? NUMBER OF SEQ ID NOS: 783  
 ? SOFTWARE: Patent in Ver. 2.1  
 ? SEQ ID NO 674  
 ? LENGTH: 10  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 US-09-935-384-674

Query Match 32.6%, Score 29; DB 12; Length 10;  
 Best Local Similarity 75.0%; Pref. No. 2.2e+02;  
 Matches 6; Conservative 1; Mismatches 1; Gaps 0;

QY 5 KKLAFEL 12  
 ||| ||  
 DB 5 KKLAFEL 10

## RESULT 5

US-09-966-782A-47  
 ? Sequence 47, Application US/09966782A  
 ? Publication No. US20030224193A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: RAITANO, ARTHUR  
 ? APPLICANT: HUBERT, RENE  
 ? APPLICANT: JAKROVITZ, AVA  
 ? APPLICANT: WISEMAN, E  
 ? APPLICANT: HAWKEN, E  
 ? APPLICANT: GAGACE, A  
 ? APPLICANT: HARBER, J  
 ? APPLICANT: KORACKI, M. G.  
 ? TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRPM7,  
 ? TITLE OF INVENTION: EXPRESSED HIGHLY IN SPINAL CORD  
 ? FILE REFERENCE: 2004481  
 ? CURRENT APPLICATION NUMBER: US/09/966,782A  
 ? PRIOR FILING DATE: 2001-09-26  
 ? PRIOR FILING DATE: 2002-09-27  
 ? PRIOR FILING DATE: 2002-09-27  
 ? PRIOR FILING DATE: 2001-02-14  
 ? PRIOR FILING DATE: 2001-02-14  
 ? PRIOR FILING DATE: 2001-02-28  
 ? NUMBER OF SEQ ID NOS: 64  
 ? SOFTWARE: Patent in Ver. 2.1  
 ? SEQ ID NO 47  
 ? LENGTH: 14  
 ? TYPE: PRT  
 ? ORGANISM: Artificially Synthesized  
 ? FEATURES:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: polypeptide  
 US 09-966-782A-47

Query Match: 31.5%; Score: 28; DP: 11; Length: 19;  
Best Local Similarity: 60.0%; pred. No. 4.5e+02;  
Matches: 6; Conservative: 2; Mismatches: 17; Indels: 0; Gaps: 0;

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3  MNKCLADEL  : 2
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      :
3  MNKCLADES  : 14

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RESISTANCE  
US-10-254-515-47

APPLICANT: BRISTOL MYERS SQUIBB COMPANY

FILE OF INVENTION: SPINAL CORD  
FILE REFERENCE: D0044 CIP  
CURRENT APPLICATION NUMBER: US/10/24,903

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; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 47

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TYPE: PRF  
ORGANISM: Homo sapiens  
US: 10 254-905.47

Query Match  
Best Local Similarity  
Matches: 6; Conservation

Qy	3	UNKLADJES	12
		:	
Ub	5	UNKLADJES	14

REF ID: A66666  
US-10-00-1-13-6

Publication No. US2006013  
GENERAL INFORMATION:  
APPLICANT: Meyers, Rache

FILE OF INVENTOR	FILE REFERENCE	CURRENT APPLICATION NUMBER
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2	2	2
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; PRIOR APPLICATION NUMBER
; PRIOR FILING DATE: 2001-
; NUMBER OF SEQ ID NOS: 7

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SEQ NO: 6  
LENGTH: 15  
TYPE: PR.

US 10 07 2006

Matches	4; (Conservation)
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93 41 156551 14

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Sequence 20, Application US/09779054  
Patent No. US202012102A1  
GENERAL INFORMATION:

APPLICANT: KAKKER, Vijay  
TITLE OF INVENTION: USE OF DENDROASPIN  
FILE REFERENCE: A-70312/TAL/AMS

CURRENT FILING DATE: 2001-02-05  
PRIOR APPLICATION NUMBER: GE 00-000000  
PRIOR FILING DATE: 2000-02-05

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; SOFTWARE: Patent version 3.0
; SEQ ID NO 20
; LENGTH: 16

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US-C9-779-054-20

Best local similarity 50.0%; Pred. No. 5.1e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels

2 CPTKQAGV 11

RESULT 9  
US-09-966-792A-43  
Sequence 43, Application:

GENERAL INFORMATION:  
APPLICANT: Battaglino, P.  
APPLICANT: Feder, C. N.

APPLICANT: Ramanathan, R.  
APPLICANT: Westphal, R.  
APPLICANT: Hawken, D. B.

APPLICANT: Barber, L.  
APPLICANT: Kornacker, M.  
TITLE OF INVENTION: A NEW

FILE REFERENCE: D0044NP  
CURRENT APPLICATION NUMBER:  
CURRENT FILING DATE: 200

PRIOR PENDING STATE CASES

PRIOR FILING DATE: 2001  
NUMBER OF SEQ. NOS.: 44  
SOFTWARE: PATENT IN VO.

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; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial S-
; STRUCTURE

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OTHER INFORMATION: POLYMER  
OTHER INFORMATION: POLYMER  
US-99-966 782A-40

Query Match:  
Best Loc: Similarity 6  
Matches 6; Conservat:

[illegible]

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RESULT 10
US-10-254-905-40
? Sequence 40, Application US/10254905
? Publication No. US20030196265A1
? GENERAL INFORMATION:
? APPLICANT: Bristol-Myers Squibb Company
? TITLE OF INVENTION: A NOVEL HUMAN G PROTEIN-RELATED PEPTIDE, HEP-907, EXPRESSED HIT
? FILE REFERENCE: SPINAL CORD
? CURRENT APPLICATION NUMBER: US/10/254,905
? CURRENT FILING DATE: 2002-03-25
? NUMBER OF SEQ ID NOS: 75
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 40
? LENGTH: 4
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-254-905-40

Query Match: 30.3%, Score 27, DB 12, Length 14
Best Local Similarity: 60.0%, Pred. No. 6.5e+05
Matches: 6, Conservative 1, Mismatches 3, Indels 0, Gaps 0

CY 3 MNKQLADEL 12
D6 1 1111
1 1 INLSADESL 12

RESULT 11
US-10-028-075B-132
? Sequence 132, Application US/10028075B
? Publication No. US2003011733A1
? GENERAL INFORMATION:
? APPLICANT: Khan, Nisar A.
? TITLE OF INVENTION: Gene regulator
? FILE REFERENCE: 2183-5223US
? CURRENT APPLICATION NUMBER: US/10/028,075B
? CURRENT FILING DATE: 2001-12-21
? PRIOR APPLICATION NUMBER: EP 01203748.7
? PRIOR FILING DATE: 2001-10-04
? NUMBER OF SEQ ID NOS: 175
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 132
? LENGTH: 4
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: pdb/19FA/19FA
US-10-028-075B-132

Query Match: 29.2%, Score 26, DB 15, Length 8
Best Local Similarity: 100.0%, Pred. No. 5.9e+05
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 11 CPRE 16
D6 1 1111
1 1 CPRE 4

RESULT 12
US-10-029-206A-132
? Sequence 132, Application US/10029206A
? Publication No. US20030119720A1
? GENERAL INFORMATION:
? APPLICANT: Khan, Nisar A.
? TITLE OF INVENTION: Glucosylpeptide treatment of anthrax
? FILE REFERENCE: 2183-5222US
? CURRENT APPLICATION NUMBER: US/10/029,206A
? CURRENT FILING DATE: 2001-12-21
? PRIOR APPLICATION NUMBER: 09/821,360
? PRIOR FILING DATE: 2001-12-21
? NUMBER OF SEQ ID NOS: 175
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 132
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: pdb/19FA/19FA
US-10-029-206A-132

Query Match: 29.0%, Score 26, DB 15, Length 8
Best Local Similarity: 100.0%, Pred. No. 5.9e+05
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 11 CPRE 16
D6 1 1111
1 1 CPRE 4

RESULT 13
US-10-028-075B-131
? Sequence 131, Application US/10028075B
? Publication No. US2003011733A1
? GENERAL INFORMATION:
? APPLICANT: Khan, Nisar A.
? TITLE OF INVENTION: Gene regulator
? FILE REFERENCE: 2183-5223US
? CURRENT APPLICATION NUMBER: US/10/028,075B
? CURRENT FILING DATE: 2001-12-21
? PRIOR APPLICATION NUMBER: EP 01203748.7
? PRIOR FILING DATE: 2001-10-04
? NUMBER OF SEQ ID NOS: 175
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 131
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: pdb/19FA/19FA
US-10-028-075B-131

Query Match: 29.2%, Score 26, DB 15, Length 8
Best Local Similarity: 100.0%, Pred. No. 5.9e+05
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 11 CPRE 16
D6 1 1111
1 1 CPRE 4

RESULT 14
US-10-029-206A-131
? Sequence 131, Application US/10029206A
? Publication No. US20030119720A1
? GENERAL INFORMATION:
? APPLICANT: Khan, Nisar A.
? TITLE OF INVENTION: Glucosylpeptide treatment of anthrax
? FILE REFERENCE: 2183-5222US
? CURRENT APPLICATION NUMBER: US/10/029,206A
? CURRENT FILING DATE: 2001-12-21
? PRIOR APPLICATION NUMBER: 09/821,360
? PRIOR FILING DATE: 2001-12-21
? NUMBER OF SEQ ID NOS: 175
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 131
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: pdb/19FA/19FA
US-10-029-206A-131

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Query Match: 29.2% Score 26; DB 15; Length 97
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 13 CPSE 16
DB 4 CPSE 7

RESULT 15
US 10 011-089 337
: Sequence 197; Application US/02211084
: Publication No. US20030104479A1
: GENERAL INFORMATION:
: APPLICANT: Bright, Gary R.
: APPLICANT: Premkumar, D. David
: APPLICANT: Choo, Yih-Tai
: TITLE OF INVENTION: No. US20030104479A1: Fusion Proteins And Assays For Molecular Bi
: FILE REFERENCE: 01 1022-US
: CURRENT APPLICATION NUMBER: US/10/211-088
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 62/309,395
: PRIOR FILING DATE: 2003-08-01
: PRIOR APPLICATION NUMBER: 62/341,599
: PRIOR FILING DATE: 2001-12-13
: NUMBER OF SEQ ID NOS: 166
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 137
: LENGTH: 17
: TYPE: PFT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: Nuclear export signal
US 10 011-089 337

Query Match: 29.2% Score 26; DB 15; Length 107
Best Local Similarity 50.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

CY 3 MMSQLADDFL 12
DB 1 LQKRELES 10

Search completed: November 5, 2003, 18:19:14
Job time 1.73 secs

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GenCore version: 5.11.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein Protein search, using sw model

Run on: November 5, 2003, 18:12:15 / Search time of 5 seconds  
(without alignment)  
32,237 million cell data/sec

Title: US-09-914-088-13

Perfect score: 89  
Sequence: 1 GEMKQLADDELCPSE 16

Scoring table: PLOSM62  
Gap: 12.0, Gapext: 6.0

Searched: 128717 seqs, 4231028 residues

Total number of hits satisfying chosen parameters: 1129.

Minimum DB seq length: 5  
Maximum DB seq length: 16

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA:  
1: /cseq2\_6/prodata1/1/aa/AA\_CVMA.pep  
2: /cseq2\_6/prodata1/1/aa/AA\_CVMA.pep  
3: /cseq2\_6/prodata1/1/aa/AA\_CVMA.pep  
4: /cseq2\_6/prodata1/1/aa/AA\_CVMA.pep  
5: /cseq2\_6/prodata1/1/aa/AA\_CVMA.pep  
6: /cseq2\_6/prodata1/1/aa/AA\_CVMA.pep

Pred. No. is the number of results predicted by chosen to have a score greater than or equal to the score of the result being listed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	31	34.8	16	6	5310729-5	1
2	30	33.7	8	6	5310729-13	1
3	30	33.7	9	1	US-09-914-088-13	1
4	30	33.7	9	7	5310729-13	1
5	30	33.7	10	6	5310729-13	1
6	30	33.7	11	6	5310729-13	1
7	24	32.9	9	6	5310729-47	1
8	28	31.5	9	6	5310729-44	1
9	28	31.5	11	1	US-07-563-413-14	1
10	28	31.5	11	1	US-07-563-413-12	1
11	28	31.5	11	1	US-08-055-530-13	1
12	28	31.5	11	1	US-08-055-530-32	1
13	28	31.5	13	4	US-09-902-641-7	1
14	28	31.5	15	3	US-09-143-590H-5	1
15	27	30.3	14	2	US-08-346-939-05	1
16	26	29.2	8	1	US-08-150-142A-10	1
17	26	29.2	12	3	US-09-258-754-43	1
18	26	29.2	12	3	US-09-542-107-02	1
19	26	29.2	12	4	US-08-346-595A-02	1
20	26	29.2	13	4	US-09-513-751A-14	1
21	26	29.2	13	4	US-09-513-781A-04	1
22	26	29.2	14	3	US-08-337-781A-10	1
23	26	29.2	15	3	US-08-308-264A-44	1
24	26	29.2	15	4	US-03-431-073-14	1
25	26	29.2	16	1	US-08-341-569-14	1
26	26	29.2	16	1	US-08-341-569-14	1
27	26	29.2	16	2	US-08-341-569-14	1

28	26	29.2	16	5	PCT-US95-54567-14	Sequence 14, Appl
29	25.5	28.7	12	1	US-08-218-026-57	Sequence 57, Appl
30	25.5	28.7	12	2	US-08-653-632-57	Sequence 57, Appl
31	25	28.1	7	4	US-09-187-859-3102	Sequence 3102, Ap
32	25	28.1	7	4	US-09-339-542B-3102	Sequence 3102, Ap
33	25	28.1	8	2	US-06-821-492-110	Sequence 110, App
34	25	28.1	8	4	US-09-187-859-3103	Sequence 3103, Ap
35	25	28.1	8	4	US-09-539-542B-3103	Sequence 3103, Ap
36	25	28.1	5	6	5310729-20	Patent No. 5310729
37	25	28.1	9	4	US-09-187-859-3104	Sequence 3104, Ap
38	25	28.1	9	4	US-09-344-040C-82	Sequence 80, Appl
39	25	28.1	9	4	US-03-839-542B-3104	Sequence 3104, Ap
40	25	28.1	9	6	5310729-21	Patent No. 5310729
41	25	28.1	10	1	US-08-750-007-17	Sequence 17, Appl
42	25	28.1	10	4	US-09-344-040C-85	Sequence 85, Appl
43	25	28.1	10	4	US-09-341-992-43	Sequence 43, Appl
44	25	28.1	10	6	5310729-22	Patent No. 5310729
45	25	28.1	10	6	5459048-17	Patent No. 5459048

ALIGNMENTS

RESULT 1  
5310729-5  
Patent No. 5310729  
APPLICANT: LERNHART, WALDEMAR  
TITLE OF INVENTION: INTERFERON-RELATED POLYPEPTIDES AS CR2  
LIGANDS AND THEIR USE FOR MODULATING IMMUNE FUNCTIONS  
NUMBER OF SEQUENCES: 47  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/512,118  
FILING DATE: 20-APR 1990  
SEQ ID NO: 5  
LENGTH: 16  
5310729-5

Query Match 34.8% Score 31; DB 6; Length 16;  
Best Local Similarity 66.7% Pred. No. 65;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CV 5 KQLADDELCP 13  
DB 5 QQLADDELCP 13

RESULT 2  
5310729-13  
Patent No. 5310729  
APPLICANT: LERNHART, WALDEMAR  
TITLE OF INVENTION: INTERFERON-RELATED POLYPEPTIDES AS CR2  
LIGANDS AND THEIR USE FOR MODULATING IMMUNE FUNCTIONS  
NUMBER OF SEQUENCES: 47  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/512,118  
FILING DATE: 20-APR 1990  
SEQ ID NO: 13  
LENGTH: 8  
5310729-13

Query Match 33.3% Score 30; DB 6; Length 9;  
Best Local Similarity 75.0% Pred. No. 2,5e+05;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CV 6 QQLADDELCP 13  
DB 1 QQLADDELCP 8

RESULT 3  
US-07-720-202-47  
Sequence 47, Applicant US/07/512,118  
Patent No. 5310729

```

GENERAL INFORMATION:
APPLICANT: Bernhardt, Waldemar
APPLICANT: Eargon, Mario
APPLICANT: Yoderian, Phil
TITLE OF INVENTION: HYBRID PROTEINS CONTAINING FOREIGN SITES
NUMBER OF SEQUENCES: 58
ORIGINATOR'S ADDRESS:
ADDRESSER: Bernhardt & Filling
STREET: 11230 Sorrento Valley Road, Suite 200
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #10, Version #1.1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/920,442
FILING DATE: 1991/06/21
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bernhardt, Doug-as A.
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: C180113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-587-3533
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: AMINO ACID
STRANDEDNESS: double
TOPOLAGY: linear
WEIGHT TYPE: DNA (genomic)
DS OF 100,000 47

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```

Query Match: 33.7%; Score 10; DB 6; Length 10;
Best Local Similarity: 75.0%; Pred No. 66;
Matches: 6; Conservative 0; Mismatches 0; Gaps 0;

```

```

QY 6 QLADELIC 13
DB 1 QNDLEAC 8

```

```

RESULT 4
5310729-14
PATENT NO. 5310729
APPLICANT: Bernhardt, Waldemar
TITLE OF INVENTION: INTERFERON RELATED POLYPEPTIDES AS CR2
LIGANDS AND THEIR USE FOR MODULATING IMMUNE FUNCTIONS
NUMBER OF SEQUENCES: 47
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/512,118
FILING DATE: 20 APR 1990

```

```

Query Match: 33.7%; Score 10; DB 6; Length 10;
Best Local Similarity: 75.0%; Pred No. 66;
Matches: 6; Conservative 0; Mismatches 0; Gaps 0;

```

```

QY 6 QLADELIC 13
DB 1 QNDLEAC 8

```

```

RESULT 5
5310729-15
PATENT NO. 5310729
APPLICANT: Bernhardt, Waldemar
TITLE OF INVENTION: INTERFERON RELATED POLYPEPTIDES AS CR2
LIGANDS AND THEIR USE FOR MODULATING IMMUNE FUNCTIONS
NUMBER OF SEQUENCES: 47
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/512,118
FILING DATE: 20 APR 1990

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```

Query Match: 33.7%; Score 10; DB 6; Length 10;
Best Local Similarity: 75.0%; Pred No. 66;
Matches: 6; Conservative 0; Mismatches 0; Gaps 0;

```

```

QY 6 QLADELIC 13
DB 1 QNDLEAC 8

```

```

5310729-15
PATENT NO. 5310729
APPLICANT: Bernhardt, Waldemar
TITLE OF INVENTION: INTERFERON RELATED POLYPEPTIDES AS CR2
LIGANDS AND THEIR USE FOR MODULATING IMMUNE FUNCTIONS
NUMBER OF SEQUENCES: 47
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/512,118
FILING DATE: 20 APR 1990

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```

Query Match: 33.7%; Score 10; DB 6; Length 10;
Best Local Similarity: 75.0%; Pred No. 66;
Matches: 6; Conservative 0; Mismatches 0; Gaps 0;

```

```

QY 6 QLADELIC 13
DB 1 QNDLEAC 8

```

```

RESULT 6
5310729-16
PATENT NO. 5310729
APPLICANT: Bernhardt, Waldemar
TITLE OF INVENTION: INTERFERON RELATED POLYPEPTIDES AS CR2
LIGANDS AND THEIR USE FOR MODULATING IMMUNE FUNCTIONS
NUMBER OF SEQUENCES: 47
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/512,118
FILING DATE: 20 APR 1990

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```

Query Match: 33.7%; Score 10; DB 6; Length 10;
Best Local Similarity: 75.0%; Pred No. 66;
Matches: 6; Conservative 0; Mismatches 0; Gaps 0;

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QY 6 QLADELIC 13
DB 1 QNDLEAC 8

```

```

RESULT 7
5310729-43
PATENT NO. 5310729
APPLICANT: Bernhardt, Waldemar
TITLE OF INVENTION: INTERFERON RELATED POLYPEPTIDES AS CR2
LIGANDS AND THEIR USE FOR MODULATING IMMUNE FUNCTIONS
NUMBER OF SEQUENCES: 47
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/512,118
FILING DATE: 20 APR 1990

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Query Match: 33.5%; Score 28; DB 6; Length 9;
Best Local Similarity: 72.5%; Pred No. 250+0;
Matches: 5; Conservative 1; Mismatches 2; Gaps 0;

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QY 6 QLADELIC 13
DB 1 QNDLEAC 8

```

```

RESULT 8
5310729-44
PATENT NO. 5310729
APPLICANT: Bernhardt, Waldemar
TITLE OF INVENTION: INTERFERON RELATED POLYPEPTIDES AS CR2

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LIGANDS AND THEIR USE FOR MODULATING IMMUNE FUNCTIONS

1  
2 NUMBER OF SEQUENCES: 47  
3  
4 CURRENT APPLICATION DATA:  
5 APPLICATION NUMBER: US/07/512.118  
6 FILING DATE: 20-APR-1990  
7  
8 SEQ ID NO: 44:  
9  
10 LENGTH: 9  
11  
12 53:0729-44

Query Match 31.5%, Score 28, DB 1, Length 11,  
Best Local Similarity 57.1%, Pred. No. 1.46+02,  
Matches 4, Conservative 2, Mismatches 1, Indels 0, Gaps 0

Cy 6 QADLELC 13  
Db 1 QADLELC 8

RESULT 9  
US-07-663-413-13  
1 Sequence 11, Application US/07663413  
2 Patent No. 5240703  
3  
4 GENERAL INFORMATION:  
5 APPLICANT: Cochran, Mark D.  
6 TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED  
7 PSEUDORABIES VIRUS S-PRV-155 AND USESTHEREOF  
8 NUMBER OF SEQUENCES: 32  
9  
10 CORRESPONDENCE ADDRESS:  
11 ADDRESSEE: John P. White, Esq.  
12 STREET: 30 Rockefeller Plaza  
13 CITY: New York  
14 STATE: New York  
15 COUNTRY: USA  
16 ZIP: 10112  
17  
18 COMPUTER READABLE FORM:  
19 MEDIUM TYPE: Floppy disk  
20 OPERATING SYSTEM: PC-DOS/MS-DOS  
21 SOFTWARE: Patent In Release #1.24  
22  
23 CURRENT APPLICATION DATA:  
24 APPLICATION NUMBER: US/07/663.413  
25 FILING DATE: 199:0301  
26  
27 CLASSIFICATION: 424  
28  
29 ATTORNEY/AGENT INFORMATION:  
30 NAME: White Esq., John P.  
31 REGISTRATION NUMBER: 28,678  
32  
33 REFERENCE/DOCKET NUMBER: 38720  
34  
35 TELECOMMUNICATION INFORMATION:  
36 TELEPHONE: (212) 977-9550  
37 TELEFAX: (212) 664-3525  
38  
39 INFORMATION FOR SEQ ID NO: 11:  
40 SEQUENCE CHARACTERISTICS:  
41 LENGTH: 11 amino acids  
42 TYPE: AMINO ACID  
43 TOPOLOGY: linear  
44 MOLECULE TYPE: protein  
45  
46 US-07-663-413-13

Query Match 31.5%, Score 28, DB 1, Length 11,  
Best Local Similarity 57.1%, Pred. No. 1.46+02,  
Matches 4, Conservative 2, Mismatches 1, Indels 0, Gaps 0

Cy 9 DLELCPR 15  
Db 1 EYDLCPR 7

RESULT 10  
US-07-663-413-32  
1 Sequence 12, Application US/07663413  
2 Patent No. 5240703  
3  
4 GENERAL INFORMATION:  
5 APPLICANT: Cochran, Mark D.  
6 TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED  
7 PSEUDORABIES VIRUS S-PRV-155 AND USESTHEREOF  
8 NUMBER OF SEQUENCES: 32  
9  
10 CORRESPONDENCE ADDRESS:  
11 ADDRESSEE: John P. White, Esq.  
12 STREET: 30 Rockefeller Plaza  
13 CITY: New York  
14 STATE: New York  
15 COUNTRY: USA  
16 ZIP: 10112  
17  
18 COMPUTER READABLE FORM:  
19 MEDIUM TYPE: Floppy disk  
20 OPERATING SYSTEM: PC-DOS/MS-DOS  
21 SOFTWARE: Patent In Release #1.24  
22  
23 CURRENT APPLICATION DATA:  
24 APPLICATION NUMBER: US/07/663.413  
25 FILING DATE: 199:0301  
26  
27 CLASSIFICATION: 424  
28  
29 ATTORNEY/AGENT INFORMATION:  
30 NAME: White Esq., John P.  
31 REGISTRATION NUMBER: 28,678  
32  
33 REFERENCE/DOCKET NUMBER: 38720  
34  
35 TELECOMMUNICATION INFORMATION:  
36 TELEPHONE: (212) 977-9550  
37 TELEFAX: (212) 664-3525  
38  
39 INFORMATION FOR SEQ ID NO: 11:  
40 SEQUENCE CHARACTERISTICS:  
41 LENGTH: 11 amino acids  
42 TYPE: AMINO ACID  
43 TOPOLOGY: linear  
44 MOLECULE TYPE: protein  
45  
46 US-07-663-413-13

Query Match 31.5%, Score 28, DB 1, Length 11,  
Best Local Similarity 57.1%, Pred. No. 1.46+02,  
Matches 4, Conservative 2, Mismatches 1, Indels 0, Gaps 0

Cy 9 DLELCPR 15  
Db 1 EYDLCPR 7

RESULT 10  
US-07-663-413-32  
1 Sequence 12, Application US/07663413  
2 Patent No. 5240703  
3  
4 GENERAL INFORMATION:  
5 APPLICANT: Cochran, Mark D.  
6 TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED  
7 PSEUDORABIES VIRUS S-PRV-155 AND USESTHEREOF  
8 NUMBER OF SEQUENCES: 32  
9  
10 CORRESPONDENCE ADDRESS:  
11 ADDRESSEE: John P. White, Esq.  
12 STREET: 30 Rockefeller Plaza  
13 CITY: New York  
14 STATE: New York  
15 COUNTRY: USA  
16 ZIP: 10112  
17  
18 COMPUTER READABLE FORM:  
19 MEDIUM TYPE: Floppy disk  
20 OPERATING SYSTEM: PC-DOS/MS-DOS  
21 SOFTWARE: Patent In Release #1.24  
22  
23 CURRENT APPLICATION DATA:  
24 APPLICATION NUMBER: US/07/663.413  
25 FILING DATE: 199:0301  
26  
27 CLASSIFICATION: 424  
28  
29 ATTORNEY/AGENT INFORMATION:  
30 NAME: White Esq., John P.  
31 REGISTRATION NUMBER: 28,678  
32  
33 REFERENCE/DOCKET NUMBER: 38720  
34  
35 TELECOMMUNICATION INFORMATION:  
36 TELEPHONE: (212) 977-9550  
37 TELEFAX: (212) 664-3525  
38  
39 INFORMATION FOR SEQ ID NO: 11:  
40 SEQUENCE CHARACTERISTICS:  
41 LENGTH: 11 amino acids  
42 TYPE: AMINO ACID  
43 TOPOLOGY: linear  
44 MOLECULE TYPE: protein  
45  
46 US-07-663-413-13

Query Match 31.5%, Score 28, DB 1, Length 11,  
Best Local Similarity 57.1%, Pred. No. 1.46+02,  
Matches 4, Conservative 2, Mismatches 1, Indels 0, Gaps 0

Cy 9 DLELCPR 15  
Db 1 EYDLCPR 7

RESULT 10  
US-07-663-413-32  
1 Sequence 12, Application US/07663413  
2 Patent No. 5240703  
3  
4 GENERAL INFORMATION:  
5 APPLICANT: Cochran, Mark D.  
6 TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED  
7 PSEUDORABIES VIRUS S-PRV-155 AND USESTHEREOF  
8 NUMBER OF SEQUENCES: 32  
9  
10 CORRESPONDENCE ADDRESS:  
11 ADDRESSEE: John P. White, Esq.  
12 STREET: 30 Rockefeller Plaza  
13 CITY: New York  
14 STATE: New York  
15 COUNTRY: USA  
16 ZIP: 10112  
17  
18 COMPUTER READABLE FORM:  
19 MEDIUM TYPE: Floppy disk  
20 OPERATING SYSTEM: PC-DOS/MS-DOS  
21 SOFTWARE: Patent In Release #1.24  
22  
23 CURRENT APPLICATION DATA:  
24 APPLICATION NUMBER: US/07/663.413  
25 FILING DATE: 199:0301  
26  
27 CLASSIFICATION: 424  
28  
29 ATTORNEY/AGENT INFORMATION:  
30 NAME: White Esq., John P.  
31 REGISTRATION NUMBER: 28,678  
32  
33 REFERENCE/DOCKET NUMBER: 38720  
34  
35 TELECOMMUNICATION INFORMATION:  
36 TELEPHONE: (212) 977-9550  
37 TELEFAX: (212) 664-3525  
38  
39 INFORMATION FOR SEQ ID NO: 11:  
40 SEQUENCE CHARACTERISTICS:  
41 LENGTH: 11 amino acids  
42 TYPE: AMINO ACID  
43 TOPOLOGY: linear  
44 MOLECULE TYPE: protein  
45  
46 US-07-663-413-13

1  
2 APPLICANT: Cochran, Mark D.  
3 TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED  
4 PSEUDORABIES VIRUS S-PRV-155 AND USESTHEREOF  
5 NUMBER OF SEQUENCES: 32  
6  
7 CORRESPONDENCE ADDRESS:  
8 ADDRESSEE: John P. White, Esq.  
9 STREET: 30 Rockefeller Plaza  
10 CITY: New York  
11 STATE: New York  
12 COUNTRY: USA  
13 ZIP: 10112  
14  
15 COMPUTER READABLE FORM:  
16 MEDIUM TYPE: Floppy disk  
17 OPERATING SYSTEM: PC-DOS/MS-DOS  
18 SOFTWARE: Patent In Release #1.24  
19  
20 CURRENT APPLICATION DATA:  
21 APPLICATION NUMBER: US/07/663.413  
22 FILING DATE: 199:0301  
23  
24 CLASSIFICATION: 424  
25  
26 ATTORNEY/AGENT INFORMATION:  
27 NAME: White Esq., John P.  
28 REGISTRATION NUMBER: 28,678  
29  
30 REFERENCE/DOCKET NUMBER: 38720  
31  
32 TELECOMMUNICATION INFORMATION:  
33 TELEPHONE: (212) 977-9550  
34 TELEFAX: (212) 664-3525  
35  
36 INFORMATION FOR SEQ ID NO: 11:  
37 SEQUENCE CHARACTERISTICS:  
38 LENGTH: 11 amino acids  
39 TYPE: AMINO ACID  
40 TOPOLOGY: linear  
41 MOLECULE TYPE: protein  
42  
43 US-07-663-413-32

Query Match 31.5%, Score 28, DB 1, Length 11,  
Best Local Similarity 57.1%, Pred. No. 1.46+02,  
Matches 4, Conservative 2, Mismatches 1, Indels 0, Gaps 0

Cy 9 DLELCPR 15  
Db 1 EYDLCPR 7

RESULT 11  
US-08-055-510-13  
1 Sequence 11, Application US/08055530  
2 Patent No. 5451499  
3  
4 GENERAL INFORMATION:  
5 APPLICANT: Cochran, Mark D.  
6 TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED  
7 PSEUDORABIES VIRUS S-PRV-155 AND USES  
8 THEREOF  
9 NUMBER OF SEQUENCES: 32  
10  
11 CORRESPONDENCE ADDRESS:  
12 ADDRESSEE: John P. White, Esq.  
13 STREET: 30 Rockefeller Plaza  
14 CITY: New York  
15 STATE: New York  
16 COUNTRY: USA  
17 ZIP: 10112  
18  
19 COMPUTER READABLE FORM:  
20 MEDIUM TYPE: Floppy disk  
21 OPERATING SYSTEM: PC-DOS/MS-DOS  
22 SOFTWARE: Patent In Release #1.24  
23  
24 CURRENT APPLICATION DATA:  
25 APPLICATION NUMBER: US/08/055.530  
26 FILING DATE: 199:0430  
27  
28 CLASSIFICATION: 436  
29  
30 ATTORNEY/AGENT INFORMATION:  
31 NAME: White Esq., John P.  
32 REGISTRATION NUMBER: 28,678  
33  
34 REFERENCE/DOCKET NUMBER: 38720  
35  
36 TELECOMMUNICATION INFORMATION:  
37 TELEPHONE: (212) 977-9550  
38 TELEFAX: (212) 664-3525  
39  
40 INFORMATION FOR SEQ ID NO: 12:  
41 SEQUENCE CHARACTERISTICS:  
42 LENGTH: 11 amino acids  
43 TYPE: AMINO ACID  
44 TOPOLOGY: linear  
45 MOLECULE TYPE: protein  
46  
47 US-07-663-413-32

Query Match 31.5%, Score 28, DB 1, Length 11,  
Best Local Similarity 57.1%, Pred. No. 1.46+02,  
Matches 4, Conservative 2, Mismatches 1, Indels 0, Gaps 0

Cy 9 DLELCPR 15  
Db 1 EYDLCPR 7

RESULT 11  
US-08-055-510-13  
1 Sequence 11, Application US/08055530  
2 Patent No. 5451499  
3  
4 GENERAL INFORMATION:  
5 APPLICANT: Cochran, Mark D.  
6 TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED  
7 PSEUDORABIES VIRUS S-PRV-155 AND USES  
8 THEREOF  
9 NUMBER OF SEQUENCES: 32  
10  
11 CORRESPONDENCE ADDRESS:  
12 ADDRESSEE: John P. White, Esq.  
13 STREET: 30 Rockefeller Plaza  
14 CITY: New York  
15 STATE: New York  
16 COUNTRY: USA  
17 ZIP: 10112  
18  
19 COMPUTER READABLE FORM:  
20 MEDIUM TYPE: Floppy disk  
21 OPERATING SYSTEM: PC-DOS/MS-DOS  
22 SOFTWARE: Patent In Release #1.24  
23  
24 CURRENT APPLICATION DATA:  
25 APPLICATION NUMBER: US/08/055.530  
26 FILING DATE: 199:0430  
27  
28 CLASSIFICATION: 436  
29  
30 ATTORNEY/AGENT INFORMATION:  
31 NAME: White Esq., John P.  
32 REGISTRATION NUMBER: 28,678  
33  
34 REFERENCE/DOCKET NUMBER: 38720  
35  
36 TELECOMMUNICATION INFORMATION:  
37 TELEPHONE: (212) 977-9550  
38 TELEFAX: (212) 664-3525  
39  
40 INFORMATION FOR SEQ ID NO: 12:  
41 SEQUENCE CHARACTERISTICS:  
42 LENGTH: 11 amino acids  
43 TYPE: AMINO ACID  
44 TOPOLOGY: linear  
45 MOLECULE TYPE: protein  
46  
47 US-07-663-413-32

Query Match 31.5%, Score 28, DB 1, Length 11,  
Best Local Similarity 57.1%, Pred. No. 1.46+02,  
Matches 4, Conservative 2, Mismatches 1, Indels 0, Gaps 0

Cy 9 DLELCPR 15  
Db 1 EYDLCPR 7

RESULT 11  
US-08-055-510-13  
1 Sequence 11, Application US/08055530  
2 Patent No. 5451499  
3  
4 GENERAL INFORMATION:  
5 APPLICANT: Cochran, Mark D.  
6 TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED  
7 PSEUDORABIES VIRUS S-PRV-155 AND USES  
8 THEREOF  
9 NUMBER OF SEQUENCES: 32  
10  
11 CORRESPONDENCE ADDRESS:  
12 ADDRESSEE: John P. White, Esq.  
13 STREET: 30 Rockefeller Plaza  
14 CITY: New York  
15 STATE: New York  
16 COUNTRY: USA  
17 ZIP: 10112  
18  
19 COMPUTER READABLE FORM:  
20 MEDIUM TYPE: Floppy disk  
21 OPERATING SYSTEM: PC-DOS/MS-DOS  
22 SOFTWARE: Patent In Release #1.24  
23  
24 CURRENT APPLICATION DATA:  
25 APPLICATION NUMBER: US/08/055.530  
26 FILING DATE: 199:0430  
27  
28 CLASSIFICATION: 436  
29  
30 ATTORNEY/AGENT INFORMATION:  
31 NAME: White Esq., John P.  
32 REGISTRATION NUMBER: 28,678  
33  
34 REFERENCE/DOCKET NUMBER: 38720  
35  
36 TELECOMMUNICATION INFORMATION:  
37 TELEPHONE: (212) 977-9550  
38 TELEFAX: (212) 664-3525  
39  
40 INFORMATION FOR SEQ ID NO: 12:  
41 SEQUENCE CHARACTERISTICS:  
42 LENGTH: 11 amino acids  
43 TYPE: AMINO ACID  
44 TOPOLOGY: linear  
45 MOLECULE TYPE: protein  
46  
47 US-07-663-413-32

Query Match 31.5%, Score 28, DB 1, Length 11,  
Best Local Similarity 57.1%, Pred. No. 1.46+02,  
Matches 4, Conservative 2, Mismatches 1, Indels 0, Gaps 0

Cy 9 DLELCPR 15  
Db 1 EYDLCPR 7

RESULT 11  
US-08-055-510-13  
1 Sequence 11, Application US/08055530  
2 Patent No. 5451499  
3  
4 GENERAL INFORMATION:  
5 APPLICANT: Cochran, Mark D.  
6 TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED  
7 PSEUDORABIES VIRUS S-PRV-155 AND USES  
8 THEREOF  
9 NUMBER OF SEQUENCES: 32  
10  
11 CORRESPONDENCE ADDRESS:  
12 ADDRESSEE: John P. White, Esq.  
13 STREET: 30 Rockefeller Plaza  
14 CITY: New York  
15 STATE: New York  
16 COUNTRY: USA  
17 ZIP: 10112  
18  
19 COMPUTER READABLE FORM:  
20 MEDIUM TYPE: Floppy disk  
21 OPERATING SYSTEM: PC-DOS/MS-DOS  
22 SOFTWARE: Patent In Release #1.24  
23  
24 CURRENT APPLICATION DATA:  
25 APPLICATION NUMBER: US/08/055.530  
26 FILING DATE: 199:0430  
27  
28 CLASSIFICATION: 436  
29  
30 ATTORNEY/AGENT INFORMATION:  
31 NAME: White Esq., John P.  
32 REGISTRATION NUMBER: 28,678  
33  
34 REFERENCE/DOCKET NUMBER: 38720  
35  
36 TELECOMMUNICATION INFORMATION:  
37 TELEPHONE: (212) 977-9550  
38 TELEFAX: (212) 664-3525  
39  
40 INFORMATION FOR SEQ ID NO: 12:  
41 SEQUENCE CHARACTERISTICS:  
42 LENGTH: 11 amino acids  
43 TYPE: AMINO ACID  
44 TOPOLOGY: linear  
45 MOLECULE TYPE: protein  
46  
47 US-07-663-413-32

REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 39726-2/JEP/350  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 977-9550  
 TELEFAX: (212) 664-0525  
 TELEX: 422523 COOP U  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acids  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-055-510 13

Query Match 31.5% Score 28; DB 13; Length 13;  
 Best Local Similarity 57.1% Pred No. 1.7e-02;  
 Matches 4; Conservative 2; Mismatches 1; Gaps 0;

QY 9 DDELEPR 15  
 DE 1 EYDLCPR 7

## RESULT 12

US-08-055-510 12  
 Sequence 32, Application US/08055530  
 Patent No. 6451499

GENERAL INFORMATION:  
 APPLICANT: Cochran, Mark D.  
 TITLE OF INVENTION: ATTENUATED, GENETICALLY ENGINEERED  
 TITLE OF INVENTION: PSEUDORABIES VIRUS S TRV 155 AND USES  
 TITLE OF INVENTION: THEREOF  
 NUMBER OF SEQUENCES: 32  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: John D. White, Esq.  
 STREET: 10 Rockefeller Plaza  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10119

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.04  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/255,510  
 FILING DATE: 19940430

CLASSIFICATION: 436  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White Esch, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 39726-2/JEP/350  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 977-9550  
 TELEFAX: (212) 664-0525  
 TELEX: 422523 COOP U  
 INFORMATION FOR SEQ ID NO: 32:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acids  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-055-510 12

Query Match 31.5% Score 28; DB 13; Length 13;  
 Best Local Similarity 57.1% Pred No. 1.7e-02;  
 Matches 4; Conservative 2; Mismatches 1; Gaps 0;

QY 9 DDELEPR 15  
 DE 1 EYDLCPR 7

RESULT 13  
 US-09-402-641-1  
 Sequence 1, Application US/09402641  
 Patent No. 6528619  
 GENERAL INFORMATION:  
 APPLICANT: BURGULE, Markus  
 APPLICANT: GRAEFF, Heinrich  
 APPLICANT: KESSLER, Holst  
 APPLICANT: MAGDOLEN, Viktor Robert  
 APPLICANT: KOENIG, Bernhard  
 APPLICANT: KOPPEL, Marius  
 APPLICANT: RIEMER, Christoph  
 APPLICANT: SCHMITT, Manfred  
 APPLICANT: WEDDE, Ulrich  
 APPLICANT: WILHELM, Olaf  
 TITLE OF INVENTION: INHIBITORS FOR UROKINASE RECEPTOR  
 FILE REFERENCE: Case 20367US  
 CURRENT APPLICATION NUMBER: US/09/402,641  
 CURRENT FILING DATE: 2000-01-10  
 PRIOR APPLICATION NUMBER: EP97106034.9  
 PRIOR FILING DATE: 1997-04-11  
 PRIOR APPLICATION NUMBER: PCT/EP98/02,728  
 PRIOR FILING DATE: 1998-04-14  
 NUMBER OF SEQ ID NOS: 10  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 1  
 LENGTH: 13  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:Peptide "peptide"  
 OTHER INFORMATION: 19,31 UPA 19 31"; Figure 3A  
 US-09-402-641-1

Query Match 31.5% Score 28; DB 4; Length 13;  
 Best Local Similarity 30.8% Pred No. 1.7e-02;  
 Matches 4; Conservative 1; Mismatches 6; Gaps 0;

QY 1 CEVKKQKAGLEK 13  
 DE 1 CVSNKYPNTHW 13

## RESULT 14

US-08-142-590B-5  
 Sequence 5, Application US/08142590B  
 Patent No. 6303246

GENERAL INFORMATION:  
 APPLICANT: HIRSH, Toshihiko; TAKAHASHI, Tadashi; HORII, Izumi; and  
 TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/142,590B  
 FILING DATE: 25 OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/042,318  
 FILING DATE: 22 APR 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WYVIS, Paul L.  
 REGISTRATION NUMBER: 35,365

Search completed: November 5, 2003, 18:15:08  
Job time : 22 secs

1 REFERENCE/DOCKET NUMBER: MGP 602AP  
2 TELECOMMUNICATION INFORMATION:  
3 TELEPHONE: (617) 227-7400  
4 TELEFAX: (617) 227-5941  
5 INFORMATION FOR SEQ ID NO: 5:  
6 SEQUENCE CHARACTERISTICS:  
7 LENGTH: 15 amino acids  
8 TYPE: amino acid  
9 TOPOLOGY: linear  
10 NCBI/GENBANK TYPE: Peptide  
11 FRAGMENT TYPE: Internal  
12 US 09-142,092B 5

Query Match 31.5% Score 25.18 E-12 Identical  
Best Local Similarity 30.8% Pident 30.19%  
Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

CY 1 CPNNKQLADLELC 13  
DB 2 CYSKVFESHWMC 14

RESULT 15  
US 09-248 6197-91  
1 Sequence 93, Application US/06248893  
2 Patent No. 5843702  
3 GENERAL INFORMATION:  
4 APPLICANT: McConnell, David  
5 APPLICANT: Derrine, Kevin  
6 APPLICANT: O'Kane, Charles  
7 TITLE OF INVENTION: A Gene Expression System  
8 NUMBER OF SEQUENCES: 185  
9 CORRESPONDENCE ADDRESS:  
10 ADDRESSEE: No. 5843702 No. 5843702disk of No. 5843702 America, Inc.  
11 STREET: 405 Lexington Avenue  
12 CITY: New York  
13 STATE: New York  
14 COUNTRY: USA  
15 ZIP: 10174-6401  
16 COMPUTER READABLE FORM:  
17 MEDIUM TYPE: Diskette  
18 COMPUTER: IBM Compatible  
19 OPERATING SYSTEM: DOS  
20 SOFTWARE: FastSeq for Windows Version 1.0  
21 CURRENT APPLICATION DATA:  
22 APPLICATION NUMBER: US/98/248,893  
23 FILING DATE: 25-MAY-1994  
24 CLASSIFICATION: 435  
25 ATTORNEY/AGENT INFORMATION:  
26 NAME: Gregg, Valinda A.  
27 REGISTRATION NUMBER: 15,127  
28 REFERENCE/DOCKET NUMBER: 3614, 214 US  
29 TELECOMMUNICATION INFORMATION:  
30 TELEPHONE: 212-867-0123  
31 TELEFAX: 212-978-9655  
32 INFORMATION FOR SEQ ID NO: 93:  
33 SEQUENCE CHARACTERISTICS:  
34 LENGTH: 14 amino acids  
35 TYPE: amino acid  
36 STRANDEDNESS: single  
37 TOPOLOGY: linear  
38 NCBI/GENBANK TYPE: Protein  
39 US-09 248 619C 93

Query Match 30.3% Score 27.18 E-11 Identical  
Best Local Similarity 100.0% Pident 100.0%  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 FHNKQ 6  
DB 4 FYNKQ 8

GenCore version 3.1.6  
Copyright (c) 1993-2003 Computer Ltd.

CM protein: protein search, using sw match

Run on: November 5, 2003, 10:18:36 / Search time 20 seconds  
(without alignment)  
96,163 Million cells/gate-sw/sec

Title: US-09-914-088-15

Perfect score: 112

Sequence: CLEMSQWMDVLCGSSGGP 20

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 28162 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 1000

Minimum DB seq length: 7

Maximum DB seq length: 20

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 76.0

1: prot.

2: para.

3: para.

4: para.

Prod. No. is the number of results predicted by chosen criteria. A score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	PIR ID	Seq Region
1	35	33.2	15	S62609	glutathione-disulf
2	34	30.4	12	S43170	kinasin light chai
3	30	26.8	13	S74110	SAGA complex, G1a
4	30	26.8	16	S65410	type 1 insulin hydroxy
5	28	25.0	14	S80240	type 1 insulin receptor a
6	27	24.1	10	A01110	type 2 insulin binding
7	27	24.1	11	PT0226	type 2 insulin receptor be
8	27	24.1	15	S43170	kinasin light chain - b
9	27	24.1	22	S43170	kinasin light chain - b
10	26	23.2	12	A58376	glutathione S-transferase
11	24	21.2	15	PA0034	glutathione S-transferase
12	24	21.2	17	SC5671	glutathione S-transferase
13	23	22.3	10	S60787	spem-activating p
14	23	22.3	10	S60788	spem-activating p
15	23	22.3	10	S60786	spem-activating p
16	23	22.3	10	S60787	spem-activating p
17	23	22.3	10	A60788	spem-activating p
18	23	22.3	10	S60589	spem-activating p
19	23	22.3	10	S60589	spem-activating p
20	23	22.3	10	PH0912	T-cell receptor be
21	23	22.3	12	J02108	CD4 molecular 1.4K
22	23	22.3	13	J02118	CD4 molecular 1.4K
23	23	22.3	18	S61110	CD4 molecular 1.4K
24	23	22.3	18	S48839	CD4 molecular 1.4K
25	24	21.4	5	PT0226	T-cell receptor be
26	24	21.4	9	PT0226	T-cell receptor be
27	24	21.4	10	PH0914	heavy chain CD4
28	24	21.4	13	PH0914	heavy chain CD4
29	24	21.4	13	S43170	kinasin light chain - b

ALIGNMENTS

RESULT 1

S62609  
glutathione-disulfide reductase (EC 1.8.1.7) - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 28-Oct-1996 Sequence\_revision 13-Mar-1997 #text\_change 03-Jun 2002  
C:Accession: S62609  
R:Krauth Stegel, R L; Mueller, J G; Lottspeich, F; Schirmer, R H.  
Eur. J. Biochem. 235, 345-350, 1996  
A:Title: Glutathione reductase and glutathione dehydrogenase of Plasmodium falciparum, th  
A:Reference number: S62609; XUID:96202957; PNCID:661352  
A:Accession: S62609  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 «KRA»  
A:Keywords: FAD; flavoprotein; NADP; oxidoreductase

Query Match: 33.2%; Score 35; DB 2; Length 15;  
Best Local Similarity: 53.8%; Pred. No. 85;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY T WCVVLCGSSGG 19  
DB : WCVVLCGSSGG 19

RESULT 2

S43170  
kinasin light chain - b (kinin fragment)  
C:Species: Homo sapiens  
C:Date: 17-Jun-1993 Sequence\_revision 13-Aug-2000 #text\_change 18-Aug-2000  
C:Accession: S43170  
R:Chernatovsky, Y; Brown, A; Jones, T A; Sheer, D.  
submitted to the EMBL Data Library, December 1993  
A:Description: Promoter: first exon/intron characterization and chromosomal location of  
A:Reference number: S43170  
A:Accession: S43170  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-12 «CHE»  
A:Cross-references: EMBL:X65658; NID:9468786; PIR:CAA49349.1; PID:9468787

Query Match: 30.4%; Score 34; DB 2; Length 12;  
Best Local Similarity: 57.8%; Pred. No. 95;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CCGSSGGP 20  
DB : CCGSSGGP 20

RESULT 3

S74110

NADH oxidase Giardia duodenalis (fragment)  
 C:Species: Giardia duodenalis  
 C:Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999  
 C:Accession: S74130  
 R:Brown, D.M.; Gierloff, J.A.; Upcroft, P.  
 Eur J Biochem 241: 155-161, 1996  
 A:Title: A H<sub>2</sub>O<sub>2</sub> producing NADH oxidase from the protozoan parasite Giardia duodenalis.  
 A:Reference number: S74130; MUID:97094524; PMID:8848521  
 A:Accession: S74130  
 A:Molecule type: protein  
 A:Residues: 113 <B>S>  
 A:Experimental source: strain: B913/83 Hapt196  
 C:Keywords: Flavoprotein; monomer; NAD

Query Match 26.88; Score 27; DB 2; Length 10;  
 Best Local Similarity 50.08; Pred. No. 7.9e+02;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 MVVLCCGSSGG 19  
 | | | | |  
 DB 1 MKVILLGGTHGG 12

RESULT 4  
 S6544C  
 Tyrosyltransferase (EC 1.9.1.12) large chain. Protein for acidimetric (frag  
 C:Species: Fecibacter acidigallici  
 C:Date: 19-Mar-1997 #sequence\_revision 23-Aug-1997 #text\_change 03-May-1998  
 C:Accession: S6544C  
 R:Reichenbacher, W.; Rudiger, A.; Krüger, F.M.H.; Schink, R.  
 Eur J Biochem 217: 426-433, 1996  
 A:Title: Gene molecule of polydopamine polymerase distributed in an associated with each subu  
 and mass spectrometry.  
 A:Reference number: S65429; MUID:96215416; PMID:8843279  
 A:Accession: S6544C  
 A:Molecule type: protein  
 A:Residues: 114 <B>E>  
 C:Keywords: oxidoreductase

Query Match 26.88; Score 27; DB 2; Length 10;  
 Best Local Similarity 50.08; Pred. No. 4.7e+02;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 GVMVVLCCGSSGG 20  
 | | | | |  
 DB 1 GVMVVLCCGSSGG 14

RESULT 5  
 F6840  
 T-cell receptor alpha chain (V<sub>H</sub> region) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 03-May-1997  
 C:Accession: F6840  
 R:Chen, Y.; Ren, P.; Aldmann, J.; Böhlinger, P.; Varykoc, J.  
 J Exp Med 174: 1311-1321, 1991  
 A:Title: T cell receptor genes in a series of transgenic mice show differential complex  
 allelic exclusion and antigen-specific repertoire  
 A:Reference number: F6846; MUID:92278845; PMID:1684115  
 A:Accession: F6840  
 A:Molecule type: mRNA  
 A:Residues: 114 <B>S>  
 A:Cross references: ENSLX65907  
 A:Experimental source: T lymphocyte  
 C:Keywords: T cell receptor

Query Match 25.08; Score 27; DB 2; Length 10;  
 Best Local Similarity 57.18; Pred. No. 1.2e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 GVRSSGG 19  
 | | | | |  
 DB 1 GVRSSGG 14

RESULT 6  
 A32195  
 Na<sup>+</sup>/K<sup>+</sup>-exchanging ATPase (EC 3.6.3.9): alpha chain - dog (fragment)  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 20-Oct-1989 #sequence\_revision 20-Oct-1989 #text\_change 19-Apr-2002  
 C:Accession: A32195  
 R:Tyson, P.A.; Steinberg, M.; Wallack, E.T.; Kiley, T.L.  
 J Biol Chem 264: 4267-44, 1989  
 A:Title: Identification of the 5'-tridocetamidofluorescein reporter site on the Na,K-ATP  
 A:Reference number: A32195; MUID:89094137; PMID:2553602  
 A:Accession: A32195  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 110 <B>Y>  
 C:Keywords: hydrolase

Query Match 24.18; Score 27; DB 2; Length 10;  
 Best Local Similarity 57.18; Pred. No. 7.9e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 VDLGGG 16  
 | | | | |  
 DB 2 FDLXGGS 8

RESULT 7  
 P70218  
 T-cell receptor beta chain V<sub>H</sub> region (710-9.3) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 11-Dec-1991 #sequence\_revision 11-Dec-1991 #text\_change 30-May-1997  
 C:Accession: P70218  
 R:Nakano, N.; Kikuchi, H.; Nishimoto, H.; Kishimoto, T.  
 J Exp Med 173: 1091-1097, 1991  
 A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restri  
 A:Reference number: P70218; MUID:91217621; PMID:1902501  
 A:Accession: P70218  
 A:Molecule type: mRNA  
 A:Residues: 111 <B>A>  
 C:Keywords: T cell receptor

Query Match 24.18; Score 27; DB 2; Length 10;  
 Best Local Similarity 57.18; Pred. No. 8.7e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GVRSSGG 19  
 | | | | |  
 DB 1 GVRSSGG 14

RESULT 8  
 S47367  
 T-cell antigen receptor V<sub>H</sub> junction beta chain human  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
 C:Accession: S47367  
 R:Lehner, P.J.  
 Submitted to the EMBL Data Library, August 1994  
 A:Description: Human HLA-A\*01: restricted recognition of influenza A is dominated by T  
 A:Reference number: S47365  
 A:Accession: S47367  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 115 <B>E>  
 A:Cross references: EMBL:Z15692; MUID:9527475; P:DN:CAA84761.1; P:ID:9527476  
 C:Keywords: T-cell receptor

Query Match 24.18; Score 27; DB 2; Length 15;  
 Best Local Similarity 57.18; Pred. No. 1.2e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 LVSRSGG 14  
 | | | | |  
 DB 1 LVSRSGG 14



at shows some, but not absolute, species restriction  
C:Superfamily: unassigned animal peptides

Query Match 22.1%; Score 25; DB 2; Length 18,  
Best Local Similarity 62.5%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 DLGGSSG 18  
          ||  
LB 3 DTGGGNG 10

RESULT 15  
E60788  
Sperm-activation peptide (Thy-5 speract) sea urchin Pseudocentrotus depressus  
C:Species: Pseudocentrotus depressus  
C:Date: 30-Sep-1991 #sequence revision 10 Sep-1991 #ext added 10 Aug-2000  
C:Accession: E60788  
R:Shizuka, M.; Kaitera, H.; Nomura, K.; Harbers, D.; Yoshino, K.; Kunita, M.; Tanaka, H.  
Comp. Biochem. Physiol. B 89, 587-694, 1988  
A:Title: Some more speract derivatives associated with eggs of sea urchins. Pseudocentrotus  
A:Reference number: A60787; MUID:86242184; PMID:3318400  
A:Accession: E60788  
A:Molecule type: protein  
A:Residues: 1-10 <SU7>  
C:Comment: This oligopeptide from egg jelly is one of several from this species, all of  
at shows some, but not absolute, species restriction.  
C:Superfamily: unassigned animal peptides

Query Match 22.1%; Score 25; DB 2; Length 18,  
Best Local Similarity 62.5%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 DLGGSSG 18  
          ||  
LB 3 DTGGGNG 10

Search completed: November 5, 2003, 18:11:49  
Job time: 0.00 sec







```

Query Match      21.4%  Score 24;  DB 1;  Length 16;
Best Local Similarity 41.7%  Pred. No. 1.4e+03;
Matches 5;  Conservative 2;  Mismatches 5;  Indels 0;  Gaps 0;

QY 7 VMDYDLCSSSQ 18
DB 3 VVDVFEGGAKG 14

RESULT 8
FNR STGR
ID FNR STGR STANDARD FRT 16 AA.
AC P24114;
DT 01-MAR-1992 (Rel. 21, Created;
DT 01-MAR-1992 (Rel. 21, Last sequence update;
DT 15-JUL-1998 (Rel. 36, Last annotation update;
DE Ferredoxin-NAD(P)+ reductase (EC 1.18.1.3) (Fragment).
CS Streptomyces griseus.
CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
CC Streptomycetaceae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID:1911;
RN 11;
RP SEQUENCE
RX MEDLINE:82041527; PubMed:193912;
RA Ramachandra M., Sentharam R., Emerage M.H., Sarislan F.S.;
RT "Purification and characterization of a soybean flour-inducible
RL J. Bacteriol. 173:7106-7112(1991).
CC 1- FUNCTION: COUPLE ELECTRON TRANSFER FROM NADH TO CYTOCHROME
CC P450(S20) IN THE PRESENCE OF FERRODOXIN.
CC 1- CATALYTIC ACTIVITY: Reduced ferredoxin + NAD(P)+ = oxidized
CC ferredoxin + NADH.
CC 1- COFACTOR: FAD; REQUIRES MAGNESIUM.
DR PIR: A41697; A44897
KW Oxidoreductase; Flavoprotein; NAD; FAD; Magnesium.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1485 MW; 27D11A7C37AC0510 CRC64;

Query Match      21.4%  Score 24;  DB 1;  Length 16;
Best Local Similarity 52.0%  Pred. No. 1.4e+03;
Matches 4;  Conservative 1;  Mismatches 3;  Indels 0;  Gaps 0;

QY 12 LGGSSSGG 19
DB 5 LGGGGGGG 12

RESULT 9
GRVS CANFA
ID GRVS CANFA STANDARD FRT 14 AA.
AC P99432;
DT 15-JUL-1998 (Rel. 46, Created;
DT 15-JUL-1998 (Rel. 46, Last sequence update;
DT 15-JUL-1998 (Rel. 46, Last annotation update;
DE Mitochondrial stress-70 protein (75 kDa glucose regulated protein;
DE (GRP 75) (Fragment).
GN HSPA9.
OS Canis familiaris (dog).
OC Eukaryota; Vertebrata; Chordata; Carnivora; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID:9615;
RN 11;
RP SEQUENCE
RX TISSUE=Heart;
RX MEDLINE:98163140; PubMed:9504812;
RA Dunn M.B., Corbett D.N., Wheeler C.H.;
RT "HSC 20PAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins."
RL Electrophoresis 14:2775-2827(1997).
CC 1- FUNCTION: IMPLICATED IN THE CONTROL OF CELL PROLIFERATION AND
CC CELLULAR GROWTH. MAY ALSO ACT AS A CHAPERONE.
CC 1- SUBCELLULAR LOCATION: Mitochondrial.
CC 1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

Query Match      21.4%  Score 24;  DB 1;  Length 16;
Best Local Similarity 57.1%  Pred. No. 1.1e+03;
Matches 4;  Conservative 1;  Mismatches 2;  Indels 0;  Gaps 0;

QY 14 GSSSGG 20
DB 1 GSRGSP 9

RESULT 7
DHEZ THUTH
ID DHEZ THUTH STANDARD FRT 16 AA.
AC P30576;
DT 31-FEB-1991 (Rel. 17, Created;
DT 31-FEB-1991 (Rel. 17, Last sequence update;
DT 01-OCT-1996 (Rel. 34, Last annotation update;
DE NAD specific glutamate dehydrogenase (EC 1.4.1.3) (Fragment).
DE (Fragment).
CS Thymus thymus (Bluefin tuna).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Eupercaria; Clupeiformes;
CC Acanthomorpha; Acanthopterygii; Delmatoidei; Perciformes; Clupeidae;
CC Scophthalmi; Thunnini.
OX NCBI_TaxID:6167;
RN 11;
RP SEQUENCE
RX TISSUE=Giver;
RX MEDLINE:76253947; PubMed:182270;
RA Veronise F.M., Bevilacqua R., Bocca E., Biava D.V.;
RT "Purification, characteristics and sequence of a protein containing
RT an essential lysine residue."
RL Biochim. Biophys. Acta 445:113-120(1996).
CC 1- CATALYTIC ACTIVITY: L-glutamate + H2O + NAD+ = L-glutamate
CC + NH3 + NADH.
CC 1- SIMILARITY: BELONGS TO THE GLUTAMATE DEHYDROGENASE FAMILY.
CC FRT: A12729; A12729.
DR InterPro; IPR026095; G5FV dehydrog
DR InterPro; IPR026097; G5FV dehydrog N
DR Pfam; PF02812; G5FV dehydrog N; 1.
DR PROSITE; PS00074; G5FV_DEHYDROGENASE; PARTIAL.
KW Oxidoreductase; NAD.
FT NON_TER 1
FT ACT_SITE 12 12
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1518 MW; FE2FAA209F0501E 8 MW

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CC -1- SUBCELLULAR LOCATION: Cytoplasmic (5y similarity);
CC -1- FUNCTION: By water stress.
CC -1- SIMILARITY: Belongs to the actin family
DR InterPro: IPR004333; Actin_like.
DR InterPro: IPR004000; Actin_like.
DR Pfam: PF00222; actin; 1.
DR PROSITE: PS00406; ACTINS_1; PARTIAL.
DR PROSITE: PS01132; ACTINS_ACT_LIKE; PARTIAL.
DR PROSITE: PS00432; ACTINS_2; PARTIAL.
KW Structural protein.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1574 MW; 47160.406 kDa; 100.00
Query Match 18.8% Score 21; DB 1; Length 20;
Best local similarity 40.0%; Pred. No. 4.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 DVPLGGSSG 17
DB 5 NVILGGST 13
RESULT 13
CON2 LITGI
ID CON2 LITGI STANDARD; PRT: 15 AA.
AC P56247;
DT 15-JUL-1998 (Rel. 16, Created)
DT 15-JUL-1998 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caerilin 2;
OS Caerilia gillnet (Australian tree frog);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Pseudoeuryloidae;
OC Pelodyadinae; Vittoria.
CX NCBI_TaxID:334405;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Parotoid gland;
RA Waigh R.M., Store D.J.M., Bowie J.H., Wallace D.C., Tyler M.J.;
RA "Peptides from Australian frogs. The structures of the Caerilins and
RA Caerilins from Vittoria gillnet";
PJ J. Chem. Res. 1993;37-96(1993)
CC -1- FUNCTION: CAERILINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC -1- ANTIBIOTIC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or vesical
CC glands.
CC -1- MASS SPECTROMETRY: MW 1478; METHOD=FAE
KW Amphibian defense peptide; Amphibian
FT MOL_FES 15
FT AVIATION 15
SQ SEQUENCE 15 AA; 1410 MW; 368786.075 kDa; 100.00
Query Match 18.8% Score 21; DB 1; Length 20;
Best local similarity 40.0%; Pred. No. 4.5e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 10 VLKGGSSGG 19
DB 5 LSLVGNALGG 15
RESULT 14
MAX6 BOMXX STANDARD; PRT: 20 AA.
AC P81065;
DT 28-FEB-2001 (Rel. 41, Created)
DT 28-FEB-2001 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Bombina maxima 6;
OS Bombina maxima (Giant fire-bellied toad); (Chinese red belly toad);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
CX NCBI_TaxID:161274;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., McClean S., Orr D.P., Boursion A.J., Rao P.F., Shaw C.;
RA "Isolation and structural characterisation of antimicrobial peptides
RA from the venom of the Chinese large webbed bell toad (Bombina
RA maxima)";
PJ J. Biol. Chem. 2001;276:19377-19383
CC -1- FUNCTION: Has antimicrobial activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
KW Amphibian defense peptide; Antibiotic.
SQ SEQUENCE 20 AA; 1914 MW; 42520.350 kDa; 100.00
Query Match 18.8% Score 21; DB 1; Length 20;
Best local similarity 40.0%; Pred. No. 4.5e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 10 VLKGGSSGG 19
DB 6 LSTGGVCG 15

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OX NCBI_TaxID:161274;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., McClean S., Orr D.P., Boursion A.J., Rao P.F., Shaw C.;
RA "Isolation and structural characterisation of antimicrobial peptides
RA from the venom of the Chinese large webbed bell toad (Bombina
RA maxima)";
PJ J. Biol. Chem. 2001;276:19377-19383
CC -1- FUNCTION: Has antimicrobial activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
KW Amphibian defense peptide; Antibiotic.
SQ SEQUENCE 20 AA; 1914 MW; 42520.350 kDa; 100.00
Query Match 18.8% Score 21; DB 1; Length 20;
Best local similarity 40.0%; Pred. No. 4.5e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 10 VLKGGSSGG 19
DB 6 LSTGGVCG 15
RESULT 15
MAX8 BOMXX STANDARD; PRT: 20 AA.
AC P81067;
DT 28-FEB-2001 (Rel. 41, Created)
DT 28-FEB-2001 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Bombina maxima 6;
OS Bombina maxima (Giant fire-bellied toad); (Chinese red belly toad);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
CX NCBI_TaxID:161274;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., McClean S., Orr D.P., Boursion A.J., Rao P.F., Shaw C.;
RA "Isolation and structural characterisation of antimicrobial peptides
RA from the venom of the Chinese large webbed bell toad (Bombina
RA maxima)";
PJ J. Biol. Chem. 2001;276:19377-19383
CC -1- FUNCTION: Has antimicrobial activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
KW Amphibian defense peptide; Antibiotic.
SQ SEQUENCE 20 AA; 1917 MW; 42742.406 kDa; 100.00
Query Match 18.8% Score 21; DB 1; Length 20;
Best local similarity 40.0%; Pred. No. 4.5e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 10 VLKGGSSGG 19
DB 5 LSLVGNALGG 15

```

Search completed: November 5, 2003, 18:20:31  
Job time : 12 secs

GenCore version 5.1.4  
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CM protein protein search, using sw mode:

Run on: November 5, 2003, 18:15:06 / Search from v. 20030401

without adjustment  
156,396 Matches found in indexed

Title: US-09-914-088-15

Perfect score: 112

Sequence: 1 BL0SGQVQVYVCGSSSGP 20

Scoring table: BLOSUM62

Gapop: 15.0, Gapext: 0.4

Search: 81325 seqs, 258052654 residues

Total number of hits satisfying chosen parameters: 406

Minimum DB seq length: 0

Maximum DB seq length: 20

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1 SPPEM51.231

- 1: sp.archaea
- 2: sp.bacteria
- 3: sp.fungi
- 4: sp.human
- 5: sp.invertebrate
- 6: sp.mammal
- 7: sp.thc
- 8: sp.organelle
- 9: sp.phage
- 10: sp.plant
- 11: sp.rodent
- 12: sp.virus
- 13: sp.vertebrate
- 14: sp.unclassified
- 15: sp.virus
- 16: sp.bacterioph
- 17: sp.archaea

Pred. No. is the number of results that satisfy the criteria. The score is greater than or equal to the score. The results are sorted and is derived by analysis of the data.

# SUMMARY

Result No.	Score	Query Match	Length	ID	Description
1	35	31.2	15	Q9TWE1	Q9TWE1 plasmodium
2	34	30.4	12	Q13865	Q13865 homo sapien
3	32	28.6	16	Q32160	Q32160 pinna past
4	29	25.9	20	Q98414	Q98414 h-sulfobir
5	29	25.9	20	Q8BXG5	Q8BXG5 mus muscu
6	28	25.0	18	Q9TWF2	Q9TWF2 inferima v
7	27	24.1	16	Q40676	Q40676 styza sativ
8	27	24.1	19	Q976F8	Q976F8 pinna gaba
9	27	24.1	19	Q9TR01	Q9TR01 sus scrofa
10	17	24.1	20	Q81223	Q81223 homo sapien
11	26	23.2	15	Q9TBE1	Q9TBE1 sus scrofa
12	26	23.2	17	Q92476	Q92476 a. alligenes
13	26	23.2	18	Q9UC14	Q9UC14 homo sapien
14	26	23.2	20	Q9UP40	Q9UP40 pinna alb
15	25.5	22.6	17	Q85019	Q85019 invertebr
16	25.0	22.8	20	Q9UCV7	Q9UCV7 homo sapien

17	25	22.3	9	11	Q9QZ48	Q9QZ48 mus muscu
18	25	22.3	17	4	Q9EP96	Q9EP96 homo sapien
19	25	22.3	18	5	Q9TWD1	Q9TWD1 der-atoprag
20	25	22.3	18	6	Q9TRX7	Q9TRX7 bos taurus
21	25	22.3	20	10	Q9S8C2	Q9S8C2 pinus sylve
22	24	21.4	17	11	Q55184	Q55184 rattus norv
23	24	21.4	12	4	Q8NEV9	Q8NEV9 homo sapien
24	24	21.4	13	4	Q9UPB1	Q9UPB1 homo sapien
25	24	21.4	14	6	Q90051	Q90051 bos taurus
26	24	21.4	15	10	Q9S8K3	Q9S8K3 g. yuice max
27	24	21.4	20	4	Q9UPA7	Q9UPA7 homo sapien
28	24	21.4	20	11	Q636F7	Q636F7 rattus norv
29	23.5	21.0	19	13	Q85117	Q85117 gallus gall
30	23	20.5	12	6	Q9N2B9	Q9N2B9 gorilla gor
31	23	20.5	12	6	Q9N2B8	Q9N2B8 pongo pygma
32	23	20.5	12	6	Q9N2C0	Q9N2C0 pan troglod
33	23	20.5	15	2	Q47892	Q47892 tremyella d
34	23	20.5	15	6	Q9TRB9	Q9TRB9 tryetolagus
35	23	20.5	17	3	Q9HEQ2	Q9HEQ2 ajellomyces
36	23	20.5	17	3	Q9HEQ3	Q9HEQ3 ajellomyces
37	23	20.5	17	3	Q9HEQ1	Q9HEQ1 paracoccidi
38	22	20.5	17	10	Q9S9C2	Q9S9C2 vigna sinen
39	23	20.5	18	11	Q8R4D7	Q8R4D7 mus muscu
40	23	20.5	18	11	Q9QV73	Q9QV73 mus sp. car
41	23	20.5	19	2	Q96140	Q96140 reisseria m
42	23	20.5	19	3	Q9UP26	Q9UP26 pinna argu
43	23	20.5	20	4	Q9N2Z6	Q9N2Z6 homo sapien
44	23	20.5	20	6	Q9TRQ4	Q9TRQ4 bos taurus
45	22.5	20.1	19	4	Q13665	Q13665 homo sapien

## ALIGNMENTS

### RESULT 1

Q9TWE1	PRELIMINARY	PRG: 15 AA
ID Q9TWE1		
AC Q9TWE1		
DT Q1-MAY-2003 (TRENBERG) 13, Created)		
DT Q1-MAY-2003 (TRENBERG) 13, Last sequence update)		
DT Q1-DEC-2001 (TRENBERG) 19, Last annotation update)		
DE Glutathione disulfide reductase (EC 1.6.4.2) (Fragment)		
OS Plasmodium falciparum		
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium		
CX NCBI_TaxID:5833		
RN 11		
RP SEQUENCE		
RX MEDLINE:96202957, PubMed:8611352		
RA Krauth Siegel R, Muller J, J, Lottspich F, Schilmer R, H		
RT "Glutathione reductase and glutathione dehydrogenase of Plasmodium		
RT falciparum, the causative agent of tropical malaria."		
RL Eut. G. Biochem. 23:3345-350(1996)		
RU SEQUENCE 15 AA; 1409 MW; 2CB94CB54DA247F6 CRC64;		

Query Match 31.2% Score 35; DB 5; Length 15;  
Best Local Similarity 53.8%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QV	7	VWDVLCSSSSG 19
QV	1	VWDVLCSSSSG 19

### RESULT 2

Q13865	PRELIMINARY	PRG: 12 AA
ID Q13865		
AC Q13865		
DT 01 NOV 1996 (TRENBERG) 01, Created)		
DT 01 NOV 1996 (TRENBERG) 01, Last sequence update)		
DT 01-DEC-2001 (TRENBERG) 19, Last annotation update)		
DE Kinesin light chain		
GN BETA KINESIN		
OS Homo sapiens; Human		

```
CC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE:97171116; PubMed:8945637;
RA Chetaniyevsky Y., Brown A., Jones T.A.
RT "Transfer first exon/intron characterization and tissue localization
RZ of the human light chain beta1 kinesin gene."
RL DNA Cell Biol 15:965-974(1996).
DR EMBL: X69652; FAY49149.1;
SQ SEQUENCE 12 AA, 1274 MW, 35690.48E04
Query Match 20.4% Score 64 DB 4 Length 12;
Best local Similarity 77.8% Pred No. 1.4e+03;
Matches 5, Conservative 0, Mismatches 2, Indels 0, Gaps 0;

CY 12 LKSSSSGP 20
DB 1
2 LKSSSSGP 10

RESULT 3
ID Q2160 PRELIMINARY; PRT, 16 AA.
AC Q2160
DT 01-MAY-2003 (TrEMBL); 01, Created;
DT 01-MAY-2003 (TrEMBL); 01, Last sequence update;
DT 01-MAY-2003 (TrEMBL); 01, Last annotation update;
DE Alcohol oxidase (fragment).
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Sacccharomycotina; Sacccharomycetes;
OX NCBI_TaxID:4922;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE:9374977; PubMed:7763609;
RA Kimura Y.H., Siewlow G.G., della Valle A., Shirai E.
RT "Conversion of starch to ethanol in a recombinant P. pastoris
RT expressing strain expressing the alpha-amylase from P.
RT putnis alcohol oxidase promoter."
RL Biotechnol Bioeng 71:11626-11636(1999).
DR EMBL: S6285; AA02548.1;
RC NCBI_TaxID:4922;
RN 1
RP SEQUENCE 16 AA, 1636 MW, 25680.48E04
Query Match 20.4% Score 64 DB 4 Length 16;
Best local Similarity 56.8% Pred No. 1.4e+03;
Matches 5, Conservative 0, Mismatches 2, Indels 0, Gaps 0;

CY 0 ELLSSSS 17
DB 0
0 ELLSSSS 16

RESULT 4
ID Q8414 PRELIMINARY; PRT, 16 AA.
AC Q8414
DT 01-MAY-2003 (TrEMBL); 13, Created;
DT 01-MAY-2003 (TrEMBL); 13, Last sequence update;
DT 01-MAY-2003 (TrEMBL); 13, Last annotation update;
DE BENZYL-tyrosine-linked aldehyde oxidoreductase (fragment).
OS Desulfovibrio gigas.
OC Bacteria; Proteobacteria; Delta-proteobacteria; Desulfarculales;
OC Desulfovibrioaceae; Desulfovibrio
OX NCBI_TaxID:809;
RN 1
RP SEQUENCE
RX MEDLINE:6004046; PubMed:7592189;
RA Bessenden W.V., Harper W.R., Hansen A.
```

```
RT "Purification and characterization of a benzylviologen-linked,
RT tungsten containing aldehyde oxidoreductase from Desulfovibrio gigas."
RL J. Bacteriol. 177:6195-6200(1995).
SQ SEQUENCE 20 AA, 2128 MW, 1A9608A188:9C2BC CRC64;

Query Match 25.9% Score 29 DB 2 Length 20;
Best local Similarity 31.3% Pred No. 1.4e+03;
Matches 5, Conservative 6, Mismatches 2, Indels 2, Gaps 1;

CY 6 QNDVDLQASRSP 20
DB 3 KLRIDV QASRSP 15

RESULT 5
ID Q8XG5 PRELIMINARY; PRT, 20 AA.
AC Q8XG5
DT 01-MAY-2003 (TrEMBL); 23, Created;
DT 01-MAY-2003 (TrEMBL); 23, Last sequence update;
DT 01-MAY-2003 (TrEMBL); 23, Last annotation update;
DE Kinesin superfamily protein 21A (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN 1
RP SEQUENCE FROM N.A.
RX STRAIN:CV981/62; Tissue=Cerebellum;
RX MEDLINE:22184681; PubMed:12468851;
RA The FANTOM Consortium.
RT "The FANTOM genome exploration research group phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL: AK047329; BA012931.1;
RC NCBI_TaxID:10090;
RN 1
RP SEQUENCE 20 AA, 2062 MW, E1DD-1EAD42A2075 CRC64;

Query Match 25.9% Score 29 DB 1 Length 20;
Best local Similarity 62.5% Pred No. 1.4e+03;
Matches 5, Conservative 2, Mismatches 1, Indels 0, Gaps 0;

CY 2 LKQGVMD 9
DB 0
0 LKQGVMD 9

RESULT 6
ID Q8W62 PRELIMINARY; PRT, 18 AA.
AC Q8W62
DT 01-MAY-2003 (TrEMBL); 14, Created;
DT 01-MAY-2003 (TrEMBL); 13, Last sequence update;
DT 01-MAY-2003 (TrEMBL); 14, Last annotation update;
DE GNG-3 tyrosine peptide (fragment).
OS Pheretima vittata (Earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplochaeta;
OC Loricifera; Megasclecidae; Pheretima.
OX NCBI_TaxID:46674;
RN 1
RP SEQUENCE
RX MEDLINE:9474592; PubMed:7486182;
RA Omi T., Ukeda K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Morio K.
RT "The GNG-3 tyrosine peptide tyrosine peptides isolated from the gut and
RT the whole body of the earthworms."
RL Biochem Biophys Res Commun. 216:1372-1378(1995).
SQ SEQUENCE 18 AA, 1937 MW, E81AD314B5B266 CRC64;

Query Match 25.9% Score 29 DB 5 Length 18;
Best local Similarity 36.8% Pred No. 1.7e+03;
Matches 4, Conservative 1, Mismatches 1, Indels 0, Gaps 0;
```

QY 13 CCGSSG 18  
DB 13 CCGGNG 18

## RESULT 7

Q00656 PRELIMINARY: PRT: 16 AA.  
ID Q00656  
AC Q00656  
DT 01-MAY-1999 (TrEMBLrel. 01, Created)  
DT 01-MAY-1999 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Actin (Fragment).  
GN ACT1.  
OS Cryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
CC Ehrhartoideae; Cryzeae; Cryza.  
CX NCBI TaxID:4532;  
FN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=CV. B-42;  
RX MEDLINE=9252956; PubMed=1753941;  
RA McElroy D., Howers A.D., Jones B., Wu R.;  
RT "Construction of expression vectors based on the rice actin-1 (act1)  
RT 5' region for use in monocot transformation";  
RL Mol. Gen. Genet. 231:150-160(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=CV. B-42;  
RA Wu R.;  
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
LR EMBL: X63830; CAA45324.1;  
LP Genbank: Q42656;  
FT NON TER 16  
SQ SEQUENCE 16 AA; 1523 MW; B6B6BA793293E2 CR764;

Query Match 24.1%; Score 27; DB 10; Length 14;  
Best Local Similarity 83.3%; Pred. No. 2.2e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GSSSG 19  
DB 14 GSSSG 12

## RESULT 8

Q07668 PRELIMINARY: PRT: 16 AA.  
ID Q07668  
AC Q07668  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Lactoferrin (Fragment).  
GN Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
CX NCBI TaxID:9796;  
FN [1]  
RP SEQUENCE FROM N.A.  
RX Brandon R.B., Giffard J.M., Bell T.K.;  
RT "Isolation of Equine Lactoferrin Gene";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF102625; AAC77463.1;  
DS HSP: 077698; ACE2  
DR InterPro: IPRO0156; Transferrin.  
DR Pfam: PF00405; Transferrin; 1.  
FT NON TER 1  
FT NON TER 18  
SQ SEQUENCE 18 AA; 1936 MW; D8FBFA20A4A6003 F7664;

Query Match 24.1%; Score 27; DB 10; Length 14;

Best Local Similarity 80.0%; Pred. No. 2.5e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEDG 5  
DB 1 CLEDG 5

## RESULT 9

Q9TRC1 PRELIMINARY: PRT: 19 AA.  
ID Q9TRC1  
AC Q9TRC1  
DT 01-MAY-2003 (TrEMBLrel. 13, Created)  
DT 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 14, Last annotation update)  
DE 20 kDa phosphorylation-dependent protein phosphatase-1 inhibitory  
DE protein (Fragment).  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
CX NCBI TaxID=9823;  
FN [1]  
RP SEQUENCE.  
RX MEDLINE=96362144; PubMed=8720121;  
RA Eto M., Ohori T., Suzuki M., Furuya K., Morita F.;  
RT "A novel protein phosphatase-1 inhibitory protein: potentiated by  
RT protein kinase C: isolation from porcine aorta media and  
RT characterization";  
RL J. Biochem. 118:1104-1107(1995).  
RN [2]  
SQ SEQUENCE 19 AA; 1850 MW; 5D94CF3EF225A922 CRC64;

Query Match 24.1%; Score 27; DB 6; Length 19;  
Best Local Similarity 83.3%; Pred. No. 2.6e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GSSSG 19  
DB 14 GSSSG 16

## RESULT 10

Q8Z13 PRELIMINARY: PRT: 20 AA.  
ID Q8Z13  
AC Q8Z13  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE LEF1 (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
CX NCBI TaxID=9606;  
FN [1]  
RP SEQUENCE FROM N.A.  
RA Filali M., Cheng N., Abbot U., Leontiev V., Engelhardt J.F.;  
RT "Wnt 3a/b-catenin Signaling Induces Transcription from the LEF-1  
RT Promoter";  
RL J. Biol. Chem. 276:21200-21202;  
DR EMBL: AY123650; AAN56089.1;  
FT NON TER 20  
SQ SEQUENCE 20 AA; 1761 MW; B4F1691E56FBA675 CRC64;

Query Match 24.1%; Score 27; DB 4; Length 20;  
Best Local Similarity 62.5%; Pred. No. 2.8e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 GCGSSG 19  
DB 4 GCGGCG 11

## RESULT 11

Q9TRP3





DR EM501:002322:AAA47284.17.10  
DR InterPro:IPROCC153:Reovirus\_cap.  
DR Pfam:PF00979:Reovirus\_cap.1  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA: 1852 MW: 47545.8464301600.90640  
  
Query March 22.8% Score 25.00 DB 100 GenBank 17.  
Best Local Similarity 54.5% Pident No 1.900000  
Matches 67 Conservative 31 Mismatches 11 Indels 11 Gaps 11  
  
CY 1 CLEDS QUMDV 10  
|||  
2b 4 CLPGRGHVWSE 14

Search completed: November 5, 2003, 18:21:17  
Job time : 14 secs





PT disulfide bridge cyclized peptide and immunogenic carrier

XX  
PS Claim 4; Page 16; 45pp; English.

XX  
CC The present invention relates to conjugates suitable for use in vaccines,  
CC where the conjugate comprises a disulfide bridge cyclised peptide and an  
CC immunogenic carrier. The vaccines can be used in the treatment of  
CC allergies. The present sequence is a cyclic peptide comprising derived  
CC from human immunoglobulin E (IgE), suitable for use in the invention.  
XX  
SQ Sequence 20 AA;

Query Match 100.0%; Score 112; Pos. 1; Ident. 100%

Best Local Similarity 100.0%; Pos. 1; Ident. 100%

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

DY : CLEDCQVNVVLGGSSGSP 20

DN : CLEDCQVNVVLGGSSGSP 20

RESULT 4

AE700544

IC ASJ08944 standard; Peptide; 20 AA.

XX ASJ08944;

XX AC AC

XX DT DT

XX GT GT

XX Human TBE cyclic immunogenic peptide SEQ ID NO: 124.

XX Immunogen; human; IgE; immunoglobulin E; allergy; third-order linkage;  
XX vaccine; antiallergic; cyclic.

XX KW Koto sapiens.

XX GS GS

XX XX

FN WU00116409 A2.

ED ED

ED 28 FEB 2002.

XX 19 AUG 2001; 2001WC-EP09576.

XX 22 AUG 2000; 2000GS-C020717.

XX USVIK I SMITHKLINE BEECHAM BIOLOGICALS.

FA (PEPT I PEPTIDE THERAPEUTICS LTD).

EI Friede X, March S, Turnell WH, Vignais Pabouls YD.

XX WIPI: 2002-089649/52.

XX Conjugate for use in vaccine for treatment of allergic diseases  
PT disulfide bridge cyclized peptide and immunogenic carrier

XX  
PS Claim 4; Page 16; 45pp; English.

XX  
CC The present invention relates to conjugates suitable for use in vaccines,  
CC where the conjugate comprises a disulfide bridge cyclised peptide and an  
CC immunogenic carrier. The vaccines can be used in the treatment of  
CC allergies. The present sequence is a cyclic peptide comprising derived  
CC from human immunoglobulin E (IgE), suitable for use in the invention.  
XX  
SQ Sequence 20 AA;

Query Match 93.8%; Score 105; Pos. 1; Ident. 89%

Best Local Similarity 100.0%; Pos. 1; Ident. 100%

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

DY : CLEDCQVNVVLGGSSGSG 19

DN : CLEDCQVNVVLGGSSGSG 19

FF 22 FEB 2000; 2000WO-BF01455.  
 XX 25-FEB 1999; 99GB-0004405.  
 PR 29 MAR 1999; 99GB-0007151.  
 PR 07 MAY 1999; 99GB-0010537.  
 PR 07 MAY 1999; 99GB-0010538.  
 PR 07-AUG 1999; 99GB-0018494.  
 PR 07-AUG 1999; 99GB-0018602.  
 PR 07 SEP 1999; 99GB-0021046.  
 PR 07 SEP 1999; 99GB-0021047.  
 PR 29-OCT 1999; 99GB-0025619.  
 PR 24 NOV 1999; 99GB-0027698.  
 XX (SMK) : SWITKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) : PEPTIDE THERAPEUTICS LTD.  
 XX Dwyer M, Friede M, Greenwood J, Hewitt R, Jones A, Van Ruyk R,  
 Randall R, Turnell WG, Van Mechelen MP, Vinals D, Wainwright W,  
 XX WPI; 2001-521967/521.  
 DR WPI; 2000-522023/53.  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX Claim 14; Page 9; 123pp; English.  
 XX The present invention describes a peptide (i) comprising an isolated  
 CC surface exposed group/epitope (E1) of C-epsilon 4 domain of an  
 CC immunoglobulin E (IgE), or its mimotope. Also described herein is an  
 CC immunogen (i) for treating allergy comprising (i) a 4 valent (ii)  
 CC for treating allergies comprising (i) a 4 valent (ii) epitope of  
 CC recombinant E1, (ii) a pharmaceutical composition comprising (i) a  
 CC (5) a peptide (i) capable of being recognised by (i) a human immunogen  
 CC (ii) comprising (i) a) and (7) products (ii) by producing (i) a (i)  
 CC can have anti-allergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (i) (ii) and (iii) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (iv) is useful for identifying mimotopes of E1.  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (v) is useful in diagnostics and in the antibody purification  
 CC of circulating anti-IgE antibodies from blood. (vi) (ii) and (iii) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (iv) is also useful in diagnosing allergy. AAU16642 to AAU16693 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX Sequence 13 AA.  
 SQ Query Match 65.2%; Score 73; DB 22; Length 13;  
 Best Local Similarity 100.0%; Posit. No. 0.021;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CUESDQWMDVLC 13  
 DP |||||  
 1 CUESDQWMDVLC 13  
 RESULT 7  
 AAU16642  
 ID AAU16642 standard; Peptide; 13 AA.  
 XX AAU16642.  
 XX 07 NOV 2001 (first entry)  
 DT 07 NOV 2001 (first entry)  
 DE Human IgE cyclic immunogenic peptide SEQ ID NO: 96.  
 XX Immunogen; Human IgE; immunoglobulin E; allergy; thio-ether linkage;  
 KW vaccing; anti-allergic; cyclic.  
 XX Homo sapiens.  
 OS WO200215409 A2.  
 XX 29-FEB 2002.  
 XX 17-AUG 2001; 2001W-BF09576.

OS Synthetic.  
 XX WO200145745-A2.  
 PD 28-JUN-2001.  
 XX 21 DEC 2000; 2000W-BF04915.  
 XX 21-DEC 1999; 99GB-0030213.  
 PR 22-FEB 2000; 2000GB-GA04096.  
 PR 22 AUG 2000; 2000GB-0022707.  
 PR 22-AUG-2000; 2000GB-0022708.  
 XX (SMK) : ACAMBI'S RES LTD.  
 PA (SMK) : SWITKLINE BEECHAM BIOLOGICALS.  
 XX Flynn M, Johnson D,  
 XX WPI; 2001-521967/521.  
 DR A linkage comprising an immunogenic conjugate useful treatment of IgE  
 PT mediated diseases  
 XX Example 4; Page 21; 45pp; English.  
 XX The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce a  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC C-epsilon 2, C-epsilon 3 or C-epsilon 4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IgE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU16632-AAU1693 represent peptides derived from or mimotopes of  
 CC the C-epsilon 2/C-epsilon 3/C-epsilon 4 region of human IgE.  
 XX Sequence 13 AA.  
 SQ Query Match 65.2%; Score 73; DB 22; Length 13;  
 Best Local Similarity 100.0%; Posit. No. 0.021;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CUESDQWMDVLC 13  
 DP |||||  
 1 CUESDQWMDVLC 13  
 RESULT 8  
 ARJ00312  
 ID ARJ00312 standard; Peptide; 13 AA.  
 XX ARJ00312.  
 XX 02 SEP 2002 (first entry)  
 DT 02 SEP 2002 (first entry)  
 DE Human IgE cyclic immunogenic peptide SEQ ID NO: 96.  
 XX Immunogen; Human IgE; immunoglobulin E; allergy; thio-ether linkage;  
 KW vaccing; anti-allergic; cyclic.  
 XX Homo sapiens.  
 OS WO200215409 A2.  
 XX 29-FEB 2002.  
 XX 17-AUG 2001; 2001W-BF09576.

XX  
PR 22 AUG 2000; 2000GB-002017.  
PA (SMITHKLINE BEECHAM BIOLOGICALS)  
PA (PEPTIDE THERAPEUTICS LTD.)  
XX  
XX Friede M, Mason S, Turner W, Vinals Bassols YC,  
XX WPI; 2002-449648/52.  
XX Conjugate for use in vaccine for treatment of allergic diseases  
XX disulfide bridge cyclized peptide and immunogen derived  
XX  
XX Claim 4; Page 11; 45pp; English.  
XX The present invention relates to conjugates suitable for use in vaccines,  
XX where the conjugate comprises a disulfide bridge cyclized peptide and an  
XX immunogenic carrier. The vaccines can be used in the treatment of  
XX allergies. The present sequence is a cyclic peptide immunogen derived  
XX from human immunoglobulin E (IgE) suitable for use in the invention.  
XX  
SQ Sequence 13 AA;  
Query Match 65.1%; Score 74; DB 21; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 CLEGGQVMQVLC 13  
DB 1 CLEGGQVMQVLC 13  
PEP11 3  
AAB20873  
XX AAB20873 standard; peptide; 13 AA.  
XX  
AC AAB20873;  
XX  
XX 01 JAN 2001 (first entry);  
XX Antiallergy peptide mimotope sequence (E1 IgE).  
XX Immunoglobulin E (IgE); immunogenic; immunoglobulin E (IgE); C-epsilon-2 domain;  
XX Pios are cancer; Haemophilus influenzae; vaccine; immunogenic disease;  
XX salivary cystostatic; antiallergic; miosis; immunogenic disease;  
XX proteinase; Alzheimer's disease; allergy.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Modified site 14  
XX Note="Hamidate"  
XX  
XX KC000050077-AL  
XX  
XX 31 AUG 2000.  
XX  
XX 22 FEB 2000; 2000C EPC1457.  
XX  
XX 25 FEB 1999; 99GB-0004405.  
XX 25 FEB 1999; 99GB-0004406.  
XX 25 FEB 1999; 99GB-0004412.  
XX 13-AUG 1999; 99GB-0019260.  
XX  
XX (SMITHKLINE BEECHAM BIOLOGICALS)  
PA Coste M, Lobet Y, Van-Mechelen ME, Vinals M,  
XX WPI; 2000-572040/53.  
XX Immunogens and vaccine comprising the immunogen derived from proteinase and  
XX cancer; comprises peptide and carrier from proteinase and immunogen

XX Claim 10; Page 15; 53pp; English.  
XX The present invention describes an immunogen (I) comprising a peptide  
XX (IIa) and a carrier (Ib) derived from protein D of Haemophilus influenzae  
XX or its fragment. Also described are: (i) a vaccine comprising (I), and  
XX an excipient; (ii) preparation of (I), comprising conjugating a peptide  
XX to protein D or its fragment; and (iii) preparation of a vaccine of (I),  
XX comprising formulating (i) with an excipient, (ii) has cytostatic,  
XX antiallergic, nootropic, neuroprotective and protozoacide activities,  
XX (iii) and the vaccine are useful for the manufacture of a medicament for  
XX preventing and treating infectious diseases such as malaria or chronic  
XX disease such as cancer; Alzheimer's disease of allergy in a patient.  
XX Unlike prior art immunogens, (i) induces high levels of antipeptide  
XX immune responses while inducing a moderate humoral response against the  
XX carrier. The present sequence represents a specifically claimed  
XX mimotope peptide sequence, which can be used in an immunogen of the  
XX present invention.  
XX  
SQ Sequence 13 AA;  
Query Match 57.1%; Score 64; DB 21; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 CLEGGQVMQVLC 12  
DB 1 CLEGGQVMQVLC 12  
RESULT 12  
AAB25914  
XX AAB25914 standard; peptide; 13 AA.  
XX  
AC AAB25914;  
XX  
XX 05 JAN 2001 (first entry);  
XX P1 mimotope peptide PT15 SEQ ID NO:3.  
XX Epitope; mimotope; human; immunoglobulin E (IgE); C-epsilon-2 domain;  
XX allergic disease; immunophylaxis; immunotherapy; antiallergic;  
XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
XX allergy; atopy.  
XX Homo sapiens.  
XX  
XX KC000050462-AL  
XX  
XX Key Location/Qualifiers  
XX Modified site 14  
XX Note="Hamidate"  
XX  
XX 22 FEB 2000; 2000C EPC1458.  
XX  
XX 25-FEB 1999; 99GB-0004405.  
XX 29-MAR 1999; 99GB-0004451.  
XX 07-MAY 1999; 99GB-0010537.  
XX 07-MAY 1999; 99GB-0010538.  
XX 07-AUG 1999; 99GB-0018594.  
XX 07-AUG 1999; 99GB-0018603.  
XX 07-SEP 1999; 99GB-0021046.  
XX 07-SEP 1999; 99GB-0021047.  
XX 29-OCT-1999; 99GB-0025619.  
XX 23-NOV-1999; 99GB-0027698.  
XX  
XX (SMITHKLINE BEECHAM BIOLOGICALS)  
PA (PEPTIDE THERAPEUTICS LTD.)  
XX  
XX Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S,  
XX Randall R, Turner W, Vinals De Bassols YC,  
XX WPI; 2000-572040/54  
XX Peptides useful for treatment, preventing and ameliorating allergic

PT diseases, comprising an isolated surface exposed at tip of a specific  
XX domain from immunoglobulin E.  
PS Claim 14, Page 9, 129pp; English.  
XX  
CC The present invention describes a peptide (I) comprising an isolated  
CC surface exposed group/epitope (E1) of C-peptide-2 domain (D) of  
CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an  
CC immunogen (II) for treating allergy comprising (i) a vaccine (III)  
CC for treating allergies comprising (i) a ligand (IV) capable of  
CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
CC (5) a peptide (a) capable of being recognised by (IV); (6) an immunogen  
CC (IIa) comprising (IIa) and (7) producing (III) by producing (II); (1)  
CC can have anti-allergic and immunosuppressive activities, and can be used  
CC as a vaccine and histamine release inhibitor. (II), (III) and (IV) are  
CC useful in medicine and in the manufacture of medicaments for treating  
CC and preventing allergies. (IV) is useful for identifying mimotopes of E1,  
CC in medicine and also in manufacturing medicaments for treating  
CC allergies. (II) is useful in diagnostics and in the affinity purification  
CC of circulating anti-IgE antibodies from blood. (II), (III) and (IV) are  
CC useful for treating a patient susceptible to or suffering from allergies.  
CC (IV) is also useful in diagnosing atopy. AAB259C7, AAB26099 represent  
CC peptide sequences which are used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 13 AA;  
Query Match 57.18; Score 64; DB 21; Length 13;  
Best Local Similarity 100.0%; Pred.No. 0.25; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGGCGVMDVCL 12  
Db 1 CAGGCGVMDVCL 12  
II III  
II III  
RESULT 12  
AAU16639  
ID AAB259C7 standard; Peptide: 13 AA  
XX  
AC AAB26099;  
XX  
DT 22 AUG 2003; first entry  
XX  
DE Peptide II derived as mimotope of C-peptide2 region of human IgE.  
XX  
KW Human linkage technology; conjugated compound; carrier vehicle;  
KW epitope; C-peptide2; C-peptide1; C-peptide; immunoglobulin E;  
KW IGE mediated disease; antibody response.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200145741 A2.  
XX  
PD 29 JUN 2001.  
XX  
PF 21-FEB-2000; 2000WC-3B04935.  
XX  
PR 21-FEB-1999; 99GB-0030233.  
PR 22-FEB-2000; 2000GB-0004096.  
PR 22-AUG-2000; 2000GB-0020787.  
PR 22-AUG-2000; 2000GB-0020788.  
XX  
PA GSKN 1 SMITHKLINE BEECHAM BIOLOGICAL AL.  
XX GSKN 1 PEPTIDE THERAPEUTICS LTD.

PT diseases, comprising an isolated surface exposed at tip of a specific  
XX domain from immunoglobulin E.  
PS Claim 14, Page 9, 129pp; English.  
XX  
CC The present invention describes a peptide (I) comprising an isolated  
CC surface exposed group/epitope (E1) of C-peptide-2 domain (D) of  
CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an  
CC immunogen (II) for treating allergy comprising (i) a vaccine (III)  
CC for treating allergies comprising (i) a ligand (IV) capable of  
CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
CC (5) a peptide (a) capable of being recognised by (IV); (6) an immunogen  
CC (IIa) comprising (IIa) and (7) producing (III) by producing (II); (1)  
CC can have anti-allergic and immunosuppressive activities, and can be used  
CC as a vaccine and histamine release inhibitor. (II), (III) and (IV) are  
CC useful in medicine and in the manufacture of medicaments for treating  
CC and preventing allergies. (IV) is useful for identifying mimotopes of E1,  
CC in medicine and also in manufacturing medicaments for treating  
CC allergies. (II) is useful in diagnostics and in the affinity purification  
CC of circulating anti-IgE antibodies from blood. (II), (III) and (IV) are  
CC useful for treating a patient susceptible to or suffering from allergies.  
CC (IV) is also useful in diagnosing atopy. AAB259C7 to AAB26099 represent  
CC peptide sequences which are used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 13 AA;  
Query Match 57.18; Score 64; DB 21; Length 13;  
Best Local Similarity 100.0%; Pred.No. 0.25; Indels 0; Gaps 0;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LERDQGVMDVCL 12  
Db 2 LERDQGVMDVCL 12  
II III  
II III  
RESULT 12  
AAU16639  
ID AAB259C7 standard; Peptide: 13 AA  
XX  
AC AAB26099;  
XX  
DT 22 AUG 2003; first entry  
XX  
DE Peptide II derived as mimotope of C-peptide2 region of human IgE.  
XX  
KW Human linkage technology; conjugated compound; carrier vehicle;  
KW epitope; C-peptide2; C-peptide1; C-peptide; immunoglobulin E;  
KW IGE mediated disease; antibody response.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200145741 A2.  
XX  
PD 29 JUN 2001.  
XX  
PF 21-FEB-2000; 2000WC-3B04935.  
XX  
PR 21-FEB-1999; 99GB-0030233.  
PR 22-FEB-2000; 2000GB-0004096.  
PR 22-AUG-2000; 2000GB-0020787.  
PR 22-AUG-2000; 2000GB-0020788.  
XX  
PA JACM 1 ROBBINS RES LTD.  
XX JSMK 1 SMITHKLINE BEECHAM BIOLOGICALS.

FI Flinn K, Johnson T;  
 DR WPI; 2001-521967/57.  
 XX  
 XX A linkage comprising an immunogenic conjugate useful treatment of IGE  
 PT mediated diseases.  
 XX  
 FS Example 4; Page 21; 48pp; English.  
 XX  
 CC The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IGE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU16612-AAU16913 represent peptides derived from or mimotopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 57.1%; Score 64; DB 13; Length 13;  
 Best Local Similarity 100.0%; Pred No. 0.25;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CEEGQVNDVLC 12  
 I I I I I I  
 DB 1 CEEGQVNDVLC 12  
 RESULT 13  
 AAU16641  
 ID AAU16641 standard; Peptide; 13 AA;  
 XX  
 AC AAU16641;  
 XX  
 DT 01-JUN-2001 (first entry)  
 XX  
 CC Peptide P15p derived as mimotope of Cepsilon4 region of human IgE.  
 XX  
 KW Biocore Linkage Technology; conjugated with P15p; used for IGE  
 XX epitope; Cepsilon4; Cepsilon3; Cepsilon2; Cepsilon1; Cepsilon0;  
 XX IGE mediated disease; antibody to IGE  
 XX Homo sapiens.  
 CS Synthetic.  
 XX  
 PN WC269014545 A2;  
 XX  
 PC 26 JUN 2001;  
 XX  
 PF 21 DEC 2000; 2003MO-GR04935.  
 XX  
 PR 21 FEB 1999; 93GB 0030233  
 PR 22-FEB 2000; 2000GB-0004096  
 PR 22-AUG 2000; 2000GB 0020707.  
 PR 22-AUG-2000; 2000GB-0020708.  
 XX  
 PA (ACAM) ACAM515 RES LTD.  
 PA (SMIR) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 FI Flinn K, Johnson T;  
 DR WPI; 2001-521967/57.  
 XX  
 PT A linkage comprising an immunogenic conjugate useful treatment of IGE

PT mediated diseases  
 XX  
 FS Example 4; Page 21; 48pp; English.  
 XX  
 CC The present invention relates to linkage methodology for use in the  
 CC conjugation of compounds (e.g. peptides) to carrier vehicles  
 CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce  
 CC biological and immunological constructs. The invention provides a  
 CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a  
 CC protein) for use in a pharmaceutical composition or a vaccine. The  
 CC invention describes peptides derived from or mimotopes of the  
 CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E  
 CC (IgE) which are used to produce conjugated compounds. The compounds or  
 CC compositions of the invention are useful in the manufacture of a  
 CC medicament for the treatment of IGE mediated diseases. The invention  
 CC allows for controlled conjugation of a peptide epitope (antigen) to a  
 CC protein so as to form an immunogenic conjugate which may be able to  
 CC raise a protective antibody response in an animal or human patient.  
 CC AAU16612-AAU16913 represent peptides derived from or mimotopes of  
 CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 57.1%; Score 64; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred No. 0.25;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LEEGQVNDVLC 13  
 I I I I I I I I  
 DB 2 LEEGQVNDVLC 13  
 RESULT 14  
 AAB51028  
 ID AAB51028 standard; Peptide; 13 AA;  
 XX  
 AC AAB51028;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE IGE peptide #6.  
 XX  
 KW Vaccine; immunoglobulin E; IgE; anti allergy.  
 XX  
 CS Mammalia.  
 XX  
 PN WC269014516 A2;  
 XX  
 PC 14-JUN-2000  
 XX  
 PF 06 JUN 2000; 2000W EP05164  
 XX  
 PR 08-JUN 1999; 95GB-0013327.  
 XX  
 PA (SMIR) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 FI Price's 07  
 XX  
 DR WPI; 2001-091150/10.  
 XX  
 PT New vaccine comprising allergy peptides linked by an inert carrier,  
 PT useful for boosting an anti-allergy immune response in an individual  
 PT susceptible to an allergic response.  
 XX  
 PS Claim 5; Page 20; 26pp; English.  
 XX  
 CC The present invention relates to a composition comprising allergy  
 CC peptides linked by an inert carrier. The allergy peptides are derived  
 CC from immunoglobulin E (IgE) or IgE receptor. The present peptide is one  
 CC such peptide from IgE. The composition is useful as a vaccine or for  
 CC manufacturing a medicament for the prophylaxis or treatment of allergy.  
 CC In particular, the medicament for an anti-allergy immune response in an  
 CC individual susceptible to an allergic response.



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XX      Sequence 13 AA;
SQ
Query Match
Best Local Similarity 57.1%; Score 64; DB 12; Length 12;
Varities 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEGGQVMDVL 12
   |||||
PB 1 CLEGGQVMDVL 12

RESULT 15
AB00024
13 AB00024 standard; Peptide; 13 AA
XX
AC AP00024;
XX
CC G1-SRP 2002 (first entry)
XX
DE Human IgE immunogenic peptide SEQ ID NO: 8;
XX
KW Immunogen; human; IgE; immunoglobulin E; allergy; this entry: linkage;
KW vaccine; anti-allergic;
XX
OS Homo sapiens.
XX
PN WC200216404-A2;
XX
PC 24 FEB-2002;
XX
PF 17 AUG-2001; 2001WC EP09576;
XX
PR 22-AUG-2000; 2000GE-0020717;
XX
PA (SVIK) SMITHKLINE BEECHAM BIOLOGICALS
PA (DEPT) PEPTIDE THERAPEUTICS INC;
XX
PC Fiedler M, Mason S, Turnell WG, Vinals-Bansale YG;
XX
DR WPI: 2002-0406487-A2;
XX
RT Conjugate for use in vaccine for treatment of allergy; description
RT disulfide bridge cyclized peptide and immunogenic carrier;
XX
CS Claim 4; Page 9; 45pp; English;
XX
The present invention relates to conjugates suitable for use in vaccines,
XX
which are conjugates comprising a disulfide bridge cyclized peptide and an
XX
immunogenic carrier. The vaccine is suitable for the treatment of
XX
allergies. The present sequence is a peptide sequence derived from human
XX
immunoglobulin E (IgE) suitable to be cyclized and used in the invention.
XX
Sequence 13 AA;
SQ
Query Match
Best Local Similarity 57.1%; Score 64; DB 12; Length 12;
Varities 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEGGQVMDVL 12
   |||||
PB 1 CLEGGQVMDVL 12

Search completed November 5, 2003, 18:23:00
Job time: 42 secs
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GenCore version 5.1.6  
Copyright (c) 1991-2003 Computer Unit

CM protein protein search, using sw model

Run on: November 5, 2003, 18:21:22 / Search time 24 seconds  
without alignment  
120 6 4 million cell of bases/sec

Title: US-09-914-088-15

Perfect score: 112

Sequence: 1 CLEGGQVMDVLLGGSSGGP 20

Scoring table: BLCSUM62

Gapop 10.0, Gapext 2.0

Searches: 644379 seqs, 17174292 residues

Total number of hits satisfying chosen parameters: 16120

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA\*  
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3: /cgn2\_6/ptodata/2/furpaa/US06\_NEW\_PRR0288.ppt  
4: /cgn2\_6/ptodata/2/furpaa/US06\_PRR0288.ppt  
5: /cgn2\_6/ptodata/2/furpaa/US06\_NEW\_PRR0288.ppt  
6: /cgn2\_6/ptodata/2/furpaa/US06\_PRR0288.ppt  
7: /cgn2\_6/ptodata/2/furpaa/US06\_PRR0288.ppt  
8: /cgn2\_6/ptodata/2/furpaa/US06\_PRR0288.ppt  
9: /cgn2\_6/ptodata/2/furpaa/US06\_PRR0288.ppt  
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18: /cgn2\_6/ptodata/2/furpaa/US06\_PRR0288.ppt

Prod. No. is the number of results from the search that have a score greater than or equal to the score of the best hit listed, and is derived by analysis of the data generated by the search.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	43.8	10	12	US-10-082-014-282
2	49	43.8	10	12	US-10-082-014-282
3	47	42.0	9	12	US-10-082-014-282
4	47	42.0	9	12	US-10-082-014-282
5	45	40.2	10	12	US-10-082-014-282
6	45	40.2	14	10	US-09-904-036-4
7	42	37.5	12	9	US-09-904-036-4
8	42	37.5	14	10	US-09-904-036-4
9	42	37.5	14	14	US-10-050-688-1
10	42	37.5	14	14	US-10-050-688-1
11	42	37.5	15	12	US-10-050-688-1
12	42	37.5	15	12	US-10-050-688-1
13	41	36.6	12	9	US-09-914-088-1
14	41	36.6	12	9	US-09-914-088-1
15	41	36.6	12	10	US-09-914-088-1

16	41	36.6	12	12	US-10-050-688-1
17	41	36.6	12	12	US-10-050-688-1
18	41	36.6	12	14	US-10-050-688-1
19	41	36.6	12	14	US-10-050-688-1
20	40	35.7	12	9	US-09-904-036-4
21	40	35.7	12	10	US-09-904-036-4
22	40	35.7	12	12	US-10-050-688-1
23	40	35.7	12	12	US-10-050-688-1
24	40	35.7	12	14	US-10-050-688-1
25	40	35.7	12	14	US-10-050-688-1
26	40	35.7	16	10	US-09-904-036-4
27	40	35.7	16	10	US-09-904-036-4
28	40	35.7	18	14	US-10-050-688-1
29	39	33.9	9	10	US-09-918-243-84
30	39	33.9	9	10	US-09-918-243-84
31	37	33.0	10	9	US-09-909-348-2
32	37	33.0	10	10	US-09-909-348-2
33	37	33.0	10	14	US-10-050-688-1
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36	36	32.1	9	9	US-09-918-243-84
37	36	32.1	9	10	US-09-918-243-84
38	36	32.1	9	12	US-10-050-688-1
39	36	32.1	9	12	US-10-050-688-1
40	36	32.1	9	15	US-10-135-795-163
41	36	32.1	9	15	US-10-135-795-163
42	36	32.1	10	9	US-09-909-348-1
43	36	32.1	10	10	US-09-909-348-1
44	36	32.1	10	14	US-10-050-688-1
45	36	32.1	10	14	US-10-050-688-1

ALIGNMENTS

RESULT 1  
US-10-082-014-282  
; Sequence 182, Application US/10082014  
; Publication No. US20030195858A1  
; GENERAL INFORMATION:  
; APPLICANT: Bickert, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL C  
; FILE REFERENCE: US-10-0466/95124  
; CURRENT APPLICATION NUMBER: US/10082014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/910,915  
; PRICE FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: Patent In Division 3.1  
; SEQ ID NO: 182  
; LENGTH: 10  
; TYPE: PPT  
; ORGANISM: HBC seqs  
US-10-082-014-282

Query Match 43.8%, Score 49; DB 12; Length 10;  
Best Loc: Similarity 90.0%; Pred. No. 1.2;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEDQVMDV 11  
DB 1 MEDQVMDV 10

RESULT 2  
US-10-312-036-136  
; Sequence 136, Application US/10172076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Page, Mark  
; APPLICANT: Filed, Martin  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; CHRONIC HEPATITIS

FILE REFERENCE: 4564/87179  
 ? CURRENT APPLICATION NUMBER: US/10/072,076  
 ? CURRENT FILING DATE: 2002-02-21  
 ? PRIOR APPLICATION NUMBER: 10/096,299  
 ? PRIOR FILING DATE: 2002-02-21  
 ? PRIOR APPLICATION NUMBER: 10/082,014  
 ? PRIOR FILING DATE: 2002-02-22  
 ? NUMBER OF SEQ ID NOS: 308  
 ? SOFTWARE: Patent in version 3.2  
 ? SEQ ID NO 136  
 ? LENGTH: 12  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 US 10-072-076-136

Query Match 43.0% Score 49; DR 12; Length 12;  
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 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 2 EDCQWQWVD 11  
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 Db 1 EDCQWQWVD 10

RESULT 4  
 US-10-072-014-273  
 ? Sequence 127, Application US/10082014  
 ? Publication No. US2003018586A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Birkett, Ashley J.  
 ? TITLE OF INVENTION: IMMUNOGENIC HBs-CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY

FILE REFERENCE: 100 130.0 4564/85124  
 ? CURRENT APPLICATION NUMBER: US/10/082,014  
 ? CURRENT FILING DATE: 2002-02-22  
 ? PRIOR APPLICATION NUMBER: 09/930,915  
 ? PRIOR FILING DATE: 2002-08-15  
 ? NUMBER OF SEQ ID NOS: 290  
 ? SOFTWARE: Patent in version 3.1  
 ? SEQ ID NO 273  
 ? LENGTH: 9  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 US 10-082-014-273

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 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 EDCQWQWVD 11  
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 Db 1 EDCQWQWVD 9

RESULT 4  
 US 10-072-076-127  
 ? Sequence 127, Application US/10/072,076  
 ? Publication No. US20030198645A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Parag, Mark  
 ? TITLE OF INVENTION: STABILIZED HBs-CHIMER PARTICLES AS HEPATITIS VACCINE FOR  
 ? TITLE OF INVENTION: CHRONIC HEPATITIS  
 ? FILE REFERENCE: 4564/87179  
 ? CURRENT APPLICATION NUMBER: US/10/072,076  
 ? CURRENT FILING DATE: 2003-02-21  
 ? PRIOR APPLICATION NUMBER: 10/086,299  
 ? PRIOR FILING DATE: 2002-02-21  
 ? PRIOR APPLICATION NUMBER: 10/082,014  
 ? PRIOR FILING DATE: 2002-02-22  
 ? NUMBER OF SEQ ID NOS: 308  
 ? SOFTWARE: Patent in version 3.2  
 ? SEQ ID NO 127  
 ? LENGTH: 9

? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 US-10-372-076-127

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 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 EDCQWQWVD 11  
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RESULT 5  
 US-10-144-148-55  
 ? Sequence 55, Application US/10144188  
 ? Publication No. US20030175212A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Cai, Zeling  
 ? APPLICANT: Jackson, Michael R.  
 ? APPLICANT: Peterson, Per A.  
 ? APPLICANT: Shi, Weixing  
 ? APPLICANT: Kong, Yan  
 ? APPLICANT: Degraw, Julia  
 ? TITLE OF INVENTION: Ex-Vivo Priming For Generating Cytotoxic T Lymphocytes Specific

FILE REFERENCE: 100 130.0 4564/85124  
 ? CURRENT APPLICATION NUMBER: US/10/144,168  
 ? CURRENT FILING DATE: 2002-05-13  
 ? PRIOR APPLICATION NUMBER: 60/291,300  
 ? PRIOR FILING DATE: 2001-05-15  
 ? NUMBER OF SEQ ID NOS: 60  
 ? SOFTWARE: Patent in version 3.2  
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 ? LENGTH: 10  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Peptide antigen  
 US-10-144-168-55

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RESULT 6  
 US-09-885-441-6  
 ? Sequence 6, Application US/09885441  
 ? Patent No. US20020146470A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Xiao, Yonghong  
 ? TITLE OF INVENTION: Regulation of Human Eosinophil Serine  
 ? TITLE OF INVENTION: Protease 1 Like Enzyme  
 ? FILE REFERENCE: 04974,00512  
 ? CURRENT APPLICATION NUMBER: US/09/885,441  
 ? CURRENT FILING DATE: 2001-06-21  
 ? PRIOR APPLICATION NUMBER: US 60/212,844  
 ? PRIOR FILING DATE: 2000-06-21  
 ? PRIOR APPLICATION NUMBER: US 60/244,171  
 ? PRIOR FILING DATE: 2000-10-31  
 ? PRIOR APPLICATION NUMBER: US 60/279,766  
 ? PRIOR FILING DATE: 2001-01-30  
 ? PRIOR APPLICATION NUMBER: PCT/\_\_\_\_\_  
 ? NUMBER OF SEQ ID NOS: 58  
 ? SOFTWARE: First SEQ for Windows Version 4.0  
 ? SEQ ID NO 6  
 ? LENGTH: 14

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1 TYPE: PPT
2 ORGANISM: Artificial Sequence
3 FEATURE:
4 OTHER INFORMATION: Peptide fragment of Thrombin
5 NAME/KEY: VARIANT
6 LOCATION: (1) - (14)
7 OTHER INFORMATION: Xaa at position six is Glu or Gln
8 OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or Val
9 US-09-914-088-15
10
11 Query Match
12 Best Local Similarity 37.5% Score 42; DB 10; Length 14;
13 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
14
15 QY 11 DLGGSSSGP 20
16 | | | | |
17 Db 3 DAXGDSGGP 12
18
19 RESULT 9
20 US-10-050-692 4
21 Sequence 4; Application US/10050692
22 Publication No. US2002018235A1
23 GENERAL INFORMATION:
24 APPLICANT: Carney, Darrell H.
25 APPLICANT: Crowther, Roger S.
26 APPLICANT: Simmons, David J.
27 APPLICANT: Yang, Cliping
28 APPLICANT: Pedin, William R.
29 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
30 TITLE OF INVENTION: PEPTIDE DERIVATIVES
31 FILE REFERENCE: 3033.1002-004
32 CURRENT APPLICATION NUMBER: US/10/050,692
33 CURRENT FILING DATE: 2002-01-16
34 PRIOR APPLICATION NUMBER: 09/929,122
35 PRIOR FILING DATE: 2001-07-19
36 PRIOR APPLICATION NUMBER: 60/219,300
37 PRIOR FILING DATE: 2000-07-19
38 NUMBER OF SEQ ID NOS: 6
39 SOFTWARE: FastSeq for Windows Version 4.0
40 SEQ ID NO: 4
41 LENGTH: 14
42 TYPE: PPT
43 ORGANISM: Artificial Sequence
44 FEATURE:
45 OTHER INFORMATION: Fragment of human prothrombin
46 NAME/KEY: VARIANT
47 LOCATION: (1) - (14)
48 OTHER INFORMATION: Xaa = Glu or Gln
49 NAME/KEY: VARIANT
50 LOCATION: (13) - (15)
51 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
52 US-10-050-692-4
53
54 Query Match
55 Best Local Similarity 37.5% Score 42; DB 14; Length 14;
56 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
57
58 QY 11 DLGGSSSGP 20
59 | | | | |
60 Db 3 DAXGDSGGP 12
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62 RESULT 10
63 US-10-050-692 4
64 Sequence 4; Application US/10050692
65 Publication No. US2002018235A1
66 GENERAL INFORMATION:
67 APPLICANT: Carney, Darrell H.
68 APPLICANT: Crowther, Roger S.
69 APPLICANT: Simmons, David J.
70 APPLICANT: Yang, Cliping
71 APPLICANT: Pedin, William R.
72 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
73 TITLE OF INVENTION: PEPTIDE DERIVATIVES
74 FILE REFERENCE: 3033.1002-001
75 CURRENT APPLICATION NUMBER: US/09/909,122
76 CURRENT FILING DATE: 2001-07-19
77 PRIOR APPLICATION NUMBER: US 60/219,300
78 PRIOR FILING DATE: 2000-07-19
79 NUMBER OF SEQ ID NOS: 5
80 SOFTWARE: FastSeq for Windows Version 4.0
81 SEQ ID NO: 4
82 LENGTH: 14
83 TYPE: PPT
84 ORGANISM: Artificial Sequence
85 FEATURE:
86 OTHER INFORMATION: Peptide fragment of Thrombin
87 NAME/KEY: VARIANT
88 LOCATION: (2, 4, 11)
89 OTHER INFORMATION: Xaa, position 2 - Ala or Ser
90 OTHER INFORMATION: Xaa, position 4 - Glu or Gln
91 OTHER INFORMATION: Xaa, position 11 - Phe, Met, Leu, His or Val
92 US-09-914-088-15
93
94 Query Match
95 Best Local Similarity 37.5% Score 42; DB 10; Length 14;
96 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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98 QY 11 DLGGSSSGP 10
99 | | | | |
100 Db 1 DAXGDSGGP 10
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102 RESULT 9
103 US-09-914-088-15 4
104 Sequence 4; Application US/09090122
105 Patent No. US20020128202A1
106 GENERAL INFORMATION:
107 APPLICANT: Carney, Darrell H.
108 APPLICANT: Crowther, Roger S.
109 APPLICANT: Simmons, David J.
110 APPLICANT: Yang, Cliping
111 APPLICANT: Pedin, William R.
112 TITLE OF INVENTION: Stimulation of Bone Growth With Thrombin
113 TITLE OF INVENTION: Peptide Derivatives
114 FILE REFERENCE: 3033.1032-001
115 CURRENT APPLICATION NUMBER: US/09/909,122
116 CURRENT FILING DATE: 2001-07-19
117 PRIOR APPLICATION NUMBER: US 60/219,300
118 PRIOR FILING DATE: 2000-07-19
119 NUMBER OF SEQ ID NOS: 5
120 SOFTWARE: FastSeq for Windows Version 4.0
121 SEQ ID NO: 4
122 LENGTH: 14
123 TYPE: PPT
124 ORGANISM: Artificial Sequence
125 FEATURE:
126 OTHER INFORMATION: Peptide fragment of Thrombin
127 NAME/KEY: VARIANT
128 LOCATION: (2, 4, 11)
129 OTHER INFORMATION: Xaa, position 2 - Ala or Ser
130 OTHER INFORMATION: Xaa, position 4 - Glu or Gln
131 OTHER INFORMATION: Xaa, position 11 - Phe, Met, Leu, His or Val
132 US-09-914-088-15
133
134 Query Match
135 Best Local Similarity 37.5% Score 42; DB 10; Length 14;
136 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
137
138 QY 11 DLGGSSSGP 20
139 | | | | |
140 Db 3 DAXGDSGGP 12
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142 RESULT 9
143 US-10-050-692 4
144 Sequence 4; Application US/10050692
145 Publication No. US2002018235A1
146 GENERAL INFORMATION:
147 APPLICANT: Carney, Darrell H.
148 APPLICANT: Crowther, Roger S.
149 APPLICANT: Simmons, David J.
150 APPLICANT: Yang, Cliping
151 APPLICANT: Pedin, William R.
152 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
153 TITLE OF INVENTION: PEPTIDE DERIVATIVES
154 FILE REFERENCE: 3033.1002-004
155 CURRENT APPLICATION NUMBER: US/10/050,692
156 CURRENT FILING DATE: 2002-01-16
157 PRIOR APPLICATION NUMBER: 09/929,122
158 PRIOR FILING DATE: 2001-07-19
159 PRIOR APPLICATION NUMBER: 60/219,300
160 PRIOR FILING DATE: 2000-07-19
161 NUMBER OF SEQ ID NOS: 6
162 SOFTWARE: FastSeq for Windows Version 4.0
163 SEQ ID NO: 4
164 LENGTH: 14
165 TYPE: PPT
166 ORGANISM: Artificial Sequence
167 FEATURE:
168 OTHER INFORMATION: Fragment of human prothrombin
169 NAME/KEY: VARIANT
170 LOCATION: (1) - (14)
171 OTHER INFORMATION: Xaa = Glu or Gln
172 NAME/KEY: VARIANT
173 LOCATION: (13) - (15)
174 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
175 US-10-050-692-4
176
177 Query Match
178 Best Local Similarity 37.5% Score 42; DB 14; Length 14;
179 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
180
181 QY 11 DLGGSSSGP 20
182 | | | | |
183 Db 3 DAXGDSGGP 12
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185 RESULT 10
186 US-10-050-692 4
187 Sequence 4; Application US/10050692
188 Publication No. US2002018235A1
189 GENERAL INFORMATION:
190 APPLICANT: Carney, Darrell H.
191 APPLICANT: Crowther, Roger S.
192 APPLICANT: Simmons, David J.
193 APPLICANT: Yang, Cliping
194 APPLICANT: Pedin, William R.
195 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
196 TITLE OF INVENTION: PEPTIDE DERIVATIVES
197 FILE REFERENCE: 3033.1002-001
198 CURRENT APPLICATION NUMBER: US/09/909,122
199 CURRENT FILING DATE: 2001-07-19
200 PRIOR APPLICATION NUMBER: US 60/219,300
201 PRIOR FILING DATE: 2000-07-19
202 NUMBER OF SEQ ID NOS: 5
203 SOFTWARE: FastSeq for Windows Version 4.0
204 SEQ ID NO: 4
205 LENGTH: 14
206 TYPE: PPT
207 ORGANISM: Artificial Sequence
208 FEATURE:
209 OTHER INFORMATION: Peptide fragment of Thrombin
210 NAME/KEY: VARIANT
211 LOCATION: (2, 4, 11)
212 OTHER INFORMATION: Xaa, position 2 - Ala or Ser
213 OTHER INFORMATION: Xaa, position 4 - Glu or Gln
214 OTHER INFORMATION: Xaa, position 11 - Phe, Met, Leu, His or Val
215 US-09-914-088-15
216
217 Query Match
218 Best Local Similarity 37.5% Score 42; DB 10; Length 14;
219 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
220
221 QY 11 DLGGSSSGP 20
222 | | | | |
223 Db 3 DAXGDSGGP 12
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225 RESULT 9
226 US-10-050-692 4
227 Sequence 4; Application US/10050692
228 Publication No. US2002018235A1
229 GENERAL INFORMATION:
230 APPLICANT: Carney, Darrell H.
231 APPLICANT: Crowther, Roger S.
232 APPLICANT: Simmons, David J.
233 APPLICANT: Yang, Cliping
234 APPLICANT: Pedin, William R.
235 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
236 TITLE OF INVENTION: PEPTIDE DERIVATIVES
237 FILE REFERENCE: 3033.1002-004
238 CURRENT APPLICATION NUMBER: US/10/050,692
239 CURRENT FILING DATE: 2002-01-16
240 PRIOR APPLICATION NUMBER: 09/929,122
241 PRIOR FILING DATE: 2001-07-19
242 PRIOR APPLICATION NUMBER: 60/219,300
243 PRIOR FILING DATE: 2000-07-19
244 NUMBER OF SEQ ID NOS: 6
245 SOFTWARE: FastSeq for Windows Version 4.0
246 SEQ ID NO: 4
247 LENGTH: 14
248 TYPE: PPT
249 ORGANISM: Artificial Sequence
250 FEATURE:
251 OTHER INFORMATION: Fragment of human prothrombin
252 NAME/KEY: VARIANT
253 LOCATION: (1) - (14)
254 OTHER INFORMATION: Xaa = Glu or Gln
255 NAME/KEY: VARIANT
256 LOCATION: (13) - (15)
257 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
258 US-10-050-692-4
259
260 Query Match
261 Best Local Similarity 37.5% Score 42; DB 14; Length 14;
262 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
263
264 QY 11 DLGGSSSGP 20
265 | | | | |
266 Db 3 DAXGDSGGP 12
267
268 RESULT 10
269 US-10-050-692 4
270 Sequence 4; Application US/10050692
271 Publication No. US2002018235A1
272 GENERAL INFORMATION:
273 APPLICANT: Carney, Darrell H.
274 APPLICANT: Crowther, Roger S.
275 APPLICANT: Simmons, David J.
276 APPLICANT: Yang, Cliping
277 APPLICANT: Pedin, William R.
278 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
279 TITLE OF INVENTION: PEPTIDE DERIVATIVES
280 FILE REFERENCE: 3033.1002-001
281 CURRENT APPLICATION NUMBER: US/09/909,122
282 CURRENT FILING DATE: 2001-07-19
283 PRIOR APPLICATION NUMBER: US 60/219,300
284 PRIOR FILING DATE: 2000-07-19
285 NUMBER OF SEQ ID NOS: 5
286 SOFTWARE: FastSeq for Windows Version 4.0
287 SEQ ID NO: 4
288 LENGTH: 14
289 TYPE: PPT
290 ORGANISM: Artificial Sequence
291 FEATURE:
292 OTHER INFORMATION: Peptide fragment of Thrombin
293 NAME/KEY: VARIANT
294 LOCATION: (2, 4, 11)
295 OTHER INFORMATION: Xaa, position 2 - Ala or Ser
296 OTHER INFORMATION: Xaa, position 4 - Glu or Gln
297 OTHER INFORMATION: Xaa, position 11 - Phe, Met, Leu, His or Val
298 US-09-914-088-15
299
300 Query Match
301 Best Local Similarity 37.5% Score 42; DB 10; Length 14;
302 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
303
304 QY 11 DLGGSSSGP 20
305 | | | | |
306 Db 3 DAXGDSGGP 12
307
308 RESULT 9
309 US-10-050-692 4
310 Sequence 4; Application US/10050692
311 Publication No. US2002018235A1
312 GENERAL INFORMATION:
313 APPLICANT: Carney, Darrell H.
314 APPLICANT: Crowther, Roger S.
315 APPLICANT: Simmons, David J.
316 APPLICANT: Yang, Cliping
317 APPLICANT: Pedin, William R.
318 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
319 TITLE OF INVENTION: PEPTIDE DERIVATIVES
320 FILE REFERENCE: 3033.1002-004
321 CURRENT APPLICATION NUMBER: US/10/050,692
322 CURRENT FILING DATE: 2002-01-16
323 PRIOR APPLICATION NUMBER: 09/929,122
324 PRIOR FILING DATE: 2001-07-19
325 PRIOR APPLICATION NUMBER: 60/219,300
326 PRIOR FILING DATE: 2000-07-19
327 NUMBER OF SEQ ID NOS: 6
328 SOFTWARE: FastSeq for Windows Version 4.0
329 SEQ ID NO: 4
330 LENGTH: 14
331 TYPE: PPT
332 ORGANISM: Artificial Sequence
333 FEATURE:
334 OTHER INFORMATION: Fragment of human prothrombin
335 NAME/KEY: VARIANT
336 LOCATION: (1) - (14)
337 OTHER INFORMATION: Xaa = Glu or Gln
338 NAME/KEY: VARIANT
339 LOCATION: (13) - (15)
340 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
341 US-10-050-692-4
342
343 Query Match
344 Best Local Similarity 37.5% Score 42; DB 14; Length 14;
345 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
346
347 QY 11 DLGGSSSGP 20
348 | | | | |
349 Db 3 DAXGDSGGP 12
350
351 RESULT 10
352 US-10-050-692 4
353 Sequence 4; Application US/10050692
354 Publication No. US2002018235A1
355 GENERAL INFORMATION:
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357 APPLICANT: Crowther, Roger S.
358 APPLICANT: Simmons, David J.
359 APPLICANT: Yang, Cliping
360 APPLICANT: Pedin, William R.
361 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
362 TITLE OF INVENTION: PEPTIDE DERIVATIVES
363 FILE REFERENCE: 3033.1002-001
364 CURRENT APPLICATION NUMBER: US/09/909,122
365 CURRENT FILING DATE: 2001-07-19
366 PRIOR APPLICATION NUMBER: US 60/219,300
367 PRIOR FILING DATE: 2000-07-19
368 NUMBER OF SEQ ID NOS: 5
369 SOFTWARE: FastSeq for Windows Version 4.0
370 SEQ ID NO: 4
371 LENGTH: 14
372 TYPE: PPT
373 ORGANISM: Artificial Sequence
374 FEATURE:
375 OTHER INFORMATION: Peptide fragment of Thrombin
376 NAME/KEY: VARIANT
377 LOCATION: (2, 4, 11)
378 OTHER INFORMATION: Xaa, position 2 - Ala or Ser
379 OTHER INFORMATION: Xaa, position 4 - Glu or Gln
380 OTHER INFORMATION: Xaa, position 11 - Phe, Met, Leu, His or Val
381 US-09-914-088-15
382
383 Query Match
384 Best Local Similarity 37.5% Score 42; DB 10; Length 14;
385 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
386
387 QY 11 DLGGSSSGP 20
388 | | | | |
389 Db 3 DAXGDSGGP 12
390
391 RESULT 9
392 US-10-050-692 4
393 Sequence 4; Application US/10050692
394 Publication No. US2002018235A1
395 GENERAL INFORMATION:
396 APPLICANT: Carney, Darrell H.
397 APPLICANT: Crowther, Roger S.
398 APPLICANT: Simmons, David J.
399 APPLICANT: Yang, Cliping
400 APPLICANT: Pedin, William R.
401 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
402 TITLE OF INVENTION: PEPTIDE DERIVATIVES
403 FILE REFERENCE: 3033.1002-004
404 CURRENT APPLICATION NUMBER: US/10/050,692
405 CURRENT FILING DATE: 2002-01-16
406 PRIOR APPLICATION NUMBER: 09/929,122
407 PRIOR FILING DATE: 2001-07-19
408 PRIOR APPLICATION NUMBER: 60/219,300
409 PRIOR FILING DATE: 2000-07-19
410 NUMBER OF SEQ ID NOS: 6
411 SOFTWARE: FastSeq for Windows Version 4.0
412 SEQ ID NO: 4
413 LENGTH: 14
414 TYPE: PPT
415 ORGANISM: Artificial Sequence
416 FEATURE:
417 OTHER INFORMATION: Fragment of human prothrombin
418 NAME/KEY: VARIANT
419 LOCATION: (1) - (14)
420 OTHER INFORMATION: Xaa = Glu or Gln
421 NAME/KEY: VARIANT
422 LOCATION: (13) - (15)
423 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
424 US-10-050-692-4
425
426 Query Match
427 Best Local Similarity 37.5% Score 42; DB 14; Length 14;
428 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
429
430 QY 11 DLGGSSSGP 20
431 | | | | |
432 Db 3 DAXGDSGGP 12
433
434 RESULT 10
435 US-10-050-692 4
436 Sequence 4; Application US/10050692
437 Publication No. US2002018235A1
438 GENERAL INFORMATION:
439 APPLICANT: Carney, Darrell H.
440 APPLICANT: Crowther, Roger S.
441 APPLICANT: Simmons, David J.
442 APPLICANT: Yang, Cliping
443 APPLICANT: Pedin, William R.
444 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
445 TITLE OF INVENTION: PEPTIDE DERIVATIVES
446 FILE REFERENCE: 3033.1002-001
447 CURRENT APPLICATION NUMBER: US/09/909,122
448 CURRENT FILING DATE: 2001-07-19
449 PRIOR APPLICATION NUMBER: US 60/219,300
450 PRIOR FILING DATE: 2000-07-19
451 NUMBER OF SEQ ID NOS: 5
452 SOFTWARE: FastSeq for Windows Version 4.0
453 SEQ ID NO: 4
454 LENGTH: 14
455 TYPE: PPT
456 ORGANISM: Artificial Sequence
457 FEATURE:
458 OTHER INFORMATION: Peptide fragment of Thrombin
459 NAME/KEY: VARIANT
460 LOCATION: (2, 4, 11)
461 OTHER INFORMATION: Xaa, position 2 - Ala or Ser
462 OTHER INFORMATION: Xaa, position 4 - Glu or Gln
463 OTHER INFORMATION: Xaa, position 11 - Phe, Met, Leu, His or Val
464 US-09-914-088-15
465
466 Query Match
467 Best Local Similarity 37.5% Score 42; DB 10; Length 14;
468 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
469
470 QY 11 DLGGSSSGP 20
471 | | | | |
472 Db 3 DAXGDSGGP 12
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474 RESULT 9
475 US-10-050-692 4
476 Sequence 4; Application US/10050692
477 Publication No. US2002018235A1
478 GENERAL INFORMATION:
479 APPLICANT: Carney, Darrell H.
480 APPLICANT: Crowther, Roger S.
481 APPLICANT: Simmons, David J.
482 APPLICANT: Yang, Cliping
483 APPLICANT: Pedin, William R.
484 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
485 TITLE OF INVENTION: PEPTIDE DERIVATIVES
486 FILE REFERENCE: 3033.1002-004
487 CURRENT APPLICATION NUMBER: US/10/050,692
488 CURRENT FILING DATE: 2002-01-16
489 PRIOR APPLICATION NUMBER: 09/929,122
490 PRIOR FILING DATE: 2001-07-19
491 PRIOR APPLICATION NUMBER: 60/219,300
492 PRIOR FILING DATE: 2000-07-19
493 NUMBER OF SEQ ID NOS: 6
494 SOFTWARE: FastSeq for Windows Version 4.0
495 SEQ ID NO: 4
496 LENGTH: 14
497 TYPE: PPT
498 ORGANISM: Artificial Sequence
499 FEATURE:
500 OTHER INFORMATION: Fragment of human prothrombin
501 NAME/KEY: VARIANT
502 LOCATION: (1) - (14)
503 OTHER INFORMATION: Xaa = Glu or Gln
504 NAME/KEY: VARIANT
505 LOCATION: (13) - (15)
506 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
507 US-10-050-692-4
508
509 Query Match
510 Best Local Similarity 37.5% Score 42; DB 14; Length 14;
511 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
512
513 QY 11 DLGGSSSGP 20
514 | | | | |
515 Db 3 DAXGDSGGP 12
516
517 RESULT 10
518 US-10-050-692 4
519 Sequence 4; Application US/10050692
520 Publication No. US2002018235A1
521 GENERAL INFORMATION:
522 APPLICANT: Carney, Darrell H.
523 APPLICANT: Crowther, Roger S.
524 APPLICANT: Simmons, David J.
525 APPLICANT: Yang, Cliping
526 APPLICANT: Pedin, William R.
527 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
528 TITLE OF INVENTION: PEPTIDE DERIVATIVES
529 FILE REFERENCE: 3033.1002-001
530 CURRENT APPLICATION NUMBER: US/09/909,122
531 CURRENT FILING DATE: 2001-07-19
532 PRIOR APPLICATION NUMBER: US 60/219,300
533 PRIOR FILING DATE: 2000-07-19
534 NUMBER OF SEQ ID NOS: 5
535 SOFTWARE: FastSeq for Windows Version 4.0
536 SEQ ID NO: 4
537 LENGTH: 14
538 TYPE: PPT
539 ORGANISM: Artificial Sequence
540 FEATURE:
541 OTHER INFORMATION: Peptide fragment of Thrombin
542 NAME/KEY: VARIANT
543 LOCATION: (2, 4, 11)
544 OTHER INFORMATION: Xaa, position 2 - Ala or Ser
545 OTHER INFORMATION: Xaa, position 4 - Glu or Gln
546 OTHER INFORMATION: Xaa, position 11 - Phe, Met, Leu, His or Val
547 US-09-914-088-15
548
549 Query Match
550 Best Local Similarity 37.5% Score 42; DB 10; Length 14;
551 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
552
553 QY 11 DLGGSSSGP 20
554 | | | | |
555 Db 3 DAXGDSGGP 12
556
557 RESULT 9
558 US-10-050-692 4
559 Sequence 4; Application US/10050692
560 Publication No. US2002018235A1
561 GENERAL INFORMATION:
562 APPLICANT: Carney, Darrell H.
563 APPLICANT: Crowther, Roger S.
564 APPLICANT: Simmons, David J.
565 APPLICANT: Yang, Cliping
566 APPLICANT: Pedin, William R.
567 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
568 TITLE OF INVENTION: PEPTIDE DERIVATIVES
569 FILE REFERENCE: 3033.1002-004
570 CURRENT APPLICATION NUMBER: US/10/050,692
571 CURRENT FILING DATE: 2002-01-16
572 PRIOR APPLICATION NUMBER: 09/929,122
573 PRIOR FILING DATE: 2001-07-19
574 PRIOR APPLICATION NUMBER: 60/219,300
575 PRIOR FILING DATE: 2000-07-19
576 NUMBER OF SEQ ID NOS: 6
577 SOFTWARE: FastSeq for Windows Version 4.0
578 SEQ ID NO: 4
579 LENGTH: 14
580 TYPE: PPT
581 ORGANISM: Artificial Sequence
582 FEATURE:
583 OTHER INFORMATION: Fragment of human prothrombin
584 NAME/KEY: VARIANT
585 LOCATION: (1) - (14)
586 OTHER INFORMATION: Xaa = Glu or Gln
587 NAME/KEY: VARIANT
588 LOCATION: (13) - (15)
589 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
590 US-10-050-692-4
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592 Query Match
593 Best Local Similarity 37.5% Score 42; DB 14; Length 14;
594 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
595
596 QY 11 DLGGSSSGP 20
597 | | | | |
598 Db 3 DAXGDSGGP 12
599
600 RESULT 10
601 US-10-050-692 4
602 Sequence 4; Application US/10050692
603 Publication No. US2002018235A1
604 GENERAL INFORMATION:
605 APPLICANT: Carney, Darrell H.
606 APPLICANT: Crowther, Roger S.
607 APPLICANT: Simmons, David J.
608 APPLICANT: Yang, Cliping
609 APPLICANT: Pedin, William R.
610 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
611 TITLE OF INVENTION: PEPTIDE DERIVATIVES
612 FILE REFERENCE: 3033.1002-001
613 CURRENT APPLICATION NUMBER: US/09/909,122
614 CURRENT FILING DATE: 2001-07-19
615 PRIOR APPLICATION NUMBER: US 60/219,300
616 PRIOR FILING DATE: 2000-07-19
617 NUMBER OF SEQ ID NOS: 5
618 SOFTWARE: FastSeq for Windows Version 4.0
619 SEQ ID NO: 4
620 LENGTH: 14
621 TYPE: PPT
622 ORGANISM: Artificial Sequence
623 FEATURE:
624 OTHER INFORMATION: Peptide fragment of Thrombin
625 NAME/KEY: VARIANT
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627 OTHER INFORMATION: Xaa, position 2 - Ala or Ser
628 OTHER INFORMATION: Xaa, position 4 - Glu or Gln
629 OTHER INFORMATION: Xaa, position 11 - Phe, Met, Leu, His or Val
630 US-09-914-088-15
631
632 Query Match
633 Best Local Similarity 37.5% Score 42; DB 10; Length 14;
634 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
635
636 QY 11 DLGGSSSGP 20
637 | | | | |
638 Db 3 DAXGDSGGP 12
639
640 RESULT 9
641 US-10-050-692 4
642 Sequence 4; Application US/10050692
643 Publication No. US2002018235A1
644 GENERAL INFORMATION:
645 APPLICANT: Carney, Darrell H.
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650 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
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652 FILE REFERENCE: 3033.1002-004
653 CURRENT APPLICATION NUMBER: US/10/050,692
654 CURRENT FILING DATE: 2002-01-16
655 PRIOR APPLICATION NUMBER: 09/929,122
656 PRIOR FILING DATE: 2001-07-19
657 PRIOR APPLICATION NUMBER: 60/219,300
658 PRIOR FILING DATE: 2000-07-19
659 NUMBER OF SEQ ID NOS: 6
660 SOFTWARE: FastSeq for Windows Version 4.0
661 SEQ ID NO: 4
662 LENGTH: 14
663 TYPE: PPT
664 ORGANISM: Artificial Sequence
665 FEATURE:
666 OTHER INFORMATION: Fragment of human prothrombin
667 NAME/KEY: VARIANT
668 LOCATION: (1) - (14)
669 OTHER INFORMATION: Xaa = Glu or Gln
670 NAME/KEY: VARIANT
671 LOCATION: (13) - (15)
672 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
673 US-10-050-692-4
674
675 Query Match
676 Best Local Similarity 37.5% Score 42; DB 14; Length 14;
677 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
678
679 QY 11 DLGGSSSGP 20
680 | | | | |
681 Db 3 DAXGDSGGP 12
682
683 RESULT 10
684 US-10-050-692 4
685 Sequence 4; Application US/10050692
686 Publication No. US2002018235A1
687 GENERAL INFORMATION:
688 APPLICANT: Carney, Darrell H.
689 APPLICANT: Crowther, Roger S.
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691 APPLICANT: Yang, Cliping
692 APPLICANT: Pedin, William R.
693 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
694 TITLE OF INVENTION: PEPTIDE DERIVATIVES
695 FILE REFERENCE: 3033.1002-001
696 CURRENT APPLICATION NUMBER: US/09/909,122
697 CURRENT FILING DATE: 2001-07-19
698 PRIOR APPLICATION NUMBER: US 60/219,300
699 PRIOR FILING DATE: 2000-07-19
700 NUMBER OF SEQ ID NOS: 5
701 SOFTWARE: FastSeq for Windows Version 4.0
702 SEQ ID NO: 4
703 LENGTH: 14
704 TYPE: PPT
705 ORGANISM: Artificial Sequence
706 FEATURE:
707 OTHER INFORMATION: Peptide fragment of Thrombin
708 NAME/KEY: VARIANT
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710 OTHER INFORMATION: Xaa, position 2 - Ala or Ser
711 OTHER INFORMATION: Xaa, position 4 - Glu or Gln
712 OTHER INFORMATION: Xaa, position 11 - Phe, Met, Leu, His or Val
713 US-09-914-088-15
714
715 Query Match
716 Best Local Similarity 37.5% Score 42; DB 10; Length 14;
717 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
718
719 QY 11 DLGGSSSGP 20
720 | | | | |
721 Db 3 DAXGDSGGP 12
722
723 RESULT 9
724 US-10-050-692 4
725 Sequence 4; Application US/10050692
726 Publication No. US2002018235A1
727 GENERAL INFORMATION:
728 APPLICANT: Carney, Darrell H.
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731 APPLICANT: Yang, Cliping
732 APPLICANT: Pedin, William R.
733 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
734 TITLE OF INVENTION: PEPTIDE DERIVATIVES
735 FILE REFERENCE: 3033.1002-004
736 CURRENT APPLICATION NUMBER: US/10/050,692
737 CURRENT FILING DATE: 2002-01-16
738 PRIOR APPLICATION NUMBER: 09/929,122
739 PRIOR FILING DATE: 2001-07-19
740 PRIOR APPLICATION NUMBER: 60/219,300
741 PRIOR FILING DATE: 2000-07-19
742 NUMBER OF SEQ ID NOS: 6
743 SOFTWARE: FastSeq for Windows Version 4.0
744 SEQ ID NO: 4
745 LENGTH: 14
746 TYPE: PPT
747 ORGANISM: Artificial Sequence
748 FEATURE:
749 OTHER INFORMATION: Fragment of human prothrombin
750 NAME/KEY: VARIANT
751 LOCATION: (1) - (14)
752 OTHER INFORMATION: Xaa = Glu or Gln
753 NAME/KEY: VARIANT
754 LOCATION: (13) - (15)
755 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
756 US-10-050-692-4
757
758 Query Match
759 Best Local Similarity 37.5% Score 42; DB 14; Length 14;
760 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
761
762 QY 11 DLGGSSSGP 20
763 | | | | |
764 Db 3 DAXGDSGGP 12
765
766 RESULT 10
767 US-10-050-692 4
768 Sequence 4; Application US/10050692
769 Publication No. US2002018235A1
770 GENERAL INFORMATION:
771 APPLICANT: Carney, Darrell H.
772 APPLICANT: Crowther, Roger S.
773 APPLICANT: Simmons, David J.
774 APPLICANT: Yang, Cliping
775 APPLICANT: Pedin, William R.
776 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
777 TITLE OF INVENTION: PEPTIDE DERIVATIVES
778 FILE REFERENCE: 3033.1002-001
779 CURRENT APPLICATION NUMBER: US/09/909,122
780 CURRENT FILING DATE: 2001-07-19
781 PRIOR APPLICATION NUMBER: US 60/219,300
782 PRIOR FILING DATE: 2000-07-19
783 NUMBER OF SEQ ID NOS: 5
784 SOFTWARE: FastSeq for Windows Version 4.0
785 SEQ ID NO: 4
786 LENGTH: 14
787 TYPE: PPT
788 ORGANISM: Artificial Sequence
789 FEATURE:
790 OTHER INFORMATION: Peptide fragment of Thrombin
791 NAME/KEY: VARIANT
792 LOCATION: (2, 4, 11)
793 OTHER INFORMATION: Xaa, position 2 - Ala or Ser
794 OTHER INFORMATION: Xaa, position 4 - Glu or Gln
795 OTHER INFORMATION: Xaa, position 11 - Phe, Met, Leu, His or Val
796 US-09-914-088-15
797
798 Query Match
799 Best Local Similarity 37.5% Score 42; DB 10; Length 14;
800 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
801
802 QY 11 DLGGSSSGP 20
803 | | | | |
804 Db 3 DAXGDSGGP 12
805
806 RESULT 9
807 US-10-050-692 4
808 Sequence 4; Application US/10050692
809 Publication No. US2002018235A1
810 GENERAL INFORMATION:
811 APPLICANT: Carney, Darrell H.
812 APPLICANT: Crowther, Roger S.
813 APPLICANT: Simmons, David J.
814 APPLICANT: Yang, Cliping
815 APPLICANT: Pedin, William R.
816 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
817 TITLE OF INVENTION: PEPTIDE DERIVATIVES
818 FILE REFERENCE: 3033.1002-004
819 CURRENT APPLICATION NUMBER: US/10/050,692
820 CURRENT FILING DATE: 2002-01-16
821 PRIOR APPLICATION NUMBER: 09/929,122
822 PRIOR FILING DATE: 2001-07-19
823 PRIOR APPLICATION NUMBER: 60/219,300
824 PRIOR FILING DATE: 2000-07-19
825 NUMBER OF SEQ ID NOS: 6
826 SOFTWARE: FastSeq for Windows Version 4.0
827 SEQ ID NO: 4
828 LENGTH: 14
829 TYPE: PPT
830 ORGANISM: Artificial Sequence
831 FEATURE:
832 OTHER INFORMATION: Fragment of human prothrombin
833 NAME/KEY: VARIANT
834 LOCATION: (1) - (14)
835 OTHER INFORMATION: Xaa = Glu or Gln
836 NAME/KEY: VARIANT
837 LOCATION: (13) - (15)
838 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val
839 US-10-050-692-4
840
841 Query Match
842 Best Local Similarity 37.5% Score 42; DB 14; Length 14;
843 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
844
845 QY 
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1 APPLICANT: Bergmann, John
2 TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
3 TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
4 TITLE OF INVENTION: RECEPTOR
5 FILE REFERENCE: 1331, 1203-024
6 CURRENT APPLICATION NUMBER: US/10/294,025
7 CURRENT FILING DATE: 2002-07-12
8 PRIOR APPLICATION NUMBER: 09/909,148
9 PRIOR FILING DATE: 2001-07-19
10 PRIOR APPLICATION NUMBER: 60/219,800
11 PRIOR FILING DATE: 2000-07-20
12 NUMBER OF SEQ ID NOS: 6
13 SOFTWARE: FastSeq for Windows Version 3.0
14 SEQ ID NO 4
15 LENGTH: 14
16 TYPE: PPT
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: peptide fragment of thrombin
20 NAME/KEY: VARIANT
21 LOCATION: (6)...(16)
22 OTHER INFORMATION: Xaa = Glu or Gln
23 FEATURE:
24 NAME/KEY: VARIANT
25 LOCATION: (1)...(14)
26 OTHER INFORMATION: Xaa = Phe, Met, Leu, His or Val.
27 US 10-294,025-4
28
29 Query Match: 37.5% Score 42; DB 14; Length 14;
30 Best Local Similarity: 70.0%; Pref. No. 18;
31 Matches: 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
32
33 QY 11 DCCGSSSRP 20
34 1 1 1 1 1
35 1 DCCGSSSRP 12
36
37 RESULT 11
38 US 10-294,025-4
39 Sequence: Application US/10/294,025
40 Publication No. US2003018430A1
41 GENERAL INFORMATION:
42 APPLICANT: Xu, Jianzhun
43 APPLICANT: Li, David
44 APPLICANT: Michael, Jennifer D.
45 APPLICANT: Barabek, Susan A.
46 APPLICANT: Li, David
47 APPLICANT: Barabek, Susan A.
48 APPLICANT: Barabek, Susan A.
49 APPLICANT: Barabek, Susan A.
50 APPLICANT: Barabek, Susan A.
51 APPLICANT: Barabek, Susan A.
52 APPLICANT: Barabek, Susan A.
53 APPLICANT: Barabek, Susan A.
54 APPLICANT: Barabek, Susan A.
55 APPLICANT: Barabek, Susan A.
56 APPLICANT: Barabek, Susan A.
57 APPLICANT: Barabek, Susan A.
58 APPLICANT: Barabek, Susan A.
59 APPLICANT: Barabek, Susan A.
60 APPLICANT: Barabek, Susan A.
61 APPLICANT: Barabek, Susan A.
62 APPLICANT: Barabek, Susan A.
63 APPLICANT: Barabek, Susan A.
64 APPLICANT: Barabek, Susan A.
65 APPLICANT: Barabek, Susan A.
66 APPLICANT: Barabek, Susan A.
67 APPLICANT: Barabek, Susan A.
68 APPLICANT: Barabek, Susan A.
69 APPLICANT: Barabek, Susan A.
70 APPLICANT: Barabek, Susan A.
71 APPLICANT: Barabek, Susan A.
72 APPLICANT: Barabek, Susan A.
73 APPLICANT: Barabek, Susan A.
74 APPLICANT: Barabek, Susan A.
75 APPLICANT: Barabek, Susan A.
76 APPLICANT: Barabek, Susan A.
77 APPLICANT: Barabek, Susan A.
78 APPLICANT: Barabek, Susan A.
79 APPLICANT: Barabek, Susan A.
80 APPLICANT: Barabek, Susan A.
81 APPLICANT: Barabek, Susan A.
82 APPLICANT: Barabek, Susan A.
83 APPLICANT: Barabek, Susan A.
84 APPLICANT: Barabek, Susan A.
85 APPLICANT: Barabek, Susan A.
86 APPLICANT: Barabek, Susan A.
87 APPLICANT: Barabek, Susan A.
88 APPLICANT: Barabek, Susan A.
89 APPLICANT: Barabek, Susan A.
90 APPLICANT: Barabek, Susan A.
91 APPLICANT: Barabek, Susan A.
92 APPLICANT: Barabek, Susan A.
93 APPLICANT: Barabek, Susan A.
94 APPLICANT: Barabek, Susan A.
95 APPLICANT: Barabek, Susan A.
96 APPLICANT: Barabek, Susan A.
97 APPLICANT: Barabek, Susan A.
98 APPLICANT: Barabek, Susan A.
99 APPLICANT: Barabek, Susan A.
100 APPLICANT: Barabek, Susan A.

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1 SOFTWARE: FastSeq for Windows Version 3.0
2 SEQ ID NO 1012
3 LENGTH: 15
4 TYPE: PPT
5 ORGANISM: Homo sapiens
6 US-10-144-088-15-1012
7
8 Query Match: 37.5% Score 42; DB 12; Length 15;
9 Best Local Similarity: 70.0%; Pref. No. 18;
10 Matches: 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
11
12 QY 11 DCCGSSSRP 20
13 1 1 1 1 1
14 1 DCCGSSSRP 11
15
16 RESULT 12
17 US-10-294-025-1032
18 Sequence: Application US/10294025
19 Publication No. US2003018430A1
20 GENERAL INFORMATION:
21 APPLICANT: Xu, Jianzhun
22 APPLICANT: Kalos, Michael F.
23 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
24 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
25 FILE REFERENCE: 21611, 427C29
26 CURRENT APPLICATION NUMBER: US/10/294,025
27 CURRENT FILING DATE: 2002-11-12
28 NUMBER OF SEQ ID NOS: 1038
29 SOFTWARE: FastSeq for Windows Version 3.0
30 SEQ ID NO 1032
31 LENGTH: 15
32 TYPE: PPT
33 ORGANISM: Homo sapiens
34 US 10-294-025-1032
35
36 Query Match: 37.5% Score 42; DB 12; Length 15;
37 Best Local Similarity: 70.0%; Pref. No. 18;
38 Matches: 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
39
40 QY 11 DCCGSSSRP 20
41 1 1 1 1 1
42 1 DCCGSSSRP 11
43
44 RESULT 13
45 US 09-904-090-1
46 Sequence: Application US/09/904,090
47 Patent No. US2003018430A1
48 GENERAL INFORMATION:
49 APPLICANT: Guiney, Daniel
50 TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
51 TITLE OF INVENTION: PEPTIDES
52 FILE REFERENCE: 12031200-021
53 CURRENT APPLICATION NUMBER: US/09/904,090
54 CURRENT FILING DATE: 2001-07-12
55 PRIOR APPLICATION NUMBER: US 60/219,800
56 PRIOR FILING DATE: 2000-07-12
57 NUMBER OF SEQ ID NOS: 4
58 SOFTWARE: FastSeq for Windows Version 4.0
59 SEQ ID NO 2
60 LENGTH: 12
61 TYPE: PPT
62 ORGANISM: Artificial Sequence
63 FEATURE:
64 OTHER INFORMATION: Polypeptide, fragment of thrombin
65 US-09-904-090-1
66
67 Query Match: 36.4% Score 41; DB 9; Length 12;
68 Best Local Similarity: 70.0%; Pref. No. 19;
69 Matches: 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Job time : 29 secs

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CY      11 DCCGGSSGSP 20
DB      1 DCCGGSSGSP 10

RESULT 14
US 09-804-156-34
? Sequence 34, Application US/0904156
? Patent No. US2007005912CA1
? GENERAL INFORMATION:
? APPLICANT: SERA ET AL.
? TITLE OF INVENTION: Serine protease polynucleotides, polypeptides, and antibodies
? FILE REFERENCE: PTO05P4
? CURRENT APPLICATION NUMBER: US/09/804,156
? CURRENT FILING DATE: 2001-03-13
? PRIOR APPLICATION NUMBER: 60/189,025
? PRIOR FILING DATE: 2000-03-14
? NUMBER OF SEQ ID NOS: 39
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO: 34
? LENGTH: 12
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-804-156-34

Query Match      36.6% Score 41 DB 3, Length 12,
Best Local Similarity 70.0% Pred. No. 19
Matches 7: Conservative 0; Mismatches 3; Gaps 0;

CY      11 DCCGGSSGSP 20
DB      1 DCCGGSSGSP 10

RESULT 15
US 09-946-643-19
? Sequence 19, Application US/09046633
? Patent No. US20070119925A1
? GENERAL INFORMATION:
? APPLICANT: NI ET AL.
? TITLE OF INVENTION: PTO05P1
? FILE REFERENCE: Serine proteases
? CURRENT APPLICATION NUMBER: US/09/946,633
? CURRENT FILING DATE: 2001-09-06
? PRIOR APPLICATION NUMBER: 09/597,839
? PRIOR FILING DATE: 2000-06-20
? PRIOR APPLICATION NUMBER: 60/533,439
? PRIOR FILING DATE: 1999-05-27
? PRIOR APPLICATION NUMBER: 62/115,174
? PRIOR FILING DATE: 1999-05-20
? PRIOR APPLICATION NUMBER: 62/147,006
? PRIOR FILING DATE: 1999-08-03
? PRIOR APPLICATION NUMBER: 60/152,935
? PRIOR FILING DATE: 1999-09-09
? PRIOR APPLICATION NUMBER: 60/162,979
? PRIOR FILING DATE: 1999-11-01
? NUMBER OF SEQ ID NOS: 19
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO: 19
? LENGTH: 12
? TYPE: PRT
? ORGANISM: Homo sapiens
US 09-946-643-19

Query Match      36.6% Score 41 DB 3, Length 12,
Best Local Similarity 70.0% Pred. No. 19,
Matches 7: Conservative 0; Mismatches 3; Gaps 0;

CY      11 DCCGGSSGSP 20
DB      1 DCCGGSSGSP 10

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GenCore version 5.0.1.6  
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ON protein - protein search, using sw -tbl

Run on: November 5, 2003, 19:13:14 / Search 150, 21 Sequences  
(without alignment)  
43,264 Million cell of hits/sec

Filter:  
Perfect score: 112  
Sequence: 1 CLEGGQWMDVLCGSSSG 20

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 3.5

Searched: 32917 seqs, 423,088 residues

Total number of hits satisfying chosen parameters: 15073

Minimum DB seq length: 2  
Maximum DB seq length: 20

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA:  
1: /cgn2\_6/prodata/1/aa/AA\_NVB pep.  
2: /cgn2\_6/prodata/1/aa/AA\_CMB pep.  
3: /cgn2\_6/prodata/1/aa/AA\_CMB pep.  
4: /cgn2\_6/prodata/1/aa/AA\_CMB pep.  
5: /cgn2\_6/prodata/1/aa/AA\_CMB pep.  
6: /cgn2\_6/prodata/1/aa/AA\_CMB pep.

Pref. No. is the number of results predicted by algorithm to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Match	Length	DB ID	Seq. Name
1	43	38.4	18	1	US-09-914-088-15
2	41	38.4	18	4	US-09-914-088-15
3	41	36.6	12	6	US-09-914-088-15
4	41	36.6	15	3	US-09-914-088-15
5	40	35.7	13	4	US-09-914-088-15
6	39	34.8	20	1	US-09-914-088-15
7	39	34.8	20	3	US-09-914-088-15
8	38	34.8	20	1	US-09-914-088-15
9	38	34.8	20	3	US-09-914-088-15
10	37	34.8	20	1	US-09-914-088-15
11	37	34.8	20	3	US-09-914-088-15
12	38	33.9	9	5	PCT/US98/09869
13	38	33.9	20	1	US-09-914-088-15
14	38	33.9	20	3	US-09-914-088-15
15	37	33.0	9	1	US-09-914-088-15
16	37	33.0	9	2	US-09-914-088-15
17	37	33.0	9	2	US-09-914-088-15
18	37	33.0	9	2	US-09-914-088-15
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21	37	33.0	9	3	US-09-914-088-15
22	37	33.0	9	3	US-09-914-088-15
23	37	33.0	9	3	US-09-914-088-15
24	37	33.0	9	3	US-09-914-088-15
25	37	33.0	9	3	US-09-914-088-15
26	37	33.0	9	3	US-09-914-088-15
27	37	33.0	9	3	PCT/US98/14445

Sequence 163, App  
Sequence 58, App  
Sequence 163, App  
Sequence 3, Appl  
Sequence 47, Appl  
Patent No. 5352664  
Sequence 34, Appl  
Sequence 34, Appl  
Sequence 7, Appl  
Sequence 7, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 64, Appl  
Sequence 4, Appl  
Sequence 64, Appl

ALIGNMENTS

RESULT 1  
US-09-914-088-15  
Sequence 25, Application US/09/67953B  
Patent No. 6287572  
GENERAL INFORMATION:  
APPLICANT: Kingsman, Alan J  
APPLICANT: Kingsman, Susan M  
TITLE OF INVENTION: Anti-HIV peptides and proteins  
FILE REFERENCE: 550 154  
CURRENT APPLICATION NUMBER: US/09/367.953B  
CURRENT FILING DATE: 1999-08-24  
PRIOR APPLICATION NUMBER: PCT/GB98/00563  
PRIOR FILING DATE: 1998-02-24  
PRIOR APPLICATION NUMBER: GB 970362.0  
PRIOR FILING DATE: 1997-02-24  
NUMBER OF SEQ ID NOS: 131  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 25  
LENGTH: 18  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Index:  
US-09-914-088-15

Query Match: 58.4% Score 43; DP 3; Length 18;  
Best Local Similarity: 53.3% Pred. No. 10;  
Matches: 8; Conservative: 3; Mismatches: 4; Gaps: 0;

QY 5 GQWMDVLCGSSSG 19  
DB 4 GRLDVPSTCGSSSG 18

RESULT 2  
US-09-914-088-15  
Sequence 26, Application US/09/254832B  
Patent No. 6541219  
GENERAL INFORMATION:  
APPLICANT: Kingsman, Alan J  
APPLICANT: Kingsman, Susan M  
TITLE OF INVENTION: THERAPEUTIC GENE  
FILE REFERENCE: 9132.10USKO  
CURRENT APPLICATION NUMBER: US/09/254.832B  
CURRENT FILING DATE: 1999-06-21  
PRIOR APPLICATION NUMBER: PCT/GB97/02969  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 962250.6  
PRIOR FILING DATE: 1996-10-29  
NUMBER OF SEQ ID NOS: 24





US-09-102-008C-34

Query Match 35.7% Score 40; DB 4; Length 19;  
 Best Local Similarity 70.0%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 11 DSCGSSGSP 20

DB 2 DSCGSSGSP 11

RESULT 6

US-08-495-302-54

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Affymax Technologies, N.V.

STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,410

FILING DATE: 07 JUN 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 16,691

REFERENCE/DOCKET NUMBER: 1068-1A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-414-312-53

Query Match 34.8% Score 39; DB 1; Length 19;  
 Best Local Similarity 44.4%; Pred. No. 39;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 2 LSCGQVNVLCGSSG 19

DB 1 LSCGQVNVLCGSSG 18

RESULT 7

US-08-495-302-54

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Affymax Technologies, N.V.

STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,410

FILING DATE: 07 JUN 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 16,691

REFERENCE/DOCKET NUMBER: 1068-1A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-414-312-53

Query Match 34.8% Score 39; DB 1; Length 19;  
 Best Local Similarity 44.4%; Pred. No. 39;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 2 LSCGQVNVLCGSSG 19

DB 1 LSCGQVNVLCGSSG 18

RESULT 7

US-08-495-302-54

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Affymax Technologies, N.V.

STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,410

FILING DATE: 07 JUN 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 16,691

REFERENCE/DOCKET NUMBER: 1068-1A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-414-312-53

Query Match 34.8% Score 39; DB 1; Length 19;  
 Best Local Similarity 44.4%; Pred. No. 39;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 2 LSCGQVNVLCGSSG 19

DB 1 LSCGQVNVLCGSSG 18

RESULT 7

US-08-495-302-54

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

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STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,410

FILING DATE: 07 JUN 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 16,691

REFERENCE/DOCKET NUMBER: 1068-1A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-414-312-53

Query Match 34.8% Score 39; DB 1; Length 19;  
 Best Local Similarity 44.4%; Pred. No. 39;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 2 LSCGQVNVLCGSSG 19

DB 1 LSCGQVNVLCGSSG 18

RESULT 7

US-08-495-302-54

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Affymax Technologies, N.V.

STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,410

FILING DATE: 07 JUN 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 16,691

REFERENCE/DOCKET NUMBER: 1068-1A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-414-312-53

Query Match 34.8% Score 39; DB 1; Length 19;  
 Best Local Similarity 44.4%; Pred. No. 39;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 2 LSCGQVNVLCGSSG 19

DB 1 LSCGQVNVLCGSSG 18

RESULT 7

US-08-495-302-54

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Affymax Technologies, N.V.

STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,410

FILING DATE: 07 JUN 1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 16,691

REFERENCE/DOCKET NUMBER: 1068-1A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-414-312-53

Query Match 34.8% Score 39; DB 1; Length 19;  
 Best Local Similarity 44.4%; Pred. No. 39;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 2 LSCGQVNVLCGSSG 19

DB 1 LSCGQVNVLCGSSG 18

RESULT 7

US-08-495-302-54

Sequence 53, Application US/08478410

Patent No. 5654276

GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.

APPLICANT: England, Bruce

APPLICANT: Schatz, Peter

APPLICANT: Sloan, Derek

APPLICANT: Chen, Min-Jia

TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Affymax Technologies, N.V.

STREET: 400 Miranda Ave.

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stevens, Lauren L.  
 REGISTRATION NUMBER: 16,691  
 REFERENCE/DOCKET NUMBER: 1088 JA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-496-2300  
 TELEFAX: 415 424-0912  
 INFORMATION FOR SEQ ID NO: 58:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08 475 169-58

Query Match: 34.8% Score: 97 DB 1: EMBL 20,  
 Best Local Similarity: 44.4% Pred No: 39,  
 Matches: 8; Conservative: 3; Mismatches: 7; Indels: 0; Gaps: 0;

QY 2 LEDGQWVHVLGGSSGS 19  
 DB 1 LEDGQWVHVLGGSSGS 18

RESULT 9  
 US-09 548 081-58  
 Sequence 58: Application: US/294840A  
 Patent No.: 5683983  
 GENERAL INFORMATION:  
 APPLICANT: Barrett, Ronald W.  
 APPLICANT: England, Bruce  
 APPLICANT: Schatz, Peter  
 APPLICANT: Sloan, Derek  
 APPLICANT: Ched, Min Cui  
 TITLE OF INVENTION: Peptides and methods for binding the IL-5  
 NUMBER OF SEQUENCES: 65  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Affymax Technologies, Inc.  
 STREET: 4001 Miranda Ave.  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version 1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/444,444  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stevens, Lauren L.  
 REGISTRATION NUMBER: 16,691  
 REFERENCE/DOCKET NUMBER: 1088 JA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-496-2300  
 TELEFAX: 415 424-0912  
 INFORMATION FOR SEQ ID NO: 58:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-474 081-58

Query Match: 44.8% Score: 97 DB 1: EMBL 20,  
 Best Local Similarity: 44.4% Pred No: 39,  
 Matches: 8; Conservative: 3; Mismatches: 7; Indels: 0; Gaps: 0;

Best Local Similarity: 44.4% Pred No: 39,  
 Matches: 8; Conservative: 3; Mismatches: 7; Indels: 0; Gaps: 0;  
 QY 2 LEDGQWVHVLGGSSGS 19  
 DB 1 LEDGQWVHVLGGSSGS 18

RESULT 10  
 US-09 548 540-91  
 Sequence 91: Application: US/208448A40  
 Patent No.: 5733711  
 GENERAL INFORMATION:  
 APPLICANT: Schatz, Peter C.  
 APPLICANT: Cull, William G.  
 APPLICANT: Miller, Jeff P.  
 APPLICANT: Steiner, Willet P.C.  
 APPLICANT: Gates, Christian M.  
 TITLE OF INVENTION: Peptide Library and Screening Method  
 NUMBER OF SEQUENCES: 162  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: William M. Smith  
 STREET: One Market Plaza, Stewart Tower, Suite 2000  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94105  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/548,540  
 FILING DATE: 26-OCT-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/290,841  
 FILING DATE: 15-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/953,421  
 FILING DATE: 15-OCT-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Smith, William M.  
 REGISTRATION NUMBER: 30,423  
 REFERENCE/DOCKET NUMBER: 165287-001240US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415 424-2400  
 TELEFAX: 415 424-2420  
 INFORMATION FOR SEQ ID NO: 91:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-548-540-91

Query Match: 44.8% Score: 19; DB 1: Length 20;  
 Best Local Similarity: 44.4% Pred No: 39;  
 Matches: 8; Conservative: 3; Mismatches: 7; Indels: 0; Gaps: 0;

QY 2 LEDGQWVHVLGGSSGS 19  
 DB 1 LEDGQWVHVLGGSSGS 18

RESULT 11  
 PC-US96-09609-91  
 Sequence 91: Application: PC/T03-009H10  
 GENERAL INFORMATION:  
 APPLICANT: Schatz, Peter C.  
 APPLICANT: Cull, William G.  
 APPLICANT: Gates, Christian M.  
 APPLICANT: Miller, Jeff P.  
 APPLICANT: Steiner, Willet P.C.

APPLICANT: Stemmer, Willem P.C.  
APPLICANT: Gates, Christian M.  
TITLE OF INVENTION: Peptide Library and Screening Method  
NUMBER OF SEQUENCES: 162  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Street Tower, Suite 100  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PC/US96/09469  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/544,543  
FILING DATE: 26-OCT-1995  
APPLICATION NUMBER: US 08/230,641  
FILING DATE: 15-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/963,131  
FILING DATE: 15-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 32,223  
REFERENCE/DOCKET NUMBER: 1652A PC1240US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2422  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 91:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96 09469-91

Query Match 34.8%; Score 18; DB 5; Length 20;  
Best Local Similarity 44.4%; Pred. No. 19;  
Matches 8; Conservative 3; Mismatches 1; Gaps 0

QY 2 LKGGCVTVLGGSSGG 19  
DB 1 LKGGCVTVLGGSSGG 19

RESULT 12  
US-09-914-088-15  
Sequence 84, Application US/9502620A  
Patent No. 6294344  
GENERAL INFORMATION:  
APPLICANT: O'Brien, Timothy J.  
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of  
FILE REFERENCE: 06223CIP-C  
CURRENT FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US/09/521,670A  
PRIOR FILING DATE: 03-14-1998  
NUMBER OF SEQ ID NOS: 136  
SEQ ID NO 84  
LENGTH: 9  
TYPE: PPT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Residues 201-210 of the above protein  
US 09-502 620-84

Query Match 33.9%; Score 18; DB 3; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2,5e+05;  
Matches 6; Conservative 0; Mismatches 2; Indels 0

QY 13 CGGSSGGP 10  
DB 4 CGGSSGGP 10

RESULT 13  
US-08-472-228A 19  
Sequence 19, Application US/041222EA  
Patent No. 5807978  
GENERAL INFORMATION:  
APPLICANT: Kokolus, William J.  
APPLICANT: Fritzsche, Herbert A.  
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES OF PROSTATE  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,228A  
FILING DATE: 27-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 17,642  
REFERENCE/DOCKET NUMBER: UTSC-188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 419-1000  
TELEFAX: (512) 474 7577  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
SWANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-472-228A 19

Query Match 33.9%; Score 18; DB 1; Length 20;  
Best Local Similarity 75.0%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 13 CGGSSGGP 20  
DB 4 CGGSSGGP 11

RESULT 14  
US-09-146-83-19  
Sequence 19, Application US/0914683;  
Patent No. 6326411  
GENERAL INFORMATION:  
APPLICANT: Kokolus, William J.  
APPLICANT: Fritzsche, Herbert A.  
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES OF PROSTATE  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/146,831A  
FILING DATE: 27-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 17,642  
REFERENCE/DOCKET NUMBER: UTSC-188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 419-1000  
TELEFAX: (512) 474 7577  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
SWANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-146-83-19

1 NUMBER OF SEQUENCES: 22  
 2 CORRESPONDENCE ADDRESS:  
 3 ADDRESSEE: Arnold, White & Durkin  
 4 STREET: P.O. Box 4433  
 5 CITY: Houston  
 6 STATE: Texas  
 7 COUNTRY: United States of America  
 8 ZIP: 77210  
 9 COMPUTER READABLE FORM:  
 10 MEDIUM TYPE: Floppy disk  
 11 COMPUTER: IBM PC compatible  
 12 OPERATING SYSTEM: PC DOS/MS-DOS  
 13 SOFTWARE: Patent In Release #11, Version #1.0  
 14 CURRENT APPLICATION DATA  
 15 APPLICATION NUMBER: US/09/14-088-15  
 16 FILING DATE:  
 17 CLASSIFICATION:  
 18 PRIORITY APPLICATION DATA:  
 19 APPLICATION NUMBER: US 08/472,116  
 20 FILING DATE: 07-JUN-1995  
 21 ATTORNEY/AGENT INFORMATION:  
 22 NAME: Highlander, Steven L.  
 23 REGISTRATION NUMBER: 37,642  
 24 REFERENCE/DOCKET NUMBER: JUS000000  
 25 TELECOMMUNICATION INFORMATION:  
 26 TELEPHONE: (512) 418-3000  
 27 TELEFAX: (512) 424-7577  
 28 TELEX: 79-9924  
 29 INFORMATION FOR SEQ ID NO: 19:  
 30 SEQUENCE CHARACTERISTICS:  
 31 LENGTH: 20 amino acids  
 32 TYPE: amino acid  
 33 STRANDEDNESS: single  
 34 TOPOLOGY: linear  
 35 MOLECULE TYPE: peptide  
 36 PS 09-146-831 19

Query Match 33.9%; Score 38; DB 5; Length 20;  
 Best Local Similarity 75.0%; Pred. No. 53;  
 Matches 6; Conservative 0; Mismatches 0; Gaps 0.

QY 13 CQSSSGSP 20  
 Db 4 CQSSSGSP 11

## RESULT 15

PCT US96-093741-15  
 1 Sequence 19, Application PCT/US96-093741-15  
 2 GENERAL INFORMATION:  
 3 APPLICANT:  
 4 TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FOR HIV  
 5 TIME OF INVENTION: SPECIFIC ACTION  
 6 NUMBER OF SEQUENCES: 22  
 7 COMPUTER READABLE FORM:  
 8 MEDIUM TYPE: Floppy disk  
 9 COMPUTER: IBM PC compatible  
 10 OPERATING SYSTEM: PC DOS/MS-DOS  
 11 SOFTWARE: Patent In Release #11, Version #1.0  
 12 CURRENT APPLICATION DATA:  
 13 APPLICATION NUMBER: PCT/US96/23963  
 14 FILING DATE:  
 15 CLASSIFICATION:  
 16 PRIORITY APPLICATION DATA:  
 17 APPLICATION NUMBER: US 08/472,116  
 18 FILING DATE: 07-JUN-1995  
 19 INFORMATION FOR SEQ ID NO: 19:  
 20 SEQUENCE CHARACTERISTICS:  
 21 LENGTH: 20 amino acids  
 22 TYPE: amino acid  
 23 STRANDEDNESS:  
 24 TOPOLOGY: linear  
 25 PCT US96-093741-15

Query Match 33.9%; Score 38; DB 5; Length 20;  
 Best Local Similarity 75.0%; Pred. No. 53;  
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

QY 13 CQSSSGSP 20  
 Db 4 CQSSSGSP 11

Search Completed: November 5, 2003, 16:22:24  
 Job time : 22 secs

GenCore Version 3.1.1  
Copyright (c) 1995-1998 Copyright LLC

CM protein - protein search, using sw method

Run on: November 5, 2003, 14:10:50 / Round time: 21 seconds

Title: US-09-914-088-16

Perfect score: 116

Sequence: 1 CLEDCQWQVDP:PREAAEQK 11

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 25308 seqs, 9616692 residues

Total number of hits satisfying chosen parameters: 458

Minimum DB seq length: 2

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 261\*

1: p111\*

2: p112\*

3: p113\*

4: p114\*

Pred. No. is the number of results predicted by choice to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	26	26.0	20	S105.0	Calpain heavy chain 2 - pig (fragment)
2	24	24.0	13	A146*	Calpain heavy chain 2 - pig (fragment)
3	23	23.0	20	B412*	Calpain heavy chain 2 - pig (fragment)
4	22	22.0	16	S105.0	Calpain heavy chain 2 - pig (fragment)
5	21	21.0	20	B412*	Calpain heavy chain 2 - pig (fragment)
6	20	20.0	15	P802.1	Calpain heavy chain 2 - pig (fragment)
7	19	19.0	20	P802.1	Calpain heavy chain 2 - pig (fragment)
8	18	18.0	20	S4894*	Calpain heavy chain 2 - pig (fragment)
9	17	17.0	12	S3684*	Calpain heavy chain 2 - pig (fragment)
10	16	16.0	14	P4072*	Calpain heavy chain 2 - pig (fragment)
11	15	15.0	15	A4917*	Calpain heavy chain 2 - pig (fragment)
12	14	14.0	17	S0567*	Calpain heavy chain 2 - pig (fragment)
13	13	13.0	19	B6112*	Calpain heavy chain 2 - pig (fragment)
14	12	12.0	20	S3684*	Calpain heavy chain 2 - pig (fragment)
15	11	11.0	21	S4727*	Calpain heavy chain 2 - pig (fragment)
16	10	10.0	11	S5624*	Calpain heavy chain 2 - pig (fragment)
17	9	9.0	15	PQ074*	Calpain heavy chain 2 - pig (fragment)
18	8	8.0	16	A4864*	Calpain heavy chain 2 - pig (fragment)
19	7	7.0	17	I5184*	Calpain heavy chain 2 - pig (fragment)
20	6	6.0	7	B3481*	Calpain heavy chain 2 - pig (fragment)
21	5	5.0	9	B2346*	Calpain heavy chain 2 - pig (fragment)
22	4	4.0	9	A2947*	Calpain heavy chain 2 - pig (fragment)
23	3	3.0	9	S0637*	Calpain heavy chain 2 - pig (fragment)
24	2	2.0	9	B6112*	Calpain heavy chain 2 - pig (fragment)
25	1	1.0	10	A6112*	Calpain heavy chain 2 - pig (fragment)
26	0	0.0	12	A2695*	Calpain heavy chain 2 - pig (fragment)
27	0	0.0	12	A3347*	Calpain heavy chain 2 - pig (fragment)
28	0	0.0	13	B2895*	Calpain heavy chain 2 - pig (fragment)
29	0	0.0	14	P0011*	Calpain heavy chain 2 - pig (fragment)

30	22	19.0	15	2	PH1631	Ig H chain V-D-J r
31	22	19.0	16	2	B484C6	annexin V: homolog
32	22	19.0	16	2	PH1589	Ig H chain V-D-J r
33	22	19.0	19	2	A49125	valine:RNA ligase
34	22	19.0	20	2	A46451	e antigen p17 pre
35	22	19.0	20	2	S28434	major outer membra
36	22	19.0	21	2	PK0078	alanine dehydrogen
37	22	19.0	21	2	140659	hypothetical: prote
38	22	19.0	21	2	143657	hypothetical: prote
39	21.5	18.5	20	2	155861	MHC H1A-DR gamma c
40	21	18.1	6	2	PT0511	T-cell receptor: be
41	21	18.1	8	2	A28719	thymic humoral fac
42	21	18.1	8	2	PT0553	T-cell receptor be
43	21	18.1	9	2	C60070	gastrin: domestic
44	21	18.1	10	2	G58501	48K bile/gallblad
45	21	18.1	11	2	A14135	DNA-binding protei

ALIGNMENTS

RESULT 1

S32502

Calpain (EC 3.4.22.17; large chain 2 - pig (fragment)

N:Alternate names: m-calpain heavy chain

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 02 Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 17-Mar-1999

C:Accession: S32502

R:Brown, N.; Crawford, C.

FEBS Lett. 322, 65-69, 1993

ArtTitle: Structural modifications associated with the change in Cal(2+)-sensitivity on ac

A:Reference number: S32502; XREF:93245962; PMID:8482370

A:Accession: S32502

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <BRC>

C:Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic domain

C:Keywords: calcium binding; cysteine proteinase; EF hand; hydrolase

Query Match 25.0% Score 29; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 REAAEQ 19

DB 3 REAAEQ 19

RESULT 2

A33660

Structural functional antigen alpha chain - green monkey (fragment)

C:Species: Cercopithecus aethiops (green monkey, grivet)

C>Date: 30-Mar-1990 #sequence\_revision 30-Mar-1990 #text\_change 23-Mar-1995

C:Accession: A33660

R:Cavies, J.; Warwick, J.; Derty, M.; Philp, R.; Helfrich, M.; Horton, M.

J. Cell Biol. 103, 1917-1926, 1993

ArtTitle: The structural functional antigen, implicated in the regulation of bone resorpt

A:Reference number: A33660; M010:30009054; PMID:2477382

A:Accession: A33660

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <DAV>

A:Experimental source: a green monkey kidney Vero cell line

Query Match 54.5% Score 28; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 MDCVPS 13

DB 13 MDCVPS 13

```

RESULT 7
P41299
Title: receptor alpha chain precursor V region (14-19) human (fragment)
Species: Homo sapiens (man)
CDate: 25-May-1992 #sequence_revision 11-May-1992 #text_change 24-Jul-1999
CAccession: B41299
R(Jomatsu, Y., Wede, H., Strass, A., Gell, M., Bankowitz, W., Bankowitz, J., Panay, G.,
Proc. Natl. Acad. Sci. U.S.A. 89, 8534-8538, 1992)
Article: The T-cell receptor repertoire in the syngeneic (B6.D) patient with rheumatoid
Arthritis number: A41299; NCBI:9201240; PMID:165444
AAccession: B41299
AStatus: preliminary
A.Molecule type: tRNA
A.Residues: 1-15 (15)
A.Cross references: G848746; NID-94-0000; EUR ADAPTS; in situ; 1992
C(Superfamily: immunoglobulin V region framework homology
C.Keywords: T-cell, receptor
Query Match 22.4% Score 25; DB 2; Length 15;
Best Local Similarity 45.5% Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;
CY 1: GAGAGAGAGAG 11
DB 1: GAGAGAGAGAG 11
RESULT 8
P41299
Title: protein VPI human poliovirus 1 (fragment)
Species: human poliovirus 1
CDate: 21-Dec-1979 #sequence_revision 11-Dec-1979 #text_change 18-Jun-1997
CAccession: S02473
R(Jomatsu, A., Wybrowski, C., O'Grady, J., Berman, R., Berman, R., Berman, R.,
EMBO J. 7, 2949-2957, 1988)
Article: Engineering a poliovirus type 1 polypeptide site 5-4 type 1 (epitope results in a
AAccession: S02473
AReference number: S02473; NCBI:900140; PMID:246443
A.Molecule type: tRNA
A.Residues: 1-15 (15)
A.Cross references: 1-15 (15)
C(Superfamily: 1-15 (15)
C.Keywords: 1-15 (15)
Query Match 22.4% Score 25; DB 2; Length 15;
Best Local Similarity 45.5% Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;
CY 1: GAGAGAGAGAG 11
DB 1: GAGAGAGAGAG 11
RESULT 9
P41299
Title: protein VPI human poliovirus 1 (fragment)
Species: human poliovirus 1
CDate: 21-Dec-1979 #sequence_revision 11-Dec-1979 #text_change 18-Jun-1997
CAccession: S02473
R(Jomatsu, A., Wybrowski, C., O'Grady, J., Berman, R., Berman, R., Berman, R.,
EMBO J. 7, 2949-2957, 1988)
Article: Engineering a poliovirus type 1 polypeptide site 5-4 type 1 (epitope results in a
AAccession: S02473
AReference number: S02473; NCBI:900140; PMID:246443
A.Molecule type: tRNA
A.Residues: 1-15 (15)
A.Cross references: 1-15 (15)
C(Superfamily: 1-15 (15)
C.Keywords: 1-15 (15)
Query Match 22.4% Score 25; DB 2; Length 15;
Best Local Similarity 45.5% Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;
CY 1: GAGAGAGAGAG 11
DB 1: GAGAGAGAGAG 11

```

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RESULT 6
P0251
Title: protein 10K rice (strain Nihonbare) (fragment)
Species: Oryza sativa (rice)
CDate: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
CAccession: P0251
R(Tsujita, A., Kimo, Y.,
Submitted to JIFID, April 1995
AReference number: P0251
AAccession: P0251
A.Molecule type: protein
A.Residues: 1-15 (15)
A.Experimental source: germ, strain Nihonbare
C(Comment: molecular weight: 15K, pI 9.2)
Query Match 21.6% Score 25; DB 2; Length 15;
Best Local Similarity 43.3% Pred. No. 2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 1: PCPRA 16
DB 1: PCPRA 16
RESULT 7
A27119
Title: precursor marbled lungfish (fragment)
Species: protopetrus aethiopicus (marbled lungfish)
CDate: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Nov-1996
CAccession: A27119
R(Herndson, M.A., Tyne, S.W., Reock, G.S., Neirath, H., Walsh, K.A.,
EMBO J. 14, 222-224, 1997)
Article: Comparison of the amino terminal sequences of bovine, dogfish, and lungfish trypsin
AReference number: A27119
AAccession: A27119
A.Molecule type: protein
A.Residues: 1-21 (21)
C(Superfamily: trypsin; trypsin homology
C.Keywords: hydrolase; protein digestion; serine proteinase
Query Match 21.6% Score 25; DB 2; Length 21;
Best Local Similarity 41.7% Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
CY 1: PCPRA 16
DB 1: PCPRA 16
RESULT 8
S48746
Title: beta tubulin b-beta-2 mouse
Species: Mus musculus (house mouse)
CDate: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
CAccession: S48746
R(Mary, J., Pedersen, V., le Caer, J.P., Prome, J.C., Rossier, J.,
FEBS Lett. 353, 39-44, 1994)
Article: Class I and IV beta tubulin isotypes expressed in adult mouse brain are glutamyl
AReference number: S48746; NCBI:9561072; PMID:792630
AAccession: S48746
AStatus: preliminary
A.Molecule type: protein
A.Residues: 1-20 (20)
Query Match 21.6% Score 24.5; DB 2; Length 20;
Best Local Similarity 46.8% Pred. No. 3.2e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
CY 1: PCPRA 16
DB 1: PCPRA 16

```

RESULT 3  
 QY 13 PREAAGCK 21  
 | | |  
 DB 7 EKKAARAK 15  
 Mismatches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 RESULT 12  
 S05671  
 hirudin 1a "medicinal leech (fragment)"  
 N:Alternate names: thrombin inhibitor  
 C:Species: Hirudo medicinalis (medicinal leech)  
 C>Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 17-Jul-1998  
 C:Accession: S05671  
 R:Scharf, M.; Engels, G.; Tripiet, D.  
 FEBS Lett. 255, 105-110, 1989  
 A:Title: Primary structures of new 'iso-hirudins'.  
 A:Reference number: S05671; PMID:9005945; PMID:2792365  
 A:Accession: S05671  
 A:Molecule type: protein  
 A:Residues: 1-17 <SCH>  
 C:Superfamily: thrombin inhibitor  
 C:Keywords: anticoagulant; serine proteinase inhibitor; sulfoproteinase  
 F:6-14/Disulfide bonds: #status predicted  
 Query Match 20.7%; Score 24; DB 2; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 3.2e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CLEGGQ 6  
 | | |  
 DB 6 CTESQ 12  
 Mismatches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 RESULT 13  
 B6110  
 66K collagen-binding protein, light form - chicken (fragments)  
 C:Species: Gallus gallus (chicken)  
 C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-Oct-1994  
 C:Accession: B6110  
 R:Tidball, J. G.  
 J. Biol. Chem. 267, 21411-21419, 1992  
 A:Title: Identification and distribution of a novel collagen-binding protein in the de  
 A:Reference number: A6110; PMID:93016046; PMID:1328225  
 A:Accession: B6110  
 A:Molecule type: protein  
 A:Residues: 1-19 <TIT>  
 C:Keywords: collagen binding  
 Query Match 20.7%; Score 24; DB 2; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CLEGGQ 6  
 | | |  
 DB 1 CLEGG 9  
 Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 14  
 S36842  
 acylaminacyl-peptidase (EC 3.4.19.1) (validated) - bovine (fragment)  
 N:Alternate names: acyl-peptide hydrolase  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 10-Dec-1993 #sequence\_revision 21-Jul-2000 #text\_change 21-Jul-2000  
 C:Accession: S36842  
 R:Sharma, P. K.; Ortiweith, B. J.  
 Eur. J. Biochem. 216, 631-637, 1993  
 A:Title: Bovine lens acyl-peptide hydrolase. Purification and characterization of a tetr  
 A:Reference number: S36842; PMID:9395716; PMID:8375399  
 A:Accession: S36842  
 A:Molecule type: protein  
 A:Residues: 1-24 <SHA>  
 A:Explosion: 1, 24 <SHA>  
 A:Explosion: 1, 24 <SHA>

RESULT 5  
 QY 13 PREAAGCK 21  
 | | |  
 DB 7 EKKAARAK 15  
 Mismatches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 RESULT 12  
 S05671  
 hirudin 1a "medicinal leech (fragment)"  
 N:Alternate names: thrombin inhibitor  
 C:Species: Hirudo medicinalis (medicinal leech)  
 C>Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 17-Jul-1998  
 C:Accession: S05671  
 R:Scharf, M.; Engels, G.; Tripiet, D.  
 FEBS Lett. 255, 105-110, 1989  
 A:Title: Primary structures of new 'iso-hirudins'.  
 A:Reference number: S05671; PMID:9005945; PMID:2792365  
 A:Accession: S05671  
 A:Molecule type: protein  
 A:Residues: 1-17 <SCH>  
 C:Superfamily: thrombin inhibitor  
 C:Keywords: anticoagulant; serine proteinase inhibitor; sulfoproteinase  
 F:6-14/Disulfide bonds: #status predicted  
 Query Match 20.7%; Score 24; DB 2; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 3.2e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CLEGGQ 6  
 | | |  
 DB 6 CTESQ 12  
 Mismatches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 RESULT 13  
 B6110  
 66K collagen-binding protein, light form - chicken (fragments)  
 C:Species: Gallus gallus (chicken)  
 C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-Oct-1994  
 C:Accession: B6110  
 R:Tidball, J. G.  
 J. Biol. Chem. 267, 21411-21419, 1992  
 A:Title: Identification and distribution of a novel collagen-binding protein in the de  
 A:Reference number: A6110; PMID:93016046; PMID:1328225  
 A:Accession: B6110  
 A:Molecule type: protein  
 A:Residues: 1-19 <TIT>  
 C:Keywords: collagen binding  
 Query Match 20.7%; Score 24; DB 2; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CLEGGQ 6  
 | | |  
 DB 1 CLEGG 9  
 Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 14  
 S36842  
 acylaminacyl-peptidase (EC 3.4.19.1) (validated) - bovine (fragment)  
 N:Alternate names: acyl-peptide hydrolase  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 10-Dec-1993 #sequence\_revision 21-Jul-2000 #text\_change 21-Jul-2000  
 C:Accession: S36842  
 R:Sharma, P. K.; Ortiweith, B. J.  
 Eur. J. Biochem. 216, 631-637, 1993  
 A:Title: Bovine lens acyl-peptide hydrolase. Purification and characterization of a tetr  
 A:Reference number: S36842; PMID:9395716; PMID:8375399  
 A:Accession: S36842  
 A:Molecule type: protein  
 A:Residues: 1-24 <SHA>  
 A:Explosion: 1, 24 <SHA>  
 A:Explosion: 1, 24 <SHA>

Q:Function:  
 A:Description: EC 3.4.19.1 [validated, MID:9388716]  
 S:Superfamily: acylaminacyl-peptidase  
 C:Keywords: hydrolase; omega peptidase

Query Match: 20.7% Score 24, DB 21, Length 21,  
 Best Local Similarity 44.4% Pred. No. 3,96+0%  
 Matches 4, Conservative 3, Mismatches 2, Indels 0, Gaps 0

CY 13 PRDAEGCK 21  
 II : II  
 DB 2 PCALKCC 10

## RESULT 15

S47207

T:Cell receptor C-alpha wvlll: Human (fragment)

C:Species: Homo Sapiens (man)

P:Date: 06 Feb 1995 #sequence\_revision 06 Feb 1995 #text\_revision 05-Nov-1999

C:Accession: S47207

R:Plaza, A.; Kono, J.H.; Theofilopoulos, A.N.

Submitted to the EMBL Data Library, February 1993

A:Reference number: S47207

A:Accession: S47207

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-21 &lt;PIA&gt;

A:Cross references: EMBL:U71032, NID:955610, GEN:CA55749.1, FID:9510318

C:Keywords: T-cell receptor

Query Match: 20.7% Score 24, DB 21, Length 21,  
 Best Local Similarity 57.1% Pred. No. 3,96+0%  
 Matches 4, Conservative 1, Mismatches 2, Indels 0, Gaps 0

CY 9 VMVDCP 13  
 I : I  
 DB 12 VPERCP 18

Search completed: November 5, 2003, 14:27 hr  
 Run time: 0.21 secs



GenCore version 3.1.1.6  
Copyright (c) 1993-2003 Comogen Inc.

CM protein protein search, using sw model

Run on: November 5, 2003, 18:22:27 Search time: 11.86 mins  
Database alignment: 100%  
49,708 Multiple Cell alignments/sec

Title: US-09-914-088-16

Perfect score: 116

Sequence: 1 CLEGGVMDVCPREAESEK .1

Scoring table: BLOSUM62

Gapop: 10.0, Gapext: 0.5

Searched: 129861 seqs, 4702675 residues

Total number of hits satisfying chosen parameters: 1,76

Minimum DB seq length: 6

Maximum DB seq length: 21

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by database to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID
1	25	21.6	21	TRYP_PPROAT
2	24	20.7	17	ITHB_HIRME
3	24	20.7	20	ACPH_PROVIN
4	24	20.7	21	ATPH_HYDPA
5	23	19.8	11	PQOC_PSEPT
6	23	19.8	14	RS14_TLBP
7	23	19.6	14	PS14_PSEPT
8	23	19.6	14	MYET_VALER
9	22	19.7	9	CCSH_VALER
10	22	19.7	9	CCSH_VALER
11	22	19.0	9	DNFI_PSEPT
12	22	19.0	9	OXVT_CVPEA
13	22	19.0	12	RS14_PSEPT
14	22	19.0	16	FIBA_CER31
15	21	18.1	11	RRED_CHAV
16	21	18.1	15	CXJA_CGNCU
17	21	18.1	21	GYRA_STRSH
18	20	17.2	10	GACU_HIVAN
19	20	17.2	19	FIBA_HISEC
20	20	17.2	19	PHSL_PSEPT
21	20	17.2	20	SC19_PESMA
22	20	17.2	21	VR9C_PSEPT
23	20	17.2	21	GRX_BUNIN
24	20	17.2	21	OMP4_PASHA
25	20	17.2	21	REV_HAZDZ
26	19.5	16.8	19	HMD_METWG
27	19	16.4	9	COMC_CERGE
28	19	16.4	14	SCK3_PSEPT
29	19	16.4	16	FIBA_MAFVA
30	19	16.4	16	KTRC_APEVA
31	19	16.4	17	TRP2_PSEPT
32	19	16.4	20	TSJ4_PSEPT
33	19	16.4	21	OMF1_ACTED

34	13	16.4	21	SP13_SQUTU
35	16.5	15.9	20	RL10_PPROVU
36	16.5	15.9	21	PER_PPROVU
37	13	15.5	9	OXVT_PAJCL
38	13	15.5	12	PPK4_PSEPT
39	13	15.5	12	PPK4_PSEPT
40	13	15.5	12	V23K_WSSV
41	13	15.5	13	FIBA_CAVPO
42	13	15.5	13	LPAA_PCRGI
43	13	15.5	14	GR75_CANFA
44	13	15.5	15	KLOM_LUNTE
45	13	15.5	15	RKGG_CARCR

## ALIGNMENTS

RESULT 1  
TRYP\_PPROAT STANDARD: PRT: 21 AA.  
AC P35051:  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Trypsin precursor (EC 3.4.21.4) (Fragment)  
CS Proteolysis: aethiopian (Mabbed lungfish)  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Dipnoi; Lepidosireniiformes; Protoperidae; Protoperus.  
OX NCBI\_TaxID=7886;  
RN 11;  
RP SEQUENCE.  
RC 1-SSUE-Paraceras;  
RA Herndonson M.A., Tyb P.W., Reock G.R., Neuzath H., Walsh K.A.;  
RT Comparison of the amino terminal sequences of bovine, dogfish, and  
RT lungfish trypsins.  
RL J. Biol. Chem. 264:4222-4224 (1991).  
CC 1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.  
CC 1- SUBCELLULAR LOCATION: Extracellular.  
CC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR PIR: A27719; A27719.  
DR MEROPS: S01.151;  
DR InterPro: IPR001254; Ser protease Try.  
DR PROSITE: PS0240; TRYPSIN\_DOM; PARTIAL.  
DR PROSITE: PS0194; TRYPSIN\_HIS; PARTIAL.  
DR PROSITE: PS0195; TRYPSIN\_SER; PARTIAL.  
KW Hydrolase; Serine protease; Zymogen.  
FT PROSERP 1 7 ACTIVATION PEPTIDE.  
FT CHAIN 8 21 TRYPSIN.  
FT NAME 8 21 TRYPSIN.  
SQ SEQUENCE 11 AA; 444 MW; 882F31D1D3C729F CRC64;

Query Match: 21.6% Score 25; DB 1; Length 21;  
Best Local Similarity: 41.7%; Pred. No. 1-2e+03;  
Matches: 5; Conservative: 2; Mismatches: 5; Indels: 0; Gaps: 0;  
Qy 3 EDGCVMDVCPRE 14  
Db 5 EDKIVGSGVCPRE 16

RESULT 2  
ITHB\_HIRME STANDARD: PRT: 17 AA.  
ID ITHB\_HIRME  
AC P28502:  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DE Hirudin 1A (Fragment)  
OS Hirudo medicinalis (Medicinal leech)  
CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
CC Ancyrodermatida; Hirudiniformes; Hirudinidae; Hirudo.  
OX NCBI\_TaxID=421.  
RN 11;

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RP SEQUENCE
EX MEDLINE:26005945; PubMed:272365;
RA Schell M, Engels J, Tripler D;
PL "Primary structures of new 'iso-Endonins'";
PEPS Int. 255:103-110(1989).
CC ! FUNCTION: Hirudin is a potent thrombin specific proteinase
CC inhibitor. It forms a stable non-covalent complex with alpha
CC 1-antitrypsin, thereby abolishing its ability to cleave fibrinogen.
CC !! SUBCELLULAR LOCATION: Secreted.
CC !! SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
CC
CR PIR: S0671; S05671.
CR HSSP: P01050; H1C3.
CR InterPro: IPSC00429; Hirudin.
CR Pfam: PF00713; Hirudin.
CR Serine protease inhibitor; Sulfatase; Multiple family.
KW MNTER 17
KW TER 17
SQ SEQUENCE 17 AA: 1877 NW; 89547.96634.1058 Q8064;
Query Match 20.78; Score 24; DB 1; Length 17;
Best Local Similarity 66.78; Pred. No. 1.70+03;
Matches 4; Conservative 0; Mismatches 3; Gaps 0;
QY 1 Q8064 6
DB 6 Q8064 11
RESULT 4
ID ATFB_PHYPA STANDARD; PRT; 21 AA.
AC P80658;
DT 21-OCT-1996 (Rel. 44, Created);
DT 21-OCT-1996 (Rel. 44, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE ATP synthase beta chain (EC 3.6.3.14) (Fragment).
GN ATFB.
OS Physcomitrella patens (Moss).
CC Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Bryophyta;
CC Bryopsida; Funariaceae; Funariaceae; Physcomitrella.
OX NCBI_TaxID:3218;
RN 1;
RP SEQUENCE.
RC TISSUE:Protonema; PubMed:9123336;
RX Kester H, Buck F, Nuske G, Reski R;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes";
RC Planta 201:261-272(1997).
CC ! FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
CC SUBUNIT.
CC ! CATALYTIC ACTIVITY: ATP + H2O -> H(-)(ir) = ADP + phosphate +
CC H(+)(ir).
CC ! SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) THE CATALYTIC
CC CORE AND CF(0) THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(3). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC ! SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC ! SIMILARITY: Belongs to the ATPase alpha/beta chains family.
CC InterPro: IPSC00194; ATPase a/b/epsilon.
DR PROSITE: PS00152; ATPase ALPHA BETA; PARTIAL.
KW ATP synthase; Chloroplast; Thylakoid; Membrane; CF(1);
KW Hydrolyase; ATP-binding; Hydrogen ion transport.
FT NON TER 21
SQ SEQUENCE 21 AA: 2298 MW; 955854F5AC89D81A CRC64;
Query Match 20.78; Score 24; DB 1; Length 21;
Best Local Similarity 44.48; Pred. No. 1.70+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 5 Q8064VP 13
DB 13 Q8064VP 21
RESULT 5
ID PQQ_PSEFP STANDARD; PRT; 11 AA.
AC P56173;
DT 21-OCT-1996 (Rel. 44, Created);
DT 21-OCT-1996 (Rel. 44, Last sequence update);
DT 21-OCT-1996 (Rel. 44, Last annotation update);
DE Coenzyme PQQ synthesis protein C (Fragment).
GN PQQC.
OS Pseudomonas fluorescens.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID:294;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN CHARI.
RX MEDLINE:9606439; PubMed:8526497;
RA Schindler U, Reski R, Delano G, Haas D;
RT "CDS directed insertion of polypeptides from Pseudomonas fluorescens Pf0-1
RT mutant into the chloroplast of the grass results in overproduction of the
RT antibiotic hygromycin".

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RP SEQUENCE
EX MEDLINE:26005945; PubMed:272365;
RA Schell M, Engels J, Tripler D;
PL "Primary structures of new 'iso-Endonins'";
PEPS Int. 255:103-110(1989).
CC ! FUNCTION: Hirudin is a potent thrombin specific proteinase
CC inhibitor. It forms a stable non-covalent complex with alpha
CC 1-antitrypsin, thereby abolishing its ability to cleave fibrinogen.
CC !! SUBCELLULAR LOCATION: Secreted.
CC !! SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
CC
CR PIR: S0671; S05671.
CR HSSP: P01050; H1C3.
CR InterPro: IPSC00429; Hirudin.
CR Pfam: PF00713; Hirudin.
CR Serine protease inhibitor; Sulfatase; Multiple family.
KW MNTER 17
KW TER 17
SQ SEQUENCE 17 AA: 1877 NW; 89547.96634.1058 Q8064;
Query Match 20.78; Score 24; DB 1; Length 17;
Best Local Similarity 66.78; Pred. No. 1.70+03;
Matches 4; Conservative 0; Mismatches 3; Gaps 0;
QY 1 Q8064 6
DB 6 Q8064 11
RESULT 4
ID ATFB_PHYPA STANDARD; PRT; 21 AA.
AC P80658;
DT 21-OCT-1996 (Rel. 44, Created);
DT 21-OCT-1996 (Rel. 44, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE ATP synthase beta chain (EC 3.6.3.14) (Fragment).
GN ATFB.
OS Physcomitrella patens (Moss).
CC Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Bryophyta;
CC Bryopsida; Funariaceae; Funariaceae; Physcomitrella.
OX NCBI_TaxID:3218;
RN 1;
RP SEQUENCE.
RC TISSUE:Protonema; PubMed:9123336;
RX Kester H, Buck F, Nuske G, Reski R;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes";
RC Planta 201:261-272(1997).
CC ! FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
CC SUBUNIT.
CC ! CATALYTIC ACTIVITY: ATP + H2O -> H(-)(ir) = ADP + phosphate +
CC H(+)(ir).
CC ! SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) THE CATALYTIC
CC CORE AND CF(0) THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(3). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC ! SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC ! SIMILARITY: Belongs to the ATPase alpha/beta chains family.
CC InterPro: IPSC00194; ATPase a/b/epsilon.
DR PROSITE: PS00152; ATPase ALPHA BETA; PARTIAL.
KW ATP synthase; Chloroplast; Thylakoid; Membrane; CF(1);
KW Hydrolyase; ATP-binding; Hydrogen ion transport.
FT NON TER 21
SQ SEQUENCE 21 AA: 2298 MW; 955854F5AC89D81A CRC64;
Query Match 20.78; Score 24; DB 1; Length 21;
Best Local Similarity 44.48; Pred. No. 1.70+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 5 Q8064VP 13
DB 13 Q8064VP 21
RESULT 5
ID PQQ_PSEFP STANDARD; PRT; 11 AA.
AC P56173;
DT 21-OCT-1996 (Rel. 44, Created);
DT 21-OCT-1996 (Rel. 44, Last sequence update);
DT 21-OCT-1996 (Rel. 44, Last annotation update);
DE Coenzyme PQQ synthesis protein C (Fragment).
GN PQQC.
OS Pseudomonas fluorescens.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID:294;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN CHARI.
RX MEDLINE:9606439; PubMed:8526497;
RA Schindler U, Reski R, Delano G, Haas D;
RT "CDS directed insertion of polypeptides from Pseudomonas fluorescens Pf0-1
RT mutant into the chloroplast of the grass results in overproduction of the
RT antibiotic hygromycin".

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CC -1 SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY
DR PIR: A29477, A29477.
DR InterPro: IPR000981; Neurohyp_horm.
DR Pfam: PF00220; hormone4.1.
DR PROSITE: PS00264; NEURGHYPOPHYS_H_4; 1.
KW Hormone; Neuropeptide; Acidic
FT DISULFID 1 6 IN F1
FT DISULFID 1 1 INTER-BRAIN WITH C-TER IN F2
FT DISULFID 3 6 INTER-BRAIN WITH C-TER IN F2
FT NGL RES 9 9 AMIDATION
SQ SEQUENCE 9 AA: 976 MW; 56EB376B845A652 (GenBank)

Query Match 19.0%; Score 20; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1; 25;
Matches 3; Conservative 1; Mismatches 0; Gaps 0;

QY 11 DCRP 14
DB 5 NCRP 9

RESULT 12
QXVT_CYPCA STANDARD; PRT; 9 AA
AC P33875;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Vasocerin.
OS Cyprinus carpio (Common carp), and
CS Petryzon latissus (Sea lamprey).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Ostariichthyes; Cyprinodontes;
CC Cyprinidae; Cyprinus.
OX NCBI TaxID:962, 7157;
PI 11
SQ SEQUENCE
AC SPECIES: Cyprinus; TISSUE: pituitary.
RA Achet R., Chauvet J., Chauvet M., Crepy B.
RT "Characterization of neurohypophyseal hormones from a fresh water bony
PT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water lony fishes".
RL Comp. Biochem. Physiol. 14:245-247 (1981).
RV 121
RP SEQUENCE.
PC SPECIES: Petryzon; TISSUE: pituitary.
EX WHILME: 98256942; PubMed: 1371646.
RA Jane T.P., Sweet S.A., Kawachi H.
RT "Arginine vasotocin from the pituitary gland of the lamprey
PT (Petryzon latissus): isolation and characterization of the
PL Gen. Comp. Endocrinol. 70:152-157 (1981).
CC -1 SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
QY PIR: B01364; B61364.
DR PIR: S63375; S66775.
DR InterPro: IPR000981; Neurohyp_horm.
DR Pfam: PF00220; hormone4.1.
DR PROSITE: PS00264; NEURGHYPOPHYS_H_4; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT NGL RES 9 9 AMIDATION
SQ SEQUENCE 9 AA: 1053 MW; 17E17FE466234P (GenBank).

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Query Match 19.0%; Score 20; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1; 25;
Matches 3; Conservative 1; Mismatches 0; Gaps 0;

QY 11 DCRP 14
DB 5 NCRP 9

RESULT 13

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RS19_ELYEP STANDARD; PRT; 12 AA.
ID RS19_ELYEP
AC Q47881;
DT 30-MAY-2000 (Rel. 13, Created)
DT 30-MAY-2000 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (fragment).
GN RPS19 OR RPS19.
OS Elr yeilows phycotasma.
CC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
CC Acholeplasmataceae; Phycoplasma.
OX NCBI TaxID:35774.
PI 11
SQ SEQUENCE FROM N.A.
RX MEDLINE:94352802; PubMed:8071198;
RA Gundersen D.E., Lee T.M., Pether S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmal): a basis for
RT their classification".
RL J. Bacteriol. 176:5244-5254 (1994).
CC -1 FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S11 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL, curators of
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/annouce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L27022; AAA91942.1;
DR HAMAP: MP_005311;
DR InterPro: IPR002422; Ribosomal_S19.
DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 12 AA: 1283 MW; 2CC47B9D58333AA8 CPC64;

Query Match 19.0%; Score 22; DB 1; Length 12;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Gaps 0;

QY 12 ABSOK 21
DB 3 ARGLX 7

RESULT 14
FIBA_CERS:
ID FIBA_CERSI STANDARD; PRT; 16 AA.
AC P14535;
DT 01-JAN-1993 (Rel. 13, Created)
DT 01-JAN-1993 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Ceratotherium simum (White rhinoceros) [Square-lipped rhinoceros].
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX NCBI TaxID:9927;
PI 11
SQ SEQUENCE.
RA O'Neill P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Syst. Zool. 22:590-595 (1973).
CC -1 FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLASMET
CC AGGREGATION.
CC -1 SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1 VISCELLAR CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA 5 BETA

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CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT AGG.

KW BLOOD COAGULATION, Plasma.  
 FT PEPTIDE 12 16 FIBRINOGENPTIDE A.

FT NON-TER 16 16  
 SQ SEQUENCE 16 AA: 1639 MW: 29587362924201 197741

Query Match 19 (1) Score 20.00 E-value 0.0  
 Best Local Similarity 66.0%, Pident No. 2 E-value  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 RAAED 20  
 DB 2 ETESD 7

## RESULT 15

RRC\_CHAV

1D RRC\_CHAV STANDARD; PRI. 11 AA.

AC P13179;

DT 01 JAN 1990 (Rel. 13, Created)

DT 01 JAN 1990 (Rel. 13, Last sequence update)

DT 28 FEB 2003 (Rel. 41, Last annotation update)

DE RNA polymerase beta subunit (EC 2.7.7.48) [a1:1- structural proteins]

DE 1; protein (Fragment);

GN 1;

CS Chandipura virus (strain 16535.4);

OC Viruses; ssRNA negative-strand viruses, Mononegavirales;

OC Rhabdoviridae; Vesiculovirus;

CX NBR: T01011272;

RN 111

PF SEQUENCE FROM N.A.

RX MEDLINE: 89299473; PubMed: 2741347.

RA Masters P.S., Beella R.S., Butcher M., Fodor B., Rucklberg J.

RA Bucherlow A.K.J.

RT "Structure and expression of the glycoprotein gene of Chandipura

RT virus";

PL Virology 111:285-290(1989).

CC 1; FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE

CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPING, AS WELL AS

CC METHYLATION OF CAPS, AND POLY A SYNTHESIS.

CC 1; CATALYTIC ACTIVITY: N nucleoside triphosphate + N dihydroxyphate +

CC (RNA) (N)

CC 1; SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE

CC NUCLEOCAPSID AND PROTEIN.

CC 1; SIMILARITY: WITH THE D PROTEIN OF OTHER GROUP 1A RNA AND

CC PARAMYXOVIRUSES.

CC This SWISS 3D entry is copy-righted by the Swiss Institute of Bioinformatics

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CC entities requires a license agreement (see <http://www.1st-3d.com/announce/>CC or send an email to [license@1st-3d.com](mailto:license@1st-3d.com)).

CC EXBL: 034150; AAA2912.1;

KW Transfrase; RNA-directed RNA polymerase

FT NON-TER 11 11

SQ SEQUENCE 11 AA: 1189 MW: 233145348.034 197741.

Query Match 18 (1) Score 20.00 E-value 0.0

Best Local Similarity 45.6%, Pident No. 2 E-value 0.0

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 MVVDCPEAAE 18

DB 1 MLNPPVCAAE 11

Search completed: November 5, 2003, 19:21:49  
 Job time: 114 secs







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OR Pfam: PF02400; transfeRin; 1
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1936 MW; D8FAFA26A6A6D3D9 C8764.4.

Query Match 23.3%; Score 27; DB 1; Length 2;
Best Local Similarity 80.0%; Pred. No. 2; 4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CQDQ 5
DB 1 CQDQ 5

RESULT 7
CQDQ15 PRELIMINARY; PRT: 20 AA.
AC CQDQ15
DT 01-MAY-2000 (TRENBlrel. 13, Created:
DT 01-MAY-2000 (TRENBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBlrel. 14, Last annotation update)
DE Membrane-associated ATPase alpha subunit (fragment)
OS Methanococcus voltae.
OC Archaea; Euryarchaeota; Methanococci; Methanococcoides
OC Methanococcaceae; Methanococcus.
CX NCBI_TaxID=2198;
FN (1)
RX SEQUENCE.
BX MEDLINE: 91374865; PubMed=9166051;
RA Chen W, Kohnsky J.;
FT "Characterization of a membrane-associated ATPase from Methanococcus
FT voltae, a methanogenic member of the Archaea".
RL J. Bacteriol. 175:5677-5682(1993).
SQ SEQUENCE 20 AA; 1965 MW; 8251D1CB444FAC C8764.4.

Query Match 23.3%; Score 27; DB 1; Length 2;
Best Local Similarity 80.0%; Pred. No. 2; 4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 CQDQVDCVCFPAAGDQ 21
DB 5 CQDQVDCVCFPAAGDQ 21

RESULT 8
CQDQ1 PRELIMINARY; PRT: 20 AA.
AC CQDQ1
DT 01-MAY-2000 (TRENBlrel. 13, Created:
DT 01-MAY-2000 (TRENBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TRENBlrel. 22, Last annotation update)
DE APYLAKYLAVINE N acetyltransferase (N-terminal fragment)
GN CAT CR CQ3316
OS Drosophila melanogaster (fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Insecta; Insecta; Diptera;
OC Neoptera; Endopterygota; Diptera; Phlebotomina; Muscidae;
OC Ephydriidae; Ephydriidae; Ephydriidae; Ephydriidae;
CX NCBI_TaxID=7227;
FN (1)
RX SEQUENCE.
BX MEDLINE=9608104; PubMed=7498465;
RA Himmerann E, Chen P, Meyer U.A.;
FT "Isolation and characterization of an apylakylavinase B
FT acetyltransferase from Drosophila melanogaster".
RL FERS Lett. 375:146-150(1995).
DR FlyBase; FBgn019643; Cat
SQ SEQUENCE 20 AA; 2215 MW; 2CFE1D1CB444FAC C8764.4.

Query Match 23.3%; Score 27; DB 1; Length 2;
Best Local Similarity 80.0%; Pred. No. 2; 4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 CQDQVDCVCFPAAGDQ 21
DB 4 CQDQVDCVCFPAAGDQ 21

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DB 1 CQDQVDCVCFPAAGDQ 21
DB 1 CQDQVDCVCFPAAGDQ 21

RESULT 9
CQDQ1 PRELIMINARY; PRT: 16 AA.
AC CQDQ1
DT 01-NOV-1998 (TRENBlrel. 38, Created:
DT 01-NOV-1998 (TRENBlrel. 38, Last sequence update)
DT 01-DEC-2001 (TRENBlrel. 19, Last annotation update)
DE D4 dopamine receptor (D4DR) (fragment)
OS Nicticebus concolor (Slow loris)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Loridae; Nycticebus.
CX NCBI_TaxID=9470;
FN (1)
RX SEQUENCE FROM N.A.
RA Inoue-Murayama Y., Takekaka O., Murayama Y.;
FT "Origin and divergence of tandem repeats of primate D4 dopamine
FT receptor genes".
RL Primates 19:217-224(1998).
DR EMBL; ABC16203; PAA12015.1;
CX NCBI_TaxID=9470;
FN (1)
RX SEQUENCE.
BX MEDLINE=91372967; PubMed=1680106;
RA Hahani F.K., Johnson D.E., Robbins D., Mobley H.L.;
FT "Protein mirabilis flagella and MR/P fimbriae: isolation,
FT purification, N-terminal analysis, and serum antibody response
FT following experimental urinary tract infection."
RL Infect. Immun. 59:3574-3580(1991).
DR InterPro; IPR000259; Fimbrin
DR Pfam; PF00419; Fimbrin; 1.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 16 AA; 1621 MW; 6B3AD0B464F4CD11 CRC64;

Query Match 22.4%; Score 26; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 4; 3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 CQDQVDCVCFPAAGDQ 21
DB 5 CQDQVDCVCFPAAGDQ 21

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[]
RP SEQUENCE FROM N.A.
RC TISSUE-SKIN
RA Strausberg P.
RG Submitted (CGI 2003) to the EMBL/GenBank/DBI databases
OR ENEM; BC019938; AAH19938.1; -.
KW Hypothetical protein.
FI NON_TER
SQ SEQUENCE 19 AA, 2067 NW, 2065224PFES54A1801 (P214)

Query Match 21.63; Score 45; DB 4; Length 19;
Best Local Similarity 49.44; Pctid 50; 50-03;
Matches 4; Conservative 1; Mismatches 4; Gap 0;

CY 11 DCPREAAE5 19
RC 10 DCAESSVAS 18

Search completed: November 5, 2003, 16:44:14
Job time : 35 secs

```

GenCore version 5.1.5  
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SW protein - protein search, using sw model

Run on: November 5, 2003, 18:21:57 : Search time 40 Seconds  
without alignment  
83,332 Million cell of database

Title: US-09-914-088-16

Perfect score: 116

Sequence: 1 CAGCGQVMDVDPREARGLK 31

Scoring table: PRC50M62

Gap: 10.0, Gapext 2.5

Sequences: 1,07869 seqs, 1,072,693 residues

Total number of hits satisfying chosen parameters: 4,9634

Minimum DB seq length: 2

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A Geneseq, 19Jun03:

1	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1980.DAT
2	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1981.DAT
3	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1982.DAT
4	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1983.DAT
5	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1984.DAT
6	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1985.DAT
7	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1986.DAT
8	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1987.DAT
9	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1988.DAT
10	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1989.DAT
11	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1990.DAT
12	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1991.DAT
13	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1992.DAT
14	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1993.DAT
15	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1994.DAT
16	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1995.DAT
17	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1996.DAT
18	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1997.DAT
19	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1998.DAT
20	/S1D51/gcgdata/geneseq/geneseq-emb1/AA1999.DAT
21	/S1D51/gcgdata/geneseq/geneseq-emb1/AA2000.DAT
22	/S1D51/gcgdata/geneseq/geneseq-emb1/AA2001.DAT
23	/S1D51/gcgdata/geneseq/geneseq-emb1/AA2002.DAT
24	/S1D51/gcgdata/geneseq/geneseq-emb1/AA2003.DAT

Pred. No is the number of results predicted by chain to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No	Query	Score	Match	Length	DB ID	Description
1		116	100.0	21	AA25942	PI mimotope peptid
2		116	100.0	21	AAU16647	Peptide P1078 der
3		116	100.0	21	AAU16647	Human IgE cyclic
4		111	95.7	20	AA25942	PI mimotope peptid
5		111	95.7	20	AAU16647	Peptide P1078 der
6		111	95.7	20	AAU16647	Human IgE cyclic
7		100.5	86.6	21	AA25942	PI mimotope peptid
8		100.5	86.6	21	AAU16647	Peptide P1078 der
9		100.5	86.6	21	AAU16647	Human IgE cyclic

10	69	59.5	14	23	AAU00540	Human IgE cyclic
11	60	51.7	13	21	AA25942	Artificially peptid
12	60	51.7	13	21	AA25942	PI mimotope peptid
13	60	51.7	13	21	AA25942	PI mimotope peptid
14	60	51.7	13	22	AAU16647	Peptide P15 deriv
15	60	51.7	13	22	AAU16647	Peptide P15 deriv
16	60	51.7	13	22	AAU16647	Human IgE immunog
17	60	51.7	13	23	AAU16647	IgE peptide #6, M
18	60	51.7	13	23	AAU16647	Human IgE cyclic
19	60	51.7	13	23	AAU16647	Human IgE cyclic
20	60	51.7	13	23	AAU16647	PI mimotope peptid
21	60	51.7	13	23	AAU16647	Peptide P1078 d
22	60	51.7	13	23	AAU16647	Human IgE cyclic
23	60	51.7	13	23	AAU16647	Human IgE cyclic
24	59.5	51.3	21	22	AAU16647	Peptide C67/8-2 de
25	51	44.0	10	21	AA25942	PI mimotope peptid
26	51	44.0	10	22	AAU16647	Peptide P15 deriv
27	51	44.0	10	23	AAU16647	Human IgE immunog
28	51	44.0	13	21	AA25942	Peptide P15 deriv
29	51	44.0	13	22	AAU16647	Human IgE immunog
30	51	44.0	13	23	AAU16647	Human IgE cyclic
31	51	44.0	13	23	AAU16647	Human IgE cyclic
32	50	43.1	13	23	AAU16647	Immunoglobulin E
33	47	40.5	9	21	AA25942	Peptide P1 deriv
34	47	40.5	9	22	AAU16647	IgE C-epsilon-2 do
35	47	40.5	9	22	AAU16647	Peptide P1 deriv
36	47	40.5	9	22	AAU16647	IgE peptide #1, M
37	47	40.5	9	23	AAU16647	Human IgE immunog
38	45	38.8	10	24	AAU16647	Immunoglobulin E
39	43.5	37.5	19	21	AA25942	PI mimotope (PMab
40	43.5	37.5	19	22	AAU16647	Peptide #34 deriv
41	43.5	37.5	19	23	AAU16647	Human IgE cyclic
42	42.5	36.6	19	21	AAU16647	PI mimotope (PMab
43	42.5	36.6	19	22	AAU16647	Peptide #36 deriv
44	42.5	36.6	19	23	AAU16647	Human IgE cyclic
45	38.5	33.2	19	21	AA25942	PI mimotope (PMab

# ALIGNMENTS

RESULT 1	
AA25942	AA25942 standard; Peptide: 21 AA
AC	AA25942
XX	
XX	05-JAN-2001 (first entry)
DE	PI mimotope peptide P1078 SEQ ID NO:16
XX	
KW	Epitope: mimotope, human; immunoglobulin E; IgE; C-epsilon-2 domain;
KW	allergic disease; immunophylaxis; immunotherapy; anti-allergic;
KW	immunosuppressive; vaccine; histamine release inhibitor; immunogen;
KW	allergy; atopy.
XX	
OS	Hom sapiens.
XX	
PN	WC200002460 A1
XX	
PD	31-AUG-2000
XX	
PF	22-FEB-2000; 2000W:EP01455
XX	
PR	25-FEB-1999; 99GB-0004405
PR	29-MAR-1999; 99GB-0007151
PR	07-MAY-1999; 99GB-0010537
PR	07-MAY-1999; 99GB-0210538
PR	07-AUG-1999; 99GB-0218594
PR	07-AUG-1999; 99GB-0218603
PR	07-SEP-1999; 99GB-0021046
PR	07-SEP-1999; 99GB-0021047
PR	29-OCT-1999; 99GB-0025619







Matches 20; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CLEGGQVWVDC-CPREAAEGD 20  
||| ||| ||| ||| |||  
DB 1 CLEGGQVWVDC-CPREAAEGD 21

RESULT 8  
AAU16692  
ID AAU16692 standard; Peptide; 21 AA.  
AC AAU16692;  
XX  
XX 02-SEP-2002 (first entry)  
XX  
XX Peptide PT1079HBC derived as mimotope of Cepsilon2 region of human IgE.  
XX  
XX Human; linkage technology; conjugated compound; carrier vehicle;  
XX C-peptide; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;  
XX IgE-mediated disease; antibody response.  
XX  
XX Homo sapiens.  
XX Synthesia.  
XX  
XX WC2002145745-A2.  
XX  
XX 28-JUN-2001.  
XX  
XX 21-DEC-2000; 2000G8-GBCA935.  
XX  
XX 21-DEC-1999; 99JB-0030233.  
XX 22-FEB-2000; 2000A8-0040364.  
XX 23-AUG-2000; 2000G8-0220707.  
XX 22-AUG-2000; 2000G8-0220708.  
XX  
XX (A)AM-1 ACAMIS RES LTD.  
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
XX Philip N. Johnson T.  
XX  
XX WPI: 2001-521967/59.  
XX  
XX A linkage comprising an immunogenic conjugate of a compound and IgE-mediated diseases.  
XX  
XX Example 4; Page 20; 48pp; English.  
XX The present invention relates to conjugates comprising a carrier molecule and a conjugation of compounds (e.g. peptides, polymers, dendrimers, proteins, liposomes, etc.) macromolecules, polymers, dendrimers, proteins, liposomes, etc. biological and immunological constructs. The invention provides a method for linking an epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a pharmaceutical composition of a vaccine. The invention describes peptides derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E (IgE) which are used to produce conjugated compounds. The compounds or compositions of the invention are useful in the manufacture of a medicament for the treatment of IgE-mediated diseases. The invention allows for controlled conjugation of a peptide epitope, in addition to a protein so as to form an immunogenic conjugate which may be able to raise a protective antibody response in an animal or human patient. ACU16632-AAU16913 represent peptides derived from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.  
XX Sequence 21 AA.

Query March 86.6%; Score 100.5; PB 20; Length 20.  
Best Local Similarity 95.2%; Pred. No. 5; Gaps 0.  
Matches 20; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CLEGGQVWVDC-CPREAAEGD 20  
||| ||| ||| ||| |||  
DB 1 CLEGGQVWVDC-CPREAAEGD 21

RESULT 9  
ABJ00359  
ID ABJ00359 standard; Peptide; 21 AA.  
XX  
XX ABJ00359;  
AC  
XX 02-SEP-2002 (first entry)  
XX  
XX Human IgE cyclic immunogenic peptide SEQ ID NO: 143.  
XX Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
XX vaccine; antiallergic; cyclic.  
XX  
XX Homo sapiens.  
XX WC200216409-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001W9-EP03576.  
XX  
XX 22-AUG-2000; 2000G8-0020717.  
XX  
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX  
XX Friede X, Mason S, Turnell WG, Vinals Passols YC;  
XX  
XX WPI: 2002-489648/52.  
XX  
XX Conjugate for use in vaccine for treatment of allergy, comprises  
XX disulfide bridge cyclized peptide and immunogenic carrier  
XX  
XX Claim 4; Page 12; 45pp; English.  
XX  
XX The present invention relates to conjugates suitable for use in vaccines, where the conjugate comprises a disulfide bridge cyclized peptide and an immunogenic carrier. The vaccines can be used in the treatment of allergies. The present sequence is a cyclic peptide immunogen derived from human immunoglobulin E (IgE) suitable for use in the invention.  
XX Sequence 21 AA.

Query March 86.6%; Score 100.5; PB 20; Length 20.  
Best Local Similarity 95.2%; Pred. No. 5; Gaps 0.  
Matches 20; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CLEGGQVWVDC-CPREAAEGD 20  
||| ||| ||| ||| |||  
DB 1 CLEGGQVWVDC-CPREAAEGD 21

RESULT 10  
ABJ00340  
ID ABJ00340 standard; Peptide; 14 AA.  
XX  
XX ABJ00340;  
AC  
XX 02-SEP-2002 (first entry)  
XX  
XX Human IgE cyclic immunogenic peptide SEQ ID NO: 324.  
XX Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;  
XX vaccine; antiallergic; cyclic.  
XX  
XX Homo sapiens.  
XX WC200216409-A2.  
XX  
XX 28-FEB-2002.  
XX



PF 12-AUG-2001; 2001WO-EP09576.  
 XX  
 XX 22-AUG-2002; 2002OR-0020717.  
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PPT) PEPTIDE THERAPEUTICS LTD.  
 XX Friede M, Mason S, Turnell WJ, Vinals De Bassols YC,  
 XX WPI; 2002-459648/52.  
 XX  
 XX Conjugate for use in vaccine for treatment of allergy, comprising  
 PT disulfide bridge cyclized peptide and immunogenic carrier.  
 XX  
 XX Claim 4; Page 16; 45pp; English.  
 XX The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccines can be used in the treatment of  
 CC allergies. The present sequence is a cyclic peptide immunogen derived  
 CC from human immunoglobulin E (IgE), suitable for use in the invention.  
 XX  
 XX Sequence 14 AA;  
 SQ  
 Query Match 59.5%; Score 69; DR 23; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.6315;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CLEDGGQWMDVC 12  
 DB 1 CLEDGGQWMDVC 14  
 RESULT 11  
 AAB25914  
 ID AAB25914 standard; Peptide; 13 AA.  
 XX  
 AC AAB25914;  
 XX  
 DT 05-JAN-2001 (first entry)  
 XX  
 DE Antiallergy peptide minitope sequence SEQ ID NO:14.  
 XX  
 KW Immunoglobulin E (IgE) immunogen; immunogen; Protein for treatment  
 KW of cancer; Haemophilus influenzae; vaccine; antiallergic; antiallergic;  
 KW malaria; cytostatic; antiallergic; peptide; immunogen; antiallergic;  
 XX  
 XX  
 OS Home sapiens.  
 XX  
 FN WO2002007411.  
 XX  
 PD location/Qualifiers  
 PT Modified site 1;  
 FT /note= "amidated"  
 XX  
 XX WO2002007411.  
 XX  
 XX 31-AUG-2002.  
 XX  
 XX 22-FEB-2002; 2002WO-EP01457.  
 XX  
 XX 25-FEB-1999; 99GB-0004405.  
 XX 25-FEB-1999; 99GB-0004408.  
 XX 25-FEB-1999; 99GB-0004412.  
 XX 13-AUG-1999; 99GB-0019260.  
 XX  
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 XX Coste M, Lobet Y, Van Vechelen MP, Verhaest C,  
 PI WPI; 2000-572040/53.  
 XX  
 XX Immunogens and vaccine comprising the group polypeptide for treatment  
 PT and treating infectious diseases such as malaria and other diseases and

PT cancer, comprises peptide and carrier from protein D of influenzae  
 XX  
 XX Claim 10; Page 38; 31pp; English.  
 XX  
 CC The present invention describes an immunogen (I) comprising a peptide  
 CC (Ia) and a carrier (It) derived from protein D of Haemophilus influenzae  
 CC or its fragment. Also described are: (1) a vaccine comprising (I), and  
 CC an excipient; (2) preparation of (I), comprising conjugating a peptide  
 CC to protein D or its fragment; and (3) preparation of a vaccine of (I),  
 CC comprising formulating (I) with an excipient. (I) has cytostatic,  
 CC antiallergic, neurotropic, neuroprotective and protozoicidal activities.  
 CC (I) and the vaccine are useful for the manufacture of a medicament for  
 CC preventing and treating infectious diseases such as malaria or chronic  
 CC disease such as cancer, Alzheimer's disease or allergy in a patient.  
 CC Unlike prior art immunogens, (I) induces high levels of anti-peptide  
 CC immune responses while inducing a moderate humoral response against the  
 CC carrier. The present sequence represents a specifically claimed  
 CC minitope peptide sequence, which can be used in an immunogen of the  
 CC present invention.  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 51.7%; Score 60; DR 21; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.031;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CLEDGGQWMDVC 11  
 DB 1 CLEDGGQWMDVC 11  
 RESULT 12  
 AAB25914  
 ID AAB25914 standard; Peptide; 13 AA.  
 XX  
 AC AAB25914;  
 XX  
 DT 05-JAN-2001 (first entry)  
 XX  
 DE P1 minitope peptide PT15 SEQ ID NO:8.  
 XX  
 KW Epitope; minitope; human; immunoglobulin E; IgE; C-peptide-2 domain;  
 KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2002058460 A1.  
 XX  
 PD 31-AUG-2002.  
 XX  
 PF 22-FEB-2002; 2002WO-EP0-455.  
 XX  
 XX 25-FEB-1999; 99GB-0004405.  
 XX 25-MAR-1999; 99GB-0001151.  
 XX 07-MAY-1999; 99GB-0010537.  
 XX 07-MAY-1999; 99GB-0010538.  
 XX 07-AUG-1999; 99GB-0018594.  
 XX 07-AUG-1999; 99GB-0018603.  
 XX 07-SEP-1999; 99GB-0021046.  
 XX 07-SEP-1999; 99GB-0021047.  
 XX 29-OCT-1999; 99GB-0025619.  
 XX 23-NOV-1999; 99GB-0027698.  
 XX  
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
 XX  
 XX Dyson M, Friede M, Greenwood C, Hewitt E, Lamont A, Mason S,  
 PI Sandhill R, Turnell WJ, Van Vechelen MP, Vinals De Bassols YC,  
 XX WPI; 2000-572040/54.  
 XX







```

1 FILE REFERENCE: 4564/9179
2 CURRENT APPLICATION NUMBER: US/10/102,076
3 CURRENT FILING DATE: 2003-02-21
4 PRIOR APPLICATION NUMBER: 10/080,249
5 PRIOR FILING DATE: 2002-02-21
6 PRIOR APPLICATION NUMBER: 10/082,014
7 PRIOR FILING DATE: 2002-02-22
8 NUMBER OF SEQ ID NOS: 128
9 SOFTWARE: Patent in version 3.2
10 SEQ ID NO: 136
11 LENGTH: 10
12 TYPE: PAT
13 ORGANISM: Homo sapiens
14 US 10 372 076 136

Query Match
Best Local Similarity: 42.8% Score 43; DB 10; Length 10;
Matches: 9; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 2 LEDGOMVVC II
DB : LEDGOMVVC I

RESULT 1
US 10 082 014 271
Sequence 271, Application US/10/082014
Publication No. US2003018458A1
GENERAL INFORMATION:
APPLICANT: BRIDGES, Ashley J.
TITLE OF INVENTION: IMMUNOGENIC HRC TUMOR PATTERNS CHARACTERIZED WITH AN N TERMINAL CY
FILE REFERENCE: 10/0 4564/9179
CURRENT APPLICATION NUMBER: US/10/082,014
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/930,945
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 296
SOFTWARE: Patent in version 3.2
SEQ ID NO: 271
LENGTH: 10
TYPE: PAT
ORGANISM: Homo sapiens
US 10 082 014 271

Query Match
Best Local Similarity: 40.8% Score 41; DB 10; Length 10;
Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 LEDGOMVVC II
DB : LEDGOMVVC I

RESULT 4
US 10 372 076 137
Sequence 137, Application US/10/372076
Publication No. US2003019845A1
GENERAL INFORMATION:
APPLICANT: Bridges, Mark
TITLE OF INVENTION: STABILIZED HRC TUMOR CARCINOGENIC VACCINE FOR
FILE REFERENCE: 10/080,249
CURRENT APPLICATION NUMBER: US/10/372,076
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 10/080,249
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/082,014
PRIOR FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 138
SOFTWARE: Patent in version 3.2
SEQ ID NO: 137
LENGTH: 10
TYPE: PAT
ORGANISM: Homo sapiens
US 10 372 076 137

Query Match
Best Local Similarity: 48.8% Score 45; DB 12; Length 10;
Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 LEDGOMVVC II
DB : LEDGOMVVC I

RESULT 6
US 10 225 567A 1477
Sequence 1477, Application US/10/225567A
Publication No. US2003011398A1
GENERAL INFORMATION:
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 10/0 4 4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 1999-12-19
NUMBER OF SEQ ID NOS: 2293
SOFTWARE: Patent in version 3.1
SEQ ID NO: 1477
LENGTH: 10
TYPE: PAT
ORGANISM: Homo sapiens
US 10 225 567A 1477

```

Query Match 31.0% Score 16; DB 16; Length 16;  
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 CPKALSGSD 20  
 DB 1 CPKALSGSD 9

## RESULT 7

US-06-927-919-62  
 ; Sequence 62, Application US/5899233;  
 ; Publication No. US6010006642A;  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOSHCH, SAMUEL  
 ; APPLICANT: BOSHCH, ELENORE S.  
 ; TITLE OF INVENTION: Compounds and methods to inhibit or  
 ; TITLE OF INVENTION: augment an inflammatory response.  
 ; FILE REFERENCE: 295,022US;  
 ; CURRENT APPLICATION NUMBER: US/08/927,919  
 ; CURRENT FILING DATE: 1997-09-11  
 ; NUMBER OF SEQ ID NOS: 83  
 ; SOFTWARE: FastSeq for Windows Version 1.0  
 ; SEQ ID NO 62  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-06-927-919-62

Query Match 29.3% Score 14; DB 14; Length 15;  
 Best Local Similarity 36.4%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 QVMDVDCPREA 16  
 DB 5 RINQCPREA 15

## RESULT 8

US-10-105-232-365  
 ; Sequence 188, Application US/10105212  
 ; Publication No. US20030180328A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOSHCH, SAMUEL  
 ; APPLICANT: BOSHCH, ELENORE S.  
 ; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS  
 ; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS  
 ; FILE REFERENCE: 09425-46904  
 ; CURRENT APPLICATION NUMBER: US/10/105,232  
 ; CURRENT FILING DATE: 2002-03-26  
 ; PRIOR APPLICATION NUMBER: 60/303,396  
 ; PRIOR FILING DATE: 2001-07-09  
 ; PRIOR APPLICATION NUMBER: 60/278,761  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: 09/146,755  
 ; PRIOR FILING DATE: 1998-09-04  
 ; PRIOR APPLICATION NUMBER: 09/817,144  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: 08/198,139  
 ; PRIOR FILING DATE: 1994-02-17  
 ; NUMBER OF SEQ ID NOS: 535  
 ; SOFTWARE: PatentIn 2.1  
 ; SEQ ID NO 188  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Plasmodium falciparum  
 US-10-105-232-365

Query Match 28.9% Score 13.5; DB 12; Length 16;  
 Best Local Similarity 42.1%; Pred. No. 1.4e+02;  
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 1;

QY 3 EDGQMDVDCPREAAEGDK 21

DB 1 KDS- -DNKTLCAQGGK 16

## RESULT 9

US-10-105-437-375  
 ; Sequence 375, Application US/10189437  
 ; Publication No. US2003019414A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOSHCH, SAMUEL  
 ; APPLICANT: BOSHCH, ELENORE S.  
 ; TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFORE  
 ; FILE REFERENCE: 09425-46905  
 ; CURRENT APPLICATION NUMBER: US/10/189,437  
 ; CURRENT FILING DATE: 2002-07-08  
 ; PRIOR APPLICATION NUMBER: 10/105,232  
 ; PRIOR FILING DATE: 2002-03-26  
 ; PRIOR APPLICATION NUMBER: 09/984,057  
 ; PRIOR FILING DATE: 2001-10-26  
 ; PRIOR APPLICATION NUMBER: 60/303,396  
 ; PRIOR FILING DATE: 2001-07-09  
 ; PRIOR APPLICATION NUMBER: 60/278,761  
 ; PRIOR FILING DATE: 2001-03-27  
 ; NUMBER OF SEQ ID NOS: 729  
 ; SOFTWARE: PatentIn 2.1  
 ; SEQ ID NO 375  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Plasmodium falciparum  
 US-10-105-437-375

Query Match 28.9% Score 13.5; DB 12; Length 16;  
 Best Local Similarity 42.1%; Pred. No. 1.4e+02;  
 Matches 8; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

QY 3 EDGQMDVDCPREAAEGDK 21  
 DB 1 KDS- -DNKTLCAQGGK 16

## RESULT 10

US-10-105-232-367  
 ; Sequence 387, Application US/10105212  
 ; Publication No. US20030180328A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOSHCH, SAMUEL  
 ; APPLICANT: BOSHCH, ELENORE S.  
 ; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS  
 ; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS  
 ; FILE REFERENCE: 09425-46904  
 ; CURRENT APPLICATION NUMBER: US/10/105,232  
 ; CURRENT FILING DATE: 2002-03-26  
 ; PRIOR APPLICATION NUMBER: 60/303,396  
 ; PRIOR FILING DATE: 2001-07-09  
 ; PRIOR APPLICATION NUMBER: 60/278,761  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: 09/146,755  
 ; PRIOR FILING DATE: 1998-09-04  
 ; PRIOR APPLICATION NUMBER: 09/817,144  
 ; PRIOR FILING DATE: 2001-03-27  
 ; PRIOR APPLICATION NUMBER: 08/198,139  
 ; PRIOR FILING DATE: 1994-02-17  
 ; NUMBER OF SEQ ID NOS: 535  
 ; SOFTWARE: PatentIn 2.1  
 ; SEQ ID NO 387  
 ; LENGTH: 21  
 ; TYPE: PRT  
 ; ORGANISM: Plasmodium falciparum  
 US-10-105-232-367

Query Match 28.9% Score 13.5; DB 12; Length 21;  
 Best Local Similarity 42.1%; Pred. No. 1.4e+02;  
 Matches 8; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

```

QY      3  EGGQNDVCCPREAEGDK 21
DE      : KGS  DTXTLECAQCK 16

RESULT 11
US-10-236-091-4
? Sequence 4, Application US/10236091
? Publication No. US2003016263A
? GENERAL INFORMATION:
? APPLICANT: DUCLOS, Marc
? TITLE OF INVENTION: Peptides Derived from the Superantigen (SAG) ENV
? TITLE OF INVENTION: Protein of HIV-X18 and Their Use in Obtaining
? TITLE OF INVENTION: SAG-Inhibitory Antibodies and in Vaccination Against
? FILE REFERENCE: 23195-506
? CURRENT APPLICATION NUMBER: US/10/236,091
? PRIOR FILING DATE: 2002-09-06
? PRIOR APPLICATION NUMBER: 60/317,703
? PRIOR FILING DATE: 2001-09-06
? PRIOR APPLICATION NUMBER: 60/317,704
? PRIOR FILING DATE: 2001-09-06
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 374
? LENGTH: 21
? TYPE: PRT
? ORGANISM: Human endogenous retrovirus
US-10-236-091-4

Query Match      28.4%; Score 13; DB 12; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3  EGGQNDVCCPREAEGDK 21
DE      : KGS  DTXTLECAQCK 16

RESULT 12
US-10-236-091-4
? Sequence 4, Application US/10236091
? Publication No. US2003016263A
? GENERAL INFORMATION:
? APPLICANT: DUCLOS, Marc
? TITLE OF INVENTION: Peptides Derived from the Superantigen (SAG) ENV
? TITLE OF INVENTION: Protein of HIV-X18 and Their Use in Obtaining
? TITLE OF INVENTION: SAG-Inhibitory Antibodies and in Vaccination Against
? FILE REFERENCE: 23195-506
? CURRENT APPLICATION NUMBER: US/10/236,091
? PRIOR FILING DATE: 2002-09-06
? PRIOR APPLICATION NUMBER: 60/317,703
? PRIOR FILING DATE: 2001-09-06
? PRIOR APPLICATION NUMBER: 60/317,704
? PRIOR FILING DATE: 2001-09-06
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 3
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Human endogenous retrovirus
US-10-236-091-4

Query Match      28.4%; Score 13; DB 12; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3  EGGQNDVCCPREAEGDK 21
DE      : KGS  DTXTLECAQCK 16

RESULT 13
US-10-236-091-4
? Sequence 4, Application US/10236091
? Publication No. US2003016263A
? GENERAL INFORMATION:
? APPLICANT: DUCLOS, Marc
? TITLE OF INVENTION: Peptides Derived from the Superantigen (SAG) ENV
? TITLE OF INVENTION: Protein of HIV-X18 and Their Use in Obtaining
? TITLE OF INVENTION: SAG-Inhibitory Antibodies and in Vaccination Against
? FILE REFERENCE: 23195-506
? CURRENT APPLICATION NUMBER: US/10/236,091
? PRIOR FILING DATE: 2002-09-06
? PRIOR APPLICATION NUMBER: 60/317,703
? PRIOR FILING DATE: 2001-09-06
? PRIOR APPLICATION NUMBER: 60/317,704
? PRIOR FILING DATE: 2001-09-06
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 4
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Human endogenous retrovirus
US-10-236-091-4

Query Match      28.4%; Score 13; DB 12; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      12  CPREAAEGDK 21
DE      : CPKEIPKQSK 10

RESULT 14
US-10-236-091-2
? Sequence 2, Application US/10236091
? Publication No. US2003016263A
? GENERAL INFORMATION:
? APPLICANT: CURRIS, Marc
? TITLE OF INVENTION: Peptides Derived from the Superantigen (SAG) ENV
? TITLE OF INVENTION: Protein of HIV-X18 and Their Use in Obtaining
? TITLE OF INVENTION: SAG-Inhibitory Antibodies and in Vaccination Against
? FILE REFERENCE: 23195-506
? CURRENT APPLICATION NUMBER: US/10/236,091
? PRIOR FILING DATE: 2002-09-06
? PRIOR APPLICATION NUMBER: 60/317,703
? PRIOR FILING DATE: 2001-09-06
? PRIOR APPLICATION NUMBER: 60/317,704
? PRIOR FILING DATE: 2001-09-06
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO 2
? LENGTH: 16
? TYPE: PRT
? ORGANISM: Human endogenous retrovirus
US-10-236-091-2

Query Match      28.4%; Score 13; DB 12; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      12  CPREAAEGDK 21
DE      : CPKEIPKQSK 10

RESULT 15
US-09-826-290-25

```

```

1 Sequence 2 : Application US/09826290
2 Patent No. US2002016468A1
3 GENERAL INFORMATION:
4 APPLICANT: Dufhem, L. Kathryn
5 APPLICANT: Friedman, David L.
6 APPLICANT: Herath, Herath Mudiyatunga Arundha Chandana
7 APPLICANT: Kimmel, Lida H.
8 APPLICANT: Parakh, Rakesh Bhikhu
9 APPLICANT: Pottier, David M.
10 APPLICANT: Rehiff, Christian
11 APPLICANT: Silber, R. Michael
12 APPLICANT: Stager, Thomas R.
13 APPLICANT: Sunderland, P. Grey
14 APPLICANT: Townsend, Robert Reid
15 APPLICANT: White, Frost
16 APPLICANT: Williams, Stephen A.
17 TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
18 Title of Invention: Uses Thereof, Including Diagnosis and Treatment of
19 Title of Invention: Alzheimer's Disease
20 FILE REFERENCE: 2572-1-C01 N2
21 CURRENT APPLICATION NUMBER: US/99/826290
22 CURRENT FILING DATE: 2001-04-30
23 PRIOR APPLICATION NUMBER: US 60/194,194
24 PRIOR FILING DATE: 2000-04-03
25 PRIOR APPLICATION NUMBER: US 60/253,643
26 PRIOR FILING DATE: 2000-11-28
27 NUMBER OF SEQ ID NOS: 492
28 SOFTWARE: FastSeq for Windows Version 4.0
29 SEQ ID NO 25
30 LENGTH: 12
31 TYPE: PRT
32 ORGANISM: Homo sapien
33 29-826-243 25
34
35 Query Watch 28.03 Score 14.00 28.00 14.00 100
36 Best Local Similarity 66.7% Pred. No. 1,500,000
37 Matches 81 Conservative 17 Mismatches 21 Indels 10 Gaps 17
38
39 1 3 EDGQVVDVQPR 14
40 10 111 11
41 2 2 EDGVDVQPR 12

```

Search completed: November 5, 2003, 06:44:14  
 Job time: 1:10 secs



GenCore version 5.1.6  
Copyright (c) 1993-2003 Computed Ltd.

CM protein - protein search, using sw-mat1

Run on: November 5, 2003, 18:27:28 / Search time: 14.5 seconds  
without alignment  
119,223 William call up times/sec

Title: US-09-914-088-16

Patent score: 116

Sequence: 1 CLEQVMDVDCPRRAAEK 21

Scoring table: PLASIM62

Gapop 13.0, Gapext 0.5

Seatched: 428757 seqs, 90991878 residues

Total number of hits satisfying chosen parameters: 944,000

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database: Pending Patents AA Main:
- 1: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 2: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 3: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 4: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 5: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 6: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 7: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 8: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 9: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 10: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 11: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 12: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 13: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 14: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 15: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 16: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 17: /cgn2\_6/prodata/1/paa/US0765086.pat
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  - 19: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 20: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 21: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 22: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 23: /cgn2\_6/prodata/1/paa/US0765086.pat
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  - 27: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 28: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 29: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 30: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 31: /cgn2\_6/prodata/1/paa/US0765086.pat
  - 32: /cgn2\_6/prodata/1/paa/US0765086.pat

Fred. No. is the number of results preferred by user to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the whole database.

Summary:

Result No.	Score	Match Length	DB ID
1	116	100.0	21 24 US-09-914-088-16, Appl

2	116	100.0	21 29 US-10-362-527-101	Sequence 101, App
3	111	95.7	20 24 US-09-914-088-65	Sequence 65, Appl
4	111	95.7	20 29 US-10-362-527-142	Sequence 142, App
5	102.5	86.6	21 24 US-09-914-088-66	Sequence 66, Appl
6	102.5	86.6	21 29 US-10-362-527-143	Sequence 143, App
7	69	59.5	14 29 US-10-362-527-324	Sequence 324, App
8	60	51.7	13 24 US-09-914-088-10	Sequence 10, Appl
9	60	51.7	13 24 US-09-914-088-8	Sequence 8, Appl
10	60	51.7	13 24 US-09-914-088-11	Sequence 11, Appl
11	60	51.7	13 29 US-10-362-527-8	Sequence 8, Appl
12	60	51.7	13 29 US-10-362-527-96	Sequence 96, Appl
13	60	51.7	13 29 US-10-362-527-326	Sequence 326, App
14	60	51.7	20 24 US-09-914-088-15	Sequence 15, Appl
15	60	51.7	20 29 US-10-362-527-100	Sequence 100, App
16	60	51.7	20 29 US-10-362-527-328	Sequence 328, App
17	51	44.0	10 24 US-09-914-088-23	Sequence 23, Appl
18	51	44.0	10 29 US-10-362-527-12	Sequence 12, Appl
19	51	44.0	13 24 US-09-914-088-10	Sequence 10, Appl
20	51	44.0	13 29 US-10-362-527-10	Sequence 10, Appl
21	50	43.1	13 29 US-10-362-527-325	Sequence 325, App
22	49	42.2	10 26 US-10-082-014-282	Sequence 282, App
23	49	42.2	10 29 US-10-372-076-136	Sequence 136, App
24	47	40.5	9 24 US-09-914-088-5	Sequence 5, Appl
25	47	40.5	9 24 US-09-914-088-1	Sequence 1, Appl
26	47	40.5	9 24 US-10-082-014-273	Sequence 273, App
27	47	40.5	9 29 US-10-372-076-127	Sequence 127, App
28	47	40.5	9 29 US-10-144-188-55	Sequence 55, Appl
29	45	38.9	10 27 US-10-144-188-62	Sequence 62, Appl
30	43.5	37.5	19 24 US-09-914-088-62	Sequence 62, Appl
31	43.5	37.5	13 29 US-10-362-527-139	Sequence 139, App
32	42.5	36.6	19 24 US-09-914-088-64	Sequence 64, Appl
33	42.5	36.6	19 29 US-10-362-527-141	Sequence 141, App
34	38.5	33.2	19 24 US-09-914-088-61	Sequence 61, Appl
35	38.5	33.2	19 29 US-10-362-527-138	Sequence 138, App
36	37.5	32.3	19 24 US-09-914-088-55	Sequence 55, Appl
37	37.5	32.3	19 29 US-10-362-527-132	Sequence 132, App
38	37	31.9	17 12 US-08-821-8275-8	Sequence 8, Appl
39	37	31.9	17 12 US-08-821-8275-8	Sequence 8, Appl
40	36.5	31.5	19 24 US-09-914-088-56	Sequence 56, Appl
41	36.5	31.5	19 24 US-09-914-088-60	Sequence 60, Appl
42	36.5	31.5	19 29 US-10-362-527-133	Sequence 133, App
43	36.5	31.5	19 29 US-10-362-527-137	Sequence 137, App
44	36	31.0	16 29 US-10-325-567A-127	Sequence 127, App
45	36	31.0	20 28 US-10-272-437A-39	Sequence 39, Appl

ALIEMENTS

RESULT 1  
US-09-914-088-16  
Sequence 16, Application US/09914088  
GENERAL INFORMATION:  
APPLICANT: DYSON, Michael  
APPLICANT: Fiedler, Martin  
APPLICANT: Greenwood, Judith  
APPLICANT: Hewitt, Ellen  
APPLICANT: Lamont, Allan  
APPLICANT: Mason, Sean  
APPLICANT: Randall, Roger  
APPLICANT: Turner, William Gordon  
APPLICANT: Van Nochem, Marcelle Paulette  
APPLICANT: Vinals y de Bassols, Carola  
TITLE OF INVENTION: Epitopes or Mimotopes Derived from the  
TITLE OF INVENTION: C-Epsilon-2 Domain of IgE, Antagonists Thereof, and Their  
TITLE OF INVENTION: Therapeutic Uses  
FILE REFERENCE: BASF 12  
CURRENT APPLICATION NUMBER: US/09/914-088  
CURRENT FILING DATE: 2001-08-12  
PRIOR APPLICATION NUMBER: US/004404-9  
PRIOR FILING DATE: 1997-02-25  
PRIOR APPLICATION NUMBER: US/97-011-6  
PRIOR FILING DATE: 1997-03-29





? PRIOR APPLICATION NUMBER: GB 991260.1  
 ? PRIOR FILING DATE: 1999-08-13  
 ? PRIOR APPLICATION NUMBER: 09/719,179  
 ? PRIOR FILING DATE: 1999-05-28  
 ? PRIOR APPLICATION NUMBER: PCT/US99/11980  
 ? PRIOR FILING DATE: 1999-05-28  
 ? PRIOR APPLICATION NUMBER: GB 981261.3  
 ? PRIOR FILING DATE: 1998-06-11  
 ? NUMBER OF SEQ ID NOS: 19  
 ? SOFTWARE: FASTSEQ for Windows Version 4.0  
 ? SEQ ID NO 10  
 ? LENGTH: 13  
 ? TYPE: PPT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Chimeric  
 US 09-914-088 10

Query Match 51.7% Score 60 DB 04 Length 13  
 Best Local Similarity 100.0% Pct. Id. 100%  
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CLEGGQVMDV 11  
 DB 1 CLEGGQVMDV 11

# RESULT 9

US-09-914-088-8

? Sequence 8, Application US/099:4088

? GENERAL INFORMATION:

? APPLICANT: Dyson, Michael

? APPLICANT: Friede, Martin

? APPLICANT: Greenwood, Judith

? APPLICANT: Hewitt, Ellen

? APPLICANT: Lamont, Alan

? APPLICANT: Mason, Sean

? APPLICANT: Randall, Roger

? APPLICANT: Turneil, William Gordon

? APPLICANT: Van Mechelen, Marcelle Paulette

? APPLICANT: Vinals y de Bassols, Carlota

? TITLE OF INVENTION: Epitopes or Mimotopes Derived from the

? TITLE OF INVENTION: 2-Epsilon-2 Domain of IgE, Antagonists Thereof, and Their

? FILE REFERENCE: B41172

? CURRENT APPLICATION NUMBER: US/09/914,088

? CURRENT FILING DATE: 2001-08-22

? PRIOR APPLICATION NUMBER: GB 9904405.9

? PRIOR FILING DATE: 1999-02-25

? PRIOR APPLICATION NUMBER: GB 9907151.6

? PRIOR FILING DATE: 1999-03-29

? PRIOR APPLICATION NUMBER: GB 9910533.1

? PRIOR FILING DATE: 1999-05-07

? PRIOR APPLICATION NUMBER: GB 9910538.9

? PRIOR FILING DATE: 1999-05-07

? PRIOR APPLICATION NUMBER: GB 9918594.4

? PRIOR FILING DATE: 1999-08-07

? PRIOR APPLICATION NUMBER: GB 9918603.3

? PRIOR FILING DATE: 1999-08-07

? NUMBER OF SEQ ID NOS: 193

? SOFTWARE: FastSEQ for Windows Version 4.0

? SEQ ID NO 8

? LENGTH: 11

? TYPE: PPT

? ORGANISM: Artificial Sequence

? FEATURE:

? OTHER INFORMATION: Chimeric

US 09-914-088 8

Query Match 51.7% Score 60 DB 04 Length 13  
 Best Local Similarity 100.0% Pct. Id. 100%  
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CLEGGQVMDV 11  
 DB 1 CLEGGQVMDV 11

# RESULT 10

US-09-914-088 11

? Sequence 11, Application US/099:4088

? GENERAL INFORMATION:

? APPLICANT: Dyson, Michael

? APPLICANT: Friede, Martin

? APPLICANT: Greenwood, Judith

? APPLICANT: Hewitt, Ellen

? APPLICANT: Lamont, Alan

? APPLICANT: Mason, Sean

? APPLICANT: Randall, Roger

? APPLICANT: Turneil, William Gordon

? APPLICANT: Van Mechelen, Marcelle Paulette

? APPLICANT: Vinals y de Bassols, Carlota

? TITLE OF INVENTION: Epitopes or Mimotopes Derived from the

? TITLE OF INVENTION: 2-Epsilon-2 Domain of IgE, Antagonists Thereof, and Their

? FILE REFERENCE: B41172

? CURRENT APPLICATION NUMBER: US/09/914,088

? CURRENT FILING DATE: 2001-08-22

? PRIOR APPLICATION NUMBER: GB 9904405.9

? PRIOR FILING DATE: 1999-02-25

? PRIOR APPLICATION NUMBER: GB 9907151.6

? PRIOR FILING DATE: 1999-03-29

? PRIOR APPLICATION NUMBER: GB 9910533.1

? PRIOR FILING DATE: 1999-05-07

? PRIOR APPLICATION NUMBER: GB 9910538.9

? PRIOR FILING DATE: 1999-05-07

? PRIOR APPLICATION NUMBER: GB 9918594.4

? PRIOR FILING DATE: 1999-08-07

? PRIOR APPLICATION NUMBER: GB 9918603.3

? PRIOR FILING DATE: 1999-08-07

? NUMBER OF SEQ ID NOS: 193

? SOFTWARE: FastSEQ for Windows Version 4.0

? SEQ ID NO 11

? LENGTH: 11

? TYPE: PPT

? ORGANISM: Artificial Sequence

? FEATURE:

? OTHER INFORMATION: Chimeric

US 09-914-088 11

Query Match 51.7% Score 60 DB 24 Length 13  
 Best Local Similarity 100.0% Pct. Id. 100%  
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 CLEGGQVMDV 11  
 DB 1 CLEGGQVMDV 11

# RESULT 11

US-09-914-088 11

? Sequence 8, Application US/099:4088

? GENERAL INFORMATION:

? APPLICANT: Dyson, Michael

? APPLICANT: Friede, Martin

? APPLICANT: Greenwood, Judith

? APPLICANT: Hewitt, Ellen

? APPLICANT: Lamont, Alan

? APPLICANT: Mason, Sean

? APPLICANT: Randall, Roger

? APPLICANT: Turneil, William Gordon

? APPLICANT: Van Mechelen, Marcelle Paulette

? APPLICANT: Vinals y de Bassols, Carlota

? TITLE OF INVENTION: Epitopes or Mimotopes Derived from the

? TITLE OF INVENTION: 2-Epsilon-2 Domain of IgE, Antagonists Thereof, and Use Thereof in the Treatment of Allergies

? FILE REFERENCE: B41172

? CURRENT APPLICATION NUMBER: US/09/914,088

? CURRENT FILING DATE: 2001-08-22

? PRIOR APPLICATION NUMBER: GB 9904405.9

? PRIOR FILING DATE: 1999-02-25

? PRIOR APPLICATION NUMBER: GB 9907151.6

? PRIOR FILING DATE: 1999-03-29

? PRIOR APPLICATION NUMBER: GB 9910533.1

? PRIOR FILING DATE: 1999-05-07

? PRIOR APPLICATION NUMBER: GB 9910538.9

? PRIOR FILING DATE: 1999-05-07

? PRIOR APPLICATION NUMBER: GB 9918594.4

? PRIOR FILING DATE: 1999-08-07

? PRIOR APPLICATION NUMBER: GB 9918603.3

? PRIOR FILING DATE: 1999-08-07

? NUMBER OF SEQ ID NOS: 193

? SOFTWARE: FastSEQ for Windows Version 4.0

? SEQ ID NO 11

? LENGTH: 11

? TYPE: PPT

? ORGANISM: Artificial Sequence

? FEATURE:

? OTHER INFORMATION: Chimeric

US 09-914-088 11

1 NUMBER OF SEQ ID NOS: 328  
2 SOFTWARE: FASTSEQ for Windows Version 4.0  
3 SEQ ID NO: 6  
4 LENGTH: 13  
5 TYPE: PRT  
6 ORGANISM: Homo sapiens  
US-10-362 527-6

Query Match 51.7% Score 60; DB 24; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.036;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEGGQWVWD 11  
11  
11  
DB 1 CLEGGQWVWD 11

RESULT 12  
US-10-362 527-96  
1 Sequence 96, Application US/10362527  
2 GENERAL INFORMATION:  
3 APPLICANT: Friede, Martin  
4 APPLICANT: Mason, Sean  
5 APPLICANT: Turnell, William Gordon  
6 APPLICANT: Vinals y de Bassols, Carola  
7 TITLE OF INVENTION: Vaccine Immunogens Comprising Disulfide-Bridged Cyclised Peptide  
8 TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies  
9 FILE REFERENCE: B45216  
10 CURRENT APPLICATION NUMBER: US/10362527  
11 CURRENT FILING DATE: 2001-02-21  
12 PRIOR APPLICATION NUMBER: PCT/EP01/00376  
13 PRIOR FILING DATE: 2001-08-17  
14 PRIOR APPLICATION NUMBER: GB 0020717.3  
15 PRIOR FILING DATE: 2000-08-22  
16 NUMBER OF SEQ ID NOS: 328  
17 SOFTWARE: FASTSEQ for Windows Version 4.0  
18 SEQ ID NO: 96  
19 LENGTH: 13  
20 TYPE: PRT  
21 ORGANISM: Artificial Sequence  
22 FEATURE:  
23 OTHER INFORMATION: Artificial variant of Homo sapiens IgE peptide  
US-10-362 527-96

Query Match 51.7% Score 60; DB 24; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.036;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEGGQWVWD 11  
11  
11  
DB 1 CLEGGQWVWD 11

RESULT 13  
US-10-362 527-100  
1 Sequence 226, Application US/10362527  
2 GENERAL INFORMATION:  
3 APPLICANT: Friede, Martin  
4 APPLICANT: Mason, Sean  
5 APPLICANT: Turnell, William Gordon  
6 APPLICANT: Vinals y de Bassols, Carola  
7 TITLE OF INVENTION: Vaccine Immunogens Comprising Disulfide-Bridged Cyclised Peptide  
8 TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies  
9 FILE REFERENCE: B45216  
10 CURRENT APPLICATION NUMBER: US/10362527  
11 CURRENT FILING DATE: 2001-02-21  
12 PRIOR APPLICATION NUMBER: PCT/EP01/00376  
13 PRIOR FILING DATE: 2001-08-17  
14 PRIOR APPLICATION NUMBER: GB 0020717.3  
15 PRIOR FILING DATE: 2000-08-22  
16 NUMBER OF SEQ ID NOS: 328  
17 SOFTWARE: FASTSEQ for Windows Version 4.0  
18 SEQ ID NO: 326

1 LENGTH: 16  
2 TYPE: PRT  
3 ORGANISM: Artificial Sequence  
4 FEATURE:  
5 OTHER INFORMATION: Artificial variant of Homo sapiens IgE peptide  
US-10-362 527-326

Query Match 51.7% Score 60; DB 29; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEGGQWVWD 11  
11  
11  
DB 1 CLEGGQWVWD 11

RESULT 14  
US-09-914-088-15  
1 Sequence 15, Application US/09914088  
2 GENERAL INFORMATION:  
3 APPLICANT: Dyson, Michael  
4 APPLICANT: Friede, Martin  
5 APPLICANT: Greenwood, Judith  
6 APPLICANT: Hewitt, Ellen  
7 APPLICANT: Lamont, Alan  
8 APPLICANT: Mason, Sean  
9 APPLICANT: Randall, Roger  
10 APPLICANT: Turrell, William Gordon  
11 APPLICANT: Vinals y de Bassols, Carola  
12 TITLE OF INVENTION: Epitopes of Mitoypes Derived from the  
13 TITLE OF INVENTION: C-Epsilon 2 Domain of IgE, Antagonists Thereof, and Their  
14 TITLE OF INVENTION: Therapeutic Uses  
15 FILE REFERENCE: B45172  
16 CURRENT APPLICATION NUMBER: US/09914088  
17 CURRENT FILING DATE: 2001-08-22  
18 PRIOR APPLICATION NUMBER: GB 9934405.9  
19 PRIOR FILING DATE: 1999-02-25  
20 PRIOR APPLICATION NUMBER: GB 9927151.6  
21 PRIOR FILING DATE: 1999-03-29  
22 PRIOR APPLICATION NUMBER: GB 9910537.1  
23 PRIOR FILING DATE: 1999-05-07  
24 PRIOR APPLICATION NUMBER: GB 9910538.9  
25 PRIOR FILING DATE: 1999-05-07  
26 PRIOR APPLICATION NUMBER: GB 9918594.4  
27 PRIOR FILING DATE: 1999-08-07  
28 PRIOR APPLICATION NUMBER: GB 9918601.3  
29 PRIOR FILING DATE: 1999-08-07  
30 NUMBER OF SEQ ID NOS: 191  
31 SOFTWARE: FASTSEQ for Windows Version 4.0  
32 SEQ ID NO: 15  
33 LENGTH: 20  
34 TYPE: PRT  
35 ORGANISM: Artificial Sequence  
36 FEATURE:  
37 OTHER INFORMATION: Chimeric  
US-09-914-088-15

Query Match 51.7% Score 60; DB 24; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLEGGQWVWD 11  
11  
11  
DB 1 CLEGGQWVWD 11

RESULT 15  
US-10-362 527-100  
1 Sequence 109, Application US/10362527  
2 GENERAL INFORMATION:  
3 APPLICANT: Friede, Martin  
4 APPLICANT: Mason, Sean  
5 APPLICANT: Turnell, William Gordon  
6 APPLICANT: Vinals y de Bassols, Carola  
7 TITLE OF INVENTION: Vaccine Immunogens Comprising Disulfide-Bridged Cyclised Peptide  
8 TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies  
9 FILE REFERENCE: B45216  
10 CURRENT APPLICATION NUMBER: US/10362527  
11 CURRENT FILING DATE: 2001-02-21  
12 PRIOR APPLICATION NUMBER: PCT/EP01/00376  
13 PRIOR FILING DATE: 2001-08-17  
14 PRIOR APPLICATION NUMBER: GB 0020717.3  
15 PRIOR FILING DATE: 2000-08-22  
16 NUMBER OF SEQ ID NOS: 328  
17 SOFTWARE: FASTSEQ for Windows Version 4.0  
18 SEQ ID NO: 326

```

1 APPLICANT: Tunnell, William Gordon
2 APPLICANT: Vinals Y De Bassols, Carlota
3 TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
4 TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
5 FILE REFERENCE: H45236
6 CURRENT APPLICATION NUMBER: US/10/362,527
7 PRIOR FILING DATE: 2003-02-21
8 PRIOR APPLICATION NUMBER: ECT/EP01/034576
9 PRIOR FILING DATE: 2001-08-17
10 PRIOR APPLICATION NUMBER: GB 0020771.5
11 PRIOR FILING DATE: 2000-08-22
12 NUMBER OF SEQ ID NOS: 328
13 SOFTWARE: FastSeq for Windows Version 4.0
14 SEQ ID NO: 100
15 LENGTH: 20
16 TYPE: PRT
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: Artificial variant of Hom. Superoxide Dismutase
20 US 10 362 527.100

Query Match 51.7% Score 637 GB 1.0, Length 20
Pair Local Similarity 100.0% Pct Id 100
Matches 11 Conservative 0 Mismatches 0 Indels 0 Gaps 0

07 1 CLEGGQWVD 11
08 1 CLEGGQWVD 11

MATCH COMPLETED: November 5, 2003, 18:41:36
Run time: 1.165 sec

```

GenCore version: 9.1.6  
Copyright (c) 1993 - 2003, CompuLink Ltd.

OX protein - protein search, using sw model

Run on: November 5, 2003, 18:16:39 / search time: 21 seconds  
without alignment  
42,311 Million cell updates/sec

Title: US-09-914-088-16

Perfect score: 116

Sequence: 1 CLEOQVMDVRCPRRAEGGX 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 421,0958 residues

Total number of hits satisfying chosen parameters: 15997

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issue Patents AA\*

- 1: /cgn2/6/prodata/1/aa/AA COMP Exp.
- 2: /cgn2/6/prodata/1/aa/AA COMP Exp.
- 3: /cgn2/6/prodata/1/aa/AA COMP Exp.
- 4: /cgn2/6/prodata/1/aa/AA COMP Exp.
- 5: /cgn2/6/prodata/1/aa/AA COMP Exp.
- 6: /cgn2/6/prodata/1/aa/AA COMP Exp.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Seq	Score	Query Match	Length	DB ID	Seq ID
1	17	31.9	17	3	US-08-329-820-107	Sequence 107, App
2	17	31.9	17	4	US-08-329-820-107	Sequence 107, App
3	17	31.9	17	4	US-08-329-820-107	Sequence 107, App
4	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
5	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
6	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
7	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
8	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
9	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
10	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
11	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
12	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
13	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
14	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
15	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
16	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
17	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
18	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
19	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
20	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
21	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
22	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
23	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
24	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
25	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
26	31	26.7	10	1	US-08-329-820-107	Sequence 107, App
27	31	26.7	10	1	US-08-329-820-107	Sequence 107, App

28	31	26.7	15	6	5202251-4	Patent No. 5202251
29	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
30	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
31	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
32	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
33	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
34	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
35	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
36	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
37	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
38	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
39	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
40	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
41	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
42	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
43	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
44	31	26.7	16	1	US-08-329-820-107	Sequence 107, App
45	31	26.7	16	1	US-08-329-820-107	Sequence 107, App

## ALIGNMENTS

RESULT 1:  
US-08-821-827C-8  
Sequence 8, Application US/08821827C  
Patent No. 6297425  
GENERAL INFORMATION:  
APPLICANT: Scelorge, Christopher J.  
APPLICANT: Bidney, Dennis L.  
TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM  
FILE OF INVENTION: ASPERGILLUS PHENICES  
FILE REFERENCE: 0561A  
CURRENT APPLICATION NUMBER: US/08/821-827C  
CURRENT FILING DATE: 1997-03-21  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 8  
LENGTH: 17  
TYPE: PPT  
ORGANISM: Aspergillus phenices  
US-08-821-827C-8

Query Match: 42.94, Score 17, DB 3, Length 17,  
Best Local Similarity: 42.94, Pred. No. 237  
Matches: 6, Conservative 5, Mismatches 4, Indels 0, Gaps 0

CY 2 LDEGQVMDVRCPRRAEGGX 16  
DB 2 LDEGQVMDVRCPRRAEGGX 16

RESULT 2:  
US-09-290-202B-8  
Sequence 8, Application US/09290202B  
Patent No. 6133846  
GENERAL INFORMATION:  
APPLICANT: Scelorge, Christopher J.  
APPLICANT: Bidney, Dennis L.  
TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM  
FILE OF INVENTION: ASPERGILLUS PHENICES  
FILE REFERENCE: 0561C  
CURRENT APPLICATION NUMBER: US/09/290-202B  
CURRENT FILING DATE: 1999-04-12  
PRIOR APPLICATION NUMBER: 08/821,827  
PRIOR FILING DATE: 1997-03-21  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 8  
LENGTH: 17  
TYPE: PPT  
ORGANISM: Aspergillus phenices  
US-09-290-202B-8

Query Match 31.8% Score 67, DB 4, Length 173  
Best Local Similarity 40.8% Pred. No. 23  
Matches 67 Conservative 57 Mismatches 10 Gaps 0

QY 2 DQGVNVDQPREA 16  
DE 1 LQGVNVDQPREA 16  
|||

RESULT 3  
US-09-377-761A-12  
Sequence 16, Application US/0817778A  
Patent No. 6102222  
GENERAL INFORMATION:  
APPLICANT: Janssen, Bradford A.  
APPLICANT: NO. 107273, Mariadale  
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz MacKenzie & N. Associates  
STREET: One Liberty Place 48th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: United States of America  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/377,761A  
FILING DATE: 24-JAN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DeLuca, Mark  
REGISTRATION NUMBER: 31,229  
REFERENCE/DOCKET NUMBER: TJC-1441  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ. ID NO. 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: 10th  
MOLECULE TYPE: Peptide  
US-09-377-761A 10

Query Match 31.8% Score 67, DB 4, Length 143  
Best Local Similarity 75.0% Pred. No. 26  
Matches 67 Conservative 0 Mismatches 0 Gaps 0

QY 14 GFEAAEG 19  
DB 1 GFEAPEG 8  
|||

RESULT 4  
US 09 329 820 154  
Sequence 154, Application US/09329820  
Patent No. 630476  
GENERAL INFORMATION:  
APPLICANT: JANCZYK, ALFRED  
APPLICANT: FELDING-HABERMANN, BRUNHILDE  
APPLICANT: DIFFENBACH, BEATE  
APPLICANT: RUDENANN, FRIEDRICH  
TITLE OF INVENTION: Linear Adhesion Inhibitors

NUMBER OF SEQUENCES: 238  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPC)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/329,820  
FILING DATE: 25-OCT-1994  
CLASSIFICATION: 510  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4336752.5  
FILING DATE: 29 OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Hawler, King, Diana  
REGISTRATION NUMBER: 33,102  
REFERENCE/DOCKET NUMBER: MERCK 1635  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6133  
TELEFAX: 703-243-6430  
INFORMATION FOR SEQ. ID NO. 154:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
HYDROTHERICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-329-820 154

Query Match 26.7% Score 31, DB 1, Length 10;  
Best Local Similarity 55.6% Pred. No. 16-02;  
Matches 57 Conservative 1 Mismatches 3 Gaps 0

QY 11 DCPRAEG 19  
DB 2 DCPRNPRG 10  
|||

RESULT 5  
US-09 057 897-11  
Sequence 11, Application US/09057897  
Patent No. 6300476  
GENERAL INFORMATION:  
APPLICANT: ILL. Antibody Y.H.  
APPLICANT: Wada, Masana W  
TITLE OF INVENTION: Anti-Peptide Antibody Against Human  
TITLE OF INVENTION: Cytochrome P450 3A4  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Meick & Co., Inc.  
STREET: P.O. Box 2002  
CITY: Rainway  
STATE: NC  
COUNTRY: US  
ZIP: 07365-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,897  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Radd, J. Mark  
REGISTRATION NUMBER: 36,543  
REFERENCE/DOCKET NUMBER: 19902  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 1420-594 3905



TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-052 837.11

Query Match 26.7%; Score 31; DB 4; Length 12;  
Best Local Similarity 53.6%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 CLEDOQVMDVD 11

DB 1 CLEDTCKHVD 11

RESULT 2

US-09-329-820-110  
Sequence 115, Application US/08129820  
Patent No. 5747457

GENERAL INFORMATION:

APPLICANT: JONCZYK, ALFRED  
APPLICANT: FELDING-HABERMANN, BRUNHILDE  
APPLICANT: DIEFENBACH, BEATE  
APPLICANT: RIPPVANN, FRIEDRICH

TITLE OF INVENTION: Linear Adhesion Inhibitors

NUMBER OF SEQUENCES: 228

COMPUTER READABLE FORM:

MEDICAL TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/329,820

FILING DATE: 27-OCT-1994

CLASSIFICATION: 530

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: DE 4336758.5

FILING DATE: 28-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet King, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: VERCK 1635

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 110:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: YES

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /product= "Res-Lys (Boc)"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 2

OTHER INFORMATION: /product= "Thr (Boc)"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /product= "Asp (Boc)"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 5  
OTHER INFORMATION: /product= "Cys (Trt)"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 7  
OTHER INFORMATION: /product= "Arg (Hx)"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 9  
OTHER INFORMATION: /product= "Asn (Trt)"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /product= "His (Trt)"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: /product= "Lys (Boc)"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: /product= "Gly-OME"  
US-09-329-820-110

Query Match 26.7%; Score 31; DB 1; Length 12;  
Best Local Similarity 55.6%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

CY 11 CDPREAREG 19

DB 4 DCPNPHKG 12

RESULT 7

US-09-329-820-115

Sequence 115, Application US/08329820

Patent No. 5747457

GENERAL INFORMATION:

APPLICANT: JONCZYK, ALFRED

APPLICANT: FELDING-HABERMANN, BRUNHILDE

APPLICANT: DIEFENBACH, BEATE

APPLICANT: RIPPVANN, FRIEDRICH

TITLE OF INVENTION: Linear Adhesion Inhibitors

NUMBER OF SEQUENCES: 228

COMPUTER READABLE FORM:

MEDICAL TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/329,820

FILING DATE: 27-OCT-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4336758.5

FILING DATE: 28-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet King, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: VERCK 1635

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 115:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: YES

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

US-08-329-820-186

Query Match 26.7% Score 317 DB 17 Length 12  
Best Local Similarity 55.6% Pref No. 130-02  
Matches 5 Conservative 17 Mismatches 7 Gaps 0

QY 11 DPREAAS 19  
DB 4 DPREAHS 12

RESULT 8

US-08-329-820-173

Sequence 173, Application US/08329810

Patent No. 5747457

GENERAL INFORMATION:

APPLICANT: JONCZYK, ALFRED

APPLICANT: FELDING-HABERMANN, BRUNHILDE

APPLICANT: DIEFENBACH, BEATE

APPLICANT: RIEMANN, FRIEDRICH

TITLE OF INVENTION: Linear Adhesion Inhibitors

NUMBER OF SEQUENCES: 228

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.00 (EPC)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/329,820

FILING DATE: 27-OCT-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4336758.5

FILING DATE: 28 OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet-King, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1635

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 173:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYDROTHERMAL: YES

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

FEATURE:

NAME KEY: Modified-site

LOCATION: 5

OTHER INFORMATION: /product= "Cys-Tyr"

FEATURE:

NAME KEY: Modified-site

LOCATION: 12

OTHER INFORMATION: /product= "Cys-Met"

US-08-329-820-173

Query Match 26.7% Score 317 DB 17 Length 12  
Best Local Similarity 55.6% Pref No. 130-02  
Matches 5 Conservative 17 Mismatches 7 Gaps 0

QY 11 DPREAAS 19  
DB 4 DPREAHS 12

RESULT 1

US-08-329-820-186

Sequence 186, Application US/08329820

Patent No. 5747457

GENERAL INFORMATION:

APPLICANT: JONCZYK, ALFRED

APPLICANT: FELDING-HABERMANN, BRUNHILDE

APPLICANT: DIEFENBACH, BEATE

APPLICANT: RIEMANN, FRIEDRICH

TITLE OF INVENTION: Linear Adhesion Inhibitors

NUMBER OF SEQUENCES: 228

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.00 (EPC)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/329,820

FILING DATE: 27-OCT-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4336758.5

FILING DATE: 28 OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet-King, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1635

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 186:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYDROTHERMAL: YES

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

FEATURE:

NAME KEY: Modified-site

LOCATION: 5

OTHER INFORMATION: /product= "Cys-Tyr"

FEATURE:

NAME KEY: Modified-site

LOCATION: 12

OTHER INFORMATION: /product= "Cys-Met"

US-08-329-820-186

Query Match 26.7% Score 317 DB 17 Length 12  
Best Local Similarity 55.6% Pref No. 130-02  
Matches 5 Conservative 17 Mismatches 7 Gaps 0

QY 11 DPREAAS 19  
DB 4 DPREAHS 12

RESULT 1

US-08-329-820-186

Sequence 186, Application US/08329820

Patent No. 5747457

GENERAL INFORMATION:

APPLICANT: JONCZYK, ALFRED

APPLICANT: FELDING-HABERMANN, BRUNHILDE

APPLICANT: DIEFENBACH, BEATE

APPLICANT: RIEMANN, FRIEDRICH

TITLE OF INVENTION: Linear Adhesion Inhibitors

NUMBER OF SEQUENCES: 228

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.00 (EPC)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/329,820

FILING DATE: 27-OCT-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4336758.5

FILING DATE: 28 OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet-King, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1635

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 186:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYDROTHERMAL: YES

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

FEATURE:

NAME KEY: Modified-site

LOCATION: 5

OTHER INFORMATION: /product= "Cys-Tyr"

FEATURE:

NAME KEY: Modified-site

LOCATION: 12

OTHER INFORMATION: /product= "Cys-Met"

US-08-329-820-186

1 APPLICATION NUMBER: DE 4336758.5  
2 FILING DATE: 28-OCT-1993  
3 ATTORNEY/AGENT INFORMATION:  
4 NAME: Hamlet-King, Diana  
5 REGISTRATION NUMBER: 33,302  
6 REFERENCE/DOCKET NUMBER: MERCK 1615  
7 TELEPHONE: 703-243-6333  
8 TELEFAX: 703-243-6410  
9 INFORMATION FOR SEQ ID NO: 186:  
10 SEQUENCE CHARACTERISTICS:  
11 LENGTH: 12 amino acids  
12 TYPE: amino acid  
13 STRANDEDNESS:  
14 TOPOLOGY: linear  
15 MOLECULE TYPE: peptide  
16 HYPOTHETICAL: YES  
17 ANTI-SENSE: NO  
18 FRAGMENT TYPE: N-terminal  
19 FEATURE:  
20 NAME/KEY: Modified-site  
21 LOCATION: 5  
22 OTHER INFORMATION: /product= "CysMe"  
23 US 08 329-820-186

Query Match: 26.7% Score 31: DB 1: Length 12;  
Best Local Similarity 55.6% Pref No. 1: 2e+02;  
Matches 5; Conservative 1; Mismatches 1; Gaps 0;

QY 1: DCFREAAEG 19

DB 4 DCFRNPKG 12

1 RESULT 11  
2 US-08-329-820-186  
3 Sequence 188, Application US/08329820  
4 Patent No. 5747457  
5 GENERAL INFORMATION:  
6 APPLICANT: JONCZYK, ALFRED  
7 APPLICANT: FELDING-HABERMANN, BRUNHILDE  
8 APPLICANT: DIEFENBACH, BEATE  
9 APPLICANT: RIPPWANN, FRIEDRICH  
10 TITLE OF INVENTION: Linear Adhesion Inhibitors  
11 NUMBER OF SEQUENCES: 228  
12 COMPUTER READABLE FORM:  
13 MEDIUM TYPE: floppy disk  
14 COMPUTER: IBM PC compatible  
15 OPERATING SYSTEM: PC-DOS/MS-DOS  
16 SOFTWARE: Patent In Release #1.0, Version #1.0  
17 CURRENT APPLICATION DATA:  
18 FILING DATE: 28-OCT-1993  
19 ATTORNEY/AGENT INFORMATION:  
20 NAME: Hamlet-King, Diana  
21 REGISTRATION NUMBER: 33,302  
22 REFERENCE/DOCKET NUMBER: MERCK 1615  
23 TELEPHONE: 703-243-6333  
24 TELEFAX: 703-243-6410  
25 INFORMATION FOR SEQ ID NO: 187:  
26 SEQUENCE CHARACTERISTICS:  
27 LENGTH: 12 amino acids  
28 TYPE: amino acid  
29 STRANDEDNESS:  
30 TOPOLOGY: linear  
31 MOLECULE TYPE: peptide  
32 HYPOTHETICAL: YES  
33 ANTI-SENSE: NO

1 FRAGMENT TYPE: N-terminal  
2 FEATURE:  
3 NAME/KEY: Modified-site  
4 LOCATION: 5  
5 OTHER INFORMATION: /product= "CysMe"  
6 US-08-329-820-187  
7  
8 Query Match: 26.7% Score 31: DB 1: Length 12;  
9 Best Local Similarity 55.6% Pref No. 1: 2e+02;  
10 Matches 5; Conservative 1; Mismatches 1; Gaps 0;

QY 1: DCFREAAEG 19

DB 4 DCFRNPKG 12

1 RESULT 12  
2 US-08-329-820-188  
3 Sequence 188, Application US/08329820  
4 Patent No. 5747457  
5 GENERAL INFORMATION:  
6 APPLICANT: JONCZYK, ALFRED  
7 APPLICANT: FELDING-HABERMANN, BRUNHILDE  
8 APPLICANT: DIEFENBACH, BEATE  
9 APPLICANT: RIPPWANN, FRIEDRICH  
10 TITLE OF INVENTION: Linear Adhesion Inhibitors  
11 NUMBER OF SEQUENCES: 228  
12 COMPUTER READABLE FORM:  
13 MEDIUM TYPE: floppy disk  
14 COMPUTER: IBM PC compatible  
15 OPERATING SYSTEM: PC-DOS/MS-DOS  
16 SOFTWARE: Patent In Release #1.0, Version #1.0 (EPC)  
17 CURRENT APPLICATION DATA:  
18 APPLICATION NUMBER: US/08329,820  
19 FILING DATE: 27 OCT 1994  
20 CLASSIFICATION: 530  
21 PRIOR APPLICATION DATA:  
22 APPLICATION NUMBER: DE 4336758.5  
23 FILING DATE: 28-OCT-1993  
24 ATTORNEY/AGENT INFORMATION:  
25 NAME: Hamlet-King, Diana  
26 REGISTRATION NUMBER: 33,302  
27 REFERENCE/DOCKET NUMBER: MERCK 1615  
28 TELEPHONE: 703-243-6333  
29 TELEFAX: 703-243-6410  
30 INFORMATION FOR SEQ ID NO: 188:  
31 SEQUENCE CHARACTERISTICS:  
32 LENGTH: 12 amino acids  
33 TYPE: amino acid  
34 STRANDEDNESS:  
35 TOPOLOGY: linear  
36 MOLECULE TYPE: peptide  
37 HYPOTHETICAL: YES  
38 ANTI-SENSE: NO  
39 FRAGMENT TYPE: N-terminal  
40 FEATURE:  
41 NAME/KEY: Modified-site  
42 LOCATION: 5  
43 OTHER INFORMATION: /product= "CysMe"  
44 US-08-329-820-188

Query Match: 26.7% Score 31: DB 1: Length 12;  
Best Local Similarity 55.6% Pref No. 1: 2e+02;  
Matches 5; Conservative 1; Mismatches 1; Gaps 0;

QY 1: DCFREAAEG 19

DB 4 DCFRNPKG 12

1 RESULT 13  
2 US-08-329-820-189

Sequence 189, Application US/08329823  
Patent No. 5747457  
GENERAL INFORMATION:  
APPLICANT: JONCZYK, ALFRED  
APPLICANT: FELDING-HABERMANN, BRUNHILDE  
APPLICANT: DIEFENBACH, BEATE  
APPLICANT: RIPPWANN, FRIEDRICH  
TITLE OF INVENTION: Linear Adhesion Inhibitors  
NUMBER OF SEQUENCES: 228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS DOS  
SOFTWARE: Patent In Release #1.0, Version #1.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/129,823  
FILING DATE: 27-OCT-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 436758.5  
FILING DATE: 28 OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Hamlet-King, Diana  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1635  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 189:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: N terminal  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 5  
OTHER INFORMATION: /product= "cystibut"  
US-08-329 820 190  
Query Match 26.7%, Score 31, DB 17, Length 12,  
Best Local Similarity 55.6%, Pred. No. 1.2e+02,  
Matches 5, Conservative 11, Mismatches 1, Indels 0,  
Cys 0, Gaps 0,  
CY 11 DECREASED 19  
DB 4 DECREASED 12  
RESULT 15  
US-08-329 820-191  
Sequence 191, Application US/08129820  
Patent No. 5747457  
GENERAL INFORMATION:  
APPLICANT: JONCZYK, ALFRED  
APPLICANT: FELDING-HABERMANN, BRUNHILDE  
APPLICANT: DIEFENBACH, BEATE  
APPLICANT: RIPPWANN, FRIEDRICH  
TITLE OF INVENTION: Linear Adhesion Inhibitors  
NUMBER OF SEQUENCES: 228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS DOS  
SOFTWARE: Patent In Release #1.0, Version #1.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/129,823  
FILING DATE: 27 OCT-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 436758.5  
FILING DATE: 28 OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Hamlet-King, Diana  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1635  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 191:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: N terminal  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 5  
OTHER INFORMATION: /product= "cys-821"  
US-08-329 820 190  
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Best Local Similarity 55.6%, Pred. No. 1.2e+02,  
Matches 5, Conservative 11, Mismatches 1, Indels 0,  
Cys 0, Gaps 0,  
CY 11 DECREASED 19  
DB 4 DECREASED 12

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 436758.5  
FILING DATE: 28 OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Hamlet-King, Diana  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1635  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 190:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: N terminal  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 5  
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US-08-329 820 190  
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Best Local Similarity 55.6%, Pred. No. 1.2e+02,  
Matches 5, Conservative 11, Mismatches 1, Indels 0,  
Cys 0, Gaps 0,  
CY 11 DECREASED 19  
DB 4 DECREASED 12  
RESULT 15  
US-08-329 820-191  
Sequence 191, Application US/08129820  
Patent No. 5747457  
GENERAL INFORMATION:  
APPLICANT: JONCZYK, ALFRED  
APPLICANT: FELDING-HABERMANN, BRUNHILDE  
APPLICANT: DIEFENBACH, BEATE  
APPLICANT: RIPPWANN, FRIEDRICH  
TITLE OF INVENTION: Linear Adhesion Inhibitors  
NUMBER OF SEQUENCES: 228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS DOS  
SOFTWARE: Patent In Release #1.0, Version #1.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/129,823  
FILING DATE: 27 OCT-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 436758.5  
FILING DATE: 28 OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Hamlet-King, Diana  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1635  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 191:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES

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1  ANTI-SENSE: NC
2  FRAGMENT TYPE: N-terminal
3  FEATURE
4  NAME: KEY: Modified-site
5  LOCATION: 5
6  OTHER INFORMATION: /product= "Cys10p2"
US-09-329 850-191

Query Match      26.7% Score 41 DB 12 Length 120
Best Local Similarity 55.6% Pred. No. 120-120
Matches 5; Conservative 1; Mismatches 1; Gaps 0;

QV      11 DCPREABE 19
      |||
LE      4 DCPREABE 12

Search completed: November 5, 2003, 18:23:41
Job time : 22 secs

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GenCore version 5.1.1  
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CM protein protein search, using sw-0.1-1  
Run on: November 5, 2003, 17:03:45, Search time 11 seconds  
(without alignment)  
87,426 Million cell updates/sec

Title: US-09-914-088-24  
Perfect score: 52  
Sequences: 1 CSTRQ9ELA 10

Scoring table: ELOSUM62  
Gapop 10.0, Gapext 0.5

Seatched: 283308 seqs, 96169802 residues  
Total number of hits satisfying chosen parameters: 1106

Minimum DB seq length: 3  
Maximum DB seq length: 10

Post processing: Minimum Match 3%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR 56.0  
1: p111  
2: p121  
3: p131  
4: p141

Pred. No. is the number of results predicted by chosen algorithm  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	34.5	9	2 PH0913	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
2	19	34.5	9	2 PH0914	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
3	18	34.6	9	2 PH0915	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
4	18	34.6	10	2 PH0916	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
5	17	32.7	10	2 PH0917	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
6	17	32.7	10	2 PH0918	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
7	16	30.8	6	2 A20146	Early anti-synthase
8	16	30.8	8	2 XGH081	Human glycoprotein
9	16	30.8	8	2 D61512	Human glycoprotein
10	16	30.8	9	2 D28854	Human glycoprotein
11	16	30.8	9	2 E28854	Human glycoprotein
12	16	30.8	9	2 F28854	Human glycoprotein
13	16	30.8	9	2 C60370	Human glycoprotein
14	16	30.8	9	2 PH0108	Human glycoprotein
15	16	30.8	9	2 PH0943	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
16	16	30.8	10	2 PH0944	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
17	16	30.8	10	2 PH0945	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
18	15	28.8	6	2 JHC0784	Human glycoprotein
19	15	28.8	9	2 A11497	Human glycoprotein
20	15	28.8	9	2 PH0919	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
21	15	28.8	10	2 PH0946	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
22	15	28.8	10	2 PH0947	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
23	14	26.9	8	2 PC1002	Human glycoprotein
24	14	26.9	9	2 A12872	Human glycoprotein
25	14	26.9	9	2 PC07076	Human glycoprotein
26	14	26.9	9	2 PH0917	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
27	14	26.9	9	2 PH0918	T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)
28	14	26.9	10	2 S74176	Human glycoprotein
29	14	26.9	10	2 A44546	Human glycoprotein

ALIGNMENTS

RESULT 1  
PH0917  
T-cell receptor beta chain V-D-J region (clone 8) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0917  
R:Gold, D.E.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.E.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy  
A:Reference number: PH0891; PMID:92078857; PMID:936012  
A:Accession: PH0917  
A:Molecule type: mRNA  
A:Residues: 1-9 <GO>  
A:Experimental source: complete Freund's adjuvant-immunized lymph node  
C:Keywords: T-cell receptor  
Query Match: 38.5%; Score 20; DB 2; Length 9;  
Best Local Similarity: 33.3%; Pred. No. 2.8e+05;  
Matches: 2; Conservative: 4; Mismatches: 0; Indels: 0; Gaps: 0;

RESULT 2  
PH0915  
T-cell receptor beta chain V-D-J region (clone 6) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0915  
R:Gold, D.E.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.E.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy  
A:Reference number: PH0891; PMID:92078857; PMID:936012  
A:Accession: PH0915  
A:Molecule type: mRNA  
A:Residues: 1-9 <GO>  
A:Experimental source: complete Freund's adjuvant-immunized lymph node  
C:Keywords: T-cell receptor  
Query Match: 36.5%; Score 19; DB 2; Length 9;  
Best Local Similarity: 28.6%; Pred. No. 2.8e+05;  
Matches: 2; Conservative: 4; Mismatches: 1; Indels: 0; Gaps: 0;

30	14	26.9	10	2	S65728	hemoglobin, extrac
31	14	26.9	10	2	E43033	T-cell receptor alpha chain
32	14	26.9	10	2	S65726	collagen alpha 1(V
33	14	26.9	10	2	PH0926	T-cell receptor beta chain
34	13	25.0	5	2	J70520	Ig kappa chain V1
35	13	25.0	6	2	S29861	Na+/K+-exchanging
36	13	25.0	7	2	E43394	glycoprotein compo
37	13	25.0	7	2	PT5581	T-cell receptor be
38	13	25.0	7	2	H49394	major fat globule
39	13	25.0	7	2	PC0777	NADH2 dehydrogenas
40	13	25.0	7	4	152382	hypothetical pesti
41	13	25.0	8	2	A32523	peptidyl dipeptida
42	13	25.0	8	2	S59622	metallothionein is
43	13	25.0	8	2	PT0613	T-cell receptor be
44	13	25.0	8	2	C39690	neural cell adhesi
45	13	25.0	9	2	A61230	calsequestrin, car

T-cell receptor beta chain V-D-J region (Hybridoma S18491) rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 09 Oct 1992 #sequence revision: 09 Oct 1992 #text\_change 30 May 1997  
 C:Accession: PH0902  
 R:Gold, D.P., Giffner, H.J. Sun, D.J. Wiley, S.J. Vandenbark, A.A.; Wilson, D.B.  
 C:Exp. Med. 174, 1467-1476, 1991  
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A:Reference number: PH0891; MIMD:92078857; PMID:183612  
 A:Accession: PH0902  
 A:Molecule type: mRNA  
 A:Residues: 1-9 <GCG>  
 A:Experimental source: myelin basic protein immunized T-cell; clones 15 and 16  
 C:Keywords: T-cell receptor

Query Match 34.6%; Score 18; DB 2; Length 9;  
 Best Local Similarity 22.2%; Pred. No. 2 He+35;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY : CATTGCGEL 9  
 DB : CASSTSGNV 9

RESULT 4  
 PH0902  
 T-cell receptor beta chain V-D-J region (Hybridoma S18491) rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 09 Oct 1992 #sequence revision: 09 Oct 1992 #text\_change 30 May 1997  
 C:Accession: PH0902  
 R:Gold, D.P., Giffner, H.J. Sun, D.J. Wiley, S.J. Vandenbark, A.A.; Wilson, D.B.  
 C:Exp. Med. 174, 1467-1476, 1991  
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A:Reference number: PH0891; MIMD:92078857; PMID:183612  
 A:Accession: PH0902  
 A:Molecule type: mRNA  
 A:Residues: 1-9 <GCG>  
 A:Experimental source: myelin basic protein immunized T-cell; clones 15 and 16  
 C:Keywords: T-cell receptor

Query Match 34.6%; Score 18; DB 2; Length 9;  
 Best Local Similarity 22.2%; Pred. No. 2 He+35;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY : CATTGCGEL 9  
 DB : CASSTSGNV 9

RESULT 5  
 PH0904  
 Protein (GenBank) - Arabidopsis thaliana (frugifer)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 07 Feb 1996 #sequence revision: 10 Apr 1996 #text\_change 30 May 1997  
 C:Accession: PH0904  
 R:Kawaguchi, A.; Kato, M.; Kawakami, M.; Oikawa, Y.  
 Submitted to JGPRD, December 1995  
 A:Description: Two dimensional electrophoresis of plant proteins and standardization of  
 A:Reference number: PH0903  
 A:Accession: PH0904  
 A:Molecule type: protein  
 A:Residues: 1-10 <TS>  
 A:Experimental source: leaf

Query Match 32.7%; Score 17; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 4 He+35;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY : TTTGG 7  
 DB : TTTGG 7

RESULT 6  
 PH0905  
 T-cell receptor beta chain V-D-J region (Hybridoma S18491) rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 09 Oct 1992 #sequence revision: 09 Oct 1992 #text\_change 30 May 1997  
 C:Accession: PH0905  
 R:Gold, D.P., Giffner, H.J. Sun, D.J. Wiley, S.J. Vandenbark, A.A.; Wilson, D.B.  
 C:Exp. Med. 174, 1467-1476, 1991  
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A:Reference number: PH0891; MIMD:92078857; PMID:183612  
 A:Accession: PH0905  
 A:Molecule type: mRNA  
 A:Residues: 1-10 <GCG>  
 A:Experimental source: myelin basic protein immunized T-cell; clones 15 and 16  
 C:Keywords: T-cell receptor

Query Match 32.7%; Score 17; DB 2; Length 10;  
 Best Local Similarity 25.0%; Pred. No. 4 He+35;  
 Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY : CATTGCGEL 9  
 DB : CASSTSGNV 5

PH0895  
 T-cell receptor beta chain V-D-J region (Hybridoma S18491) rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 09 Oct 1992 #sequence revision: 09 Oct 1992 #text\_change 30 May 1997  
 C:Accession: PH0895  
 R:Gold, D.P., Giffner, H.J. Sun, D.J. Wiley, S.J. Vandenbark, A.A.; Wilson, D.B.  
 C:Exp. Med. 174, 1467-1476, 1991  
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A:Reference number: PH0891; MIMD:92078857; PMID:183612  
 A:Accession: PH0895  
 A:Molecule type: mRNA  
 A:Residues: 1-10 <GCG>  
 A:Experimental source: myelin basic protein immunized T-cell; clones 15 and 16  
 C:Keywords: T-cell receptor

Query Match 32.7%; Score 17; DB 2; Length 10;  
 Best Local Similarity 25.0%; Pred. No. 4 He+35;  
 Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY : CATTGCGEL 9  
 DB : CASSTSGNV 5

RESULT 7  
 A20186  
 fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)  
 C:Species: Cytolagus cuniculus (domestic rabbit)  
 C:Date: 05 Jun 1997 #sequence revision: 05 Jun 1997 #text\_change 05 May 2000  
 C:Accession: A20186  
 R:McCarthy, A.D.; Atkeson, A.; Hardie, G.; Santikarn, S.; Williams, D.H.  
 FEBS Lett. 160, 296-300, 1983  
 A:Title: Amino acid sequence around the active serine in the acyl: transference domain of  
 A:Reference number: A20186; MIMD:84287768; PMID:6554204  
 A:Accession: A20186  
 A:Molecule type: protein  
 A:Residues: 1-6 <KCG>  
 C:Keywords: acyl:transference; coenzyme A

Query Match 40.8%; Score 16; DB 2; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 2 He+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : TGGTA 10  
 DB : TGGTA 4

RESULT 8  
 XGH05U  
 Urine glycopeptide (man)  
 C:Species: Homo sapiens (man)  
 C:Date: 20 Jun 2000 #sequence revision: 20 Jun 2000 #text\_change 20 Jun 2000  
 C:Accession: XGH05U  
 R:Lote, C.; Weiss, J.F.  
 Biochem. J. 123, 257, 1977  
 A:Title: Identification in urine of a low-molecular weight polar glycopeptide containing  
 A:Reference number: XGH05U; MIMD:72662338; PMID:5126985  
 A:Accession: XGH05U  
 A:Molecule type: protein  
 A:Residues: 1-8 <CG>  
 C:Comment: The identity of the glycoprotein from which this peptide is derived is unknown  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: glycoprotein  
 C:Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 20.8%; Score 16; DB 2; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 2 He+35;  
 Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY : TGGTA 10  
 DB : TGGTA 4

Db : CDSIDS 7

RESULT 9

P28854  
Fibrinopeptide B - olive baboon  
C:Species: Trypanosoma brucei  
C:Date: 28-Oct-1994 #sequence\_revision 19-May 1999 #text\_change 19-May 1999  
C:Accession: D61512  
R:Nakamura, S.; Takenaka, O.; Takahashi, K.  
J. Biochem. Parasitol. 2, 135-150, 1991

A:Title: Glycophorin-like protein of Trypanosoma brucei. C-terminal  
A:Reference number: A61512; MUID:84161821; PMID:1728361  
A:Accession: D61512  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <NA>  
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 30.8%; Score 16; DP 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EGG 8

Db 2 EGG 4

RESULT 10

P28854  
Fibrinopeptide B - olive baboon  
C:Species: Trypanosoma brucei  
C:Date: 28-Oct-1994 #sequence\_revision 19-May 1999 #text\_change 19-May 1999  
C:Accession: D61512  
R:Nakamura, S.; Takenaka, O.; Takahashi, K.  
J. Biochem. Parasitol. 2, 135-150, 1991

A:Title: Glycophorin-like protein of Trypanosoma brucei. C-terminal  
A:Reference number: A61512; MUID:84161821; PMID:1728361  
A:Accession: D61512  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <NA>  
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 30.8%; Score 16; DP 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EGG 8

Db 2 EGG 4

RESULT 11

P28854  
Fibrinopeptide B - hamadryas baboon  
C:Species: Trypanosoma brucei  
C:Date: 28-Oct-1994 #sequence\_revision 19-May 1999 #text\_change 19-May 1999  
C:Accession: D61512  
R:Nakamura, S.; Takenaka, O.; Takahashi, K.  
J. Biochem. Parasitol. 2, 135-150, 1991

A:Title: Glycophorin-like protein of Trypanosoma brucei. C-terminal  
A:Reference number: A61512; MUID:84161821; PMID:1728361  
A:Accession: D61512  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <NA>  
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 30.8%; Score 16; DP 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EGG 8

Db 2 EGG 4

Db 2 EGG 4

RESULT 12

P28854  
Fibrinopeptide B - gelada baboon  
C:Species: Theropithecus gelada (gelada baboon)  
C:Date: 19-May-1989 #sequence\_revision 19-May 1989 #text\_change 19-Aug-2000  
C:Accession: P28854  
R:Nakamura, S.; Takenaka, O.; Takahashi, K.  
J. Biochem. Parasitol. 2, 135-150, 1991

A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada).  
A:Reference number: A91973; MUID:84161821; PMID:1728361  
A:Accession: P28854  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <NA>  
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 30.8%; Score 16; DP 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EGG 7

Db 2 EGG 4

RESULT 13

C60070  
gastrin, domestic ferret (fragment)  
C:Species: Mustela putorius furo (domestic ferret)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 18-Jun-1993  
C:Accession: C60070  
R:Desmond, H.; Varro, A.; Young, C.; Gregory, H.; Nemeth, J.; Dockray, G.  
Regul. Pept. 25, 223-231, 1989

A:Title: The constitution and properties of phosphorylated and unphosphorylated C-terminal  
A:Reference number: A60070; MUID:8931947; PMID:2756156  
A:Accession: C60070  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <RES>

Query Match 30.8%; Score 16; DP 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EGG 8

Db 1 SAEED 6

RESULT 14

PH0108  
late G1-69 protein - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: PH0108  
R:Nikaido, T.; Bradley, D.W.; Pardee, A.B.  
Exp. Cell Res. 192, 102-109, 1991

A:Title: Molecular cloning of transcripts that accumulate during the late G1 phase in  
A:Reference number: PH0108; MUID:91078351; PMID:1984406  
A:Accession: PH0108  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-9 <NIK>

Query Match 30.8%; Score 16; DP 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EGG 8

Db 5 EGG 8



```

RESULT 15
PH0413
T-cell receptor beta chain V-D-J region (clone 14) rat (Eidmann)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09 Oct 1992 #sequence revision 09 Oct 1992 #text change 10 May 1997
C:Accession: PH0413
R:Gold, D.P., Offner, H., Sun, D., Wiley, S., Vandenbark, A.A., Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A:Reference number: PH0413; MUID:32078557; PMID:11516512
A:Accession: PH0413
A:Molecule type: mRNA
A:Residues: 13 aaCL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A:Note: the authors translated the coding GAG for residue 4 as GAA.
C:Keywords: T-cell receptor

Query Match          30.8%  Score 167  DP 27  Length 67
Best Local Similarity 50.3%  Pred No. 2 Re-25
Matches  2;  Conservative  2;  Mismatches  0;  Indels  0;  Gaps  0;

Cq      1 CSIT 4
DB      1  CASI 4

Search completed: November  5, 2003, 10:15:12
Job time 1:12 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2003, 17:23:40 : Search time: 2.3333 seconds  
(without alignment)  
64.127 Million cell updates/sec

Title: US-09-914-088-24  
Perfect score: 52  
Sequence: 1 CSTTQSGSLA 10

Scoring table: HLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 172

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41\*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARY:

Result No.	Score	Query Match	Length	DB ID	Description
1	18	34.6	10	1 SPI_HAIRO	C18997 Halocynthia
2	16	30.6	7	1 UF03_MOUSE	P38641 Mus musculus
3	16	30.8	8	1 CLP_THUOB	P4188 Thicbacillus
4	16	30.8	8	1 GLUR_HUMAN	P60729 Homo sapiens
5	16	30.9	9	1 FIBR_FAPAR	P18744 Fibrinogen
6	16	30.9	9	1 FIBR_FAPAR	P18744 Fibrinogen
7	16	30.9	9	1 FIBR_FAPAR	P18744 Fibrinogen
8	16	30.8	10	1 AMEN_HUMAN	P4188 Homo sapiens
9	16	30.8	10	1 URAL_HUMAN	P4188 Homo sapiens
10	16	30.8	10	1 TALI_PICHA	P4188 Homo sapiens
11	14	26.9	7	1 E105_LITPU	P4188 Homo sapiens
12	14	26.9	9	1 TALI_PICHA	P4188 Homo sapiens
13	13	25.0	7	1 MNP_LEPDE	P4188 Homo sapiens
14	13	25.0	7	1 UH11_RAT	P4188 Homo sapiens
15	13	25.0	8	1 LMT2_LGCM	P4188 Homo sapiens
16	13	25.0	9	1 FARD_CALVO	P4188 Homo sapiens
17	13	25.0	9	1 OXYT_ESFC	P4188 Homo sapiens
18	13	25.0	10	1 COXC_RAT	P4188 Homo sapiens
19	13	25.0	10	1 PPCK_FASHA	P4188 Homo sapiens
20	12	23.1	5	1 BIOA_CITFR	P4188 Homo sapiens
21	12	23.1	7	1 PPH2_LYCES	P4188 Homo sapiens
22	12	23.1	8	1 RSL_EKACH	P4188 Homo sapiens
23	12	23.1	9	1 ALC_CHRE	P4188 Homo sapiens
24	12	23.1	9	1 SAP_STOVA	P4188 Homo sapiens
25	11	21.2	8	1 UPAL_HUMAN	P4188 Homo sapiens
26	11	21.2	8	1 WPI_PBRAT	P4188 Homo sapiens
27	11	21.2	9	1 ALI1_CARMA	P4188 Homo sapiens
28	11	21.2	9	1 DI_NEPNC	P4188 Homo sapiens
29	11	21.2	9	1 DNFL_LGCM	P4188 Homo sapiens
30	11	21.2	9	1 DSIF_RABIT	P4188 Homo sapiens
31	11	21.2	9	1 FARI_CALVO	P4188 Homo sapiens
32	11	21.2	9	1 FARI_CALVO	P4188 Homo sapiens
33	11	21.2	9	1 UF02_MOUSE	P38640 Mus musculus

RESULT 1  
SPI\_HAIRO  
ID SPI\_HAIRO STANDARD: PRT: 10 AA.  
AC C18997  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Serine proteinase inhibitor (Fragment)  
OS Halocynthia roretzi (Sea squirt)  
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
OC Stolidobranchia; Pyrosidae; Halocynthia  
OX NCBI\_TaxID=7729;  
RN 11  
RP SEQUENCE  
RC Tissue: Hemolymph  
RA MEDLINE=96321313; PubMed=9759295;  
RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.  
RT "Purification and characterization of a 58,000-Da proteinase  
inhibitor from the hemolymph of a solitary ascidian, Halocynthia  
roretzi".  
RL Comp. Biochem. Physiol. 114B:1-9(1996).  
CC 1- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.  
CC 2- SUBUNIT: Monomer.  
CC 3- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR InterPro: IPR000215: Serpin.  
DR PROSITE: PS00284; SERPIN; PARTIAL.  
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA, 1254 YW; 4225AT3E181RTAA3 CRC64;  
Query Match: 34.6% Score 18; DB 1; Length 10;  
Best local similarity 50.0%; Pred. No. 9.2e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Query Match: 34.6% Score 18; DB 1; Length 10;  
Best local similarity 50.0%; Pred. No. 9.2e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 3 TQSGE 8  
Db 1 TRKGE 6

RESULT 2  
UF03\_MOUSE  
ID UF03\_MOUSE STANDARD: PRT: 7 AA.  
AC P38641  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment)  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN 11  
RP SEQUENCE  
RC Tissue=Fibroblast  
RA MEDLINE=95039907; PubMed=7523109;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Seikirk C.K.;

P31934 homo sapien  
P80128 oncorhynchu  
P80982 thunnus oce  
P02728 homo sapien  
P22103 homo sapien  
P21996 rattus norv  
P34990 homo sapien  
P58261 daucus caro  
P80630 zea mays lm  
P81675 pinus pinas  
P82455 orochetres  
P56575 rattus norv

## ALIGNMENTS

```

RT "Separation and sequencing of familial and novel murine proteins
  using preparative two-dimensional gel electrophoresis";
PL Electrophoresis 15:735-745(1994);
CC - MISCELLANEOUS; ON THE 2D GEL THE DETERMINED P1 OF THIS UNKNOWN
CC PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
FT NON TER
SQ SEQUENCE 7 AA; 842 MW; 6AA72B100519150 CRC64;

Query Match 30.8%; Score 16; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.3e-05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 QCG 9
DB 2 EFAEL 6

RESULT 5
ID CLP THICU STANDARD; PRT; 8 AA.
AC P2488;
DT 01-OCT-1996 (Rel. 14, Created);
DT 01-OCT-1996 (Rel. 14, Last sequence update);
DT 01-OCT-1996 (Rel. 14, Last annotation update);
DE Chemokine receptor specific protein (Fragment);
OS Thrombocytus capitatus;
CC Bacteria; Proteobacteria; Betaproteobacteria; Rhizobiaceae;
CC Rhizobium;
CX NCBI TaxID 16962;
RN 1;
RP SEQUENCE;
RX MEDLINE=84161822; PubMed=6423521;
RA Nakamura S., Takekura G., Takahashi K.;
RT "Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment);
R1 and Thrombocytus gelatae: their amino acid sequences and
R2 evolutionary rates and a molecular phylogeny for the baboons.";
R3 J. Biochem. 94:1973-1978(1983);
CC - FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC - SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC - MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THIS EXPOSES THEN TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT GEL.
DR F0112954; Unpub.
DR INTERPRO:PRO0111; Fibrinogen_C.
DR PROSITE: PS00514; FIBRIN AGGREGATION; PARTIAL.
KW Blood Coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1076 MW; DCFE6409C7287H06 CRC64;

Query Match 30.8%; Score 16; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QCG 7
DB 2 QCG 4

RESULT 6
ID FIBB JAPHA STANDARD; PRT; 9 AA.
AC P19347;
DT 01-NOV-1990 (Rel. 16, Created);
DT 01-NOV-1990 (Rel. 16, Last sequence update);
DT 26-FEB-2003 (Rel. 41, Last annotation update);
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment);
OS FGR;
CC Papio hamadryas Hamadryas baboon;
CC Sukaryata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

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KW Glycoprotein. 1 1 S-LINKED (GALNA...);
FT CARBOHYD
SQ SEQUENCE 8 AA; 855 MW; C2D87A4AF59EB1E CRC64;

Query Match 30.8%; Score 16; DB 1; Length 8;
Best Local Similarity 29.6%; Pred. No. 1.3e-05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSTQCG 7
DB 1 CEFHCG 7

RESULT 5
ID FIBB JAPAN STANDARD; PRT; 9 AA.
AC P19347;
DT 01-NOV-1990 (Rel. 16, Created);
DT 01-NOV-1990 (Rel. 16, Last sequence update);
DT 26-FEB-2003 (Rel. 41, Last annotation update);
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment);
OS FGR;
CC Papio anubis (Olive baboon);
CC Sukaryata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
CC Cercopithecoidea; Papio.
CX NCBI TaxID=9555;
RN 1;
RP SEQUENCE;
RX MEDLINE=84161822; PubMed=6423521;
RA Nakamura S., Takekura G., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
R1 and Thrombocytus gelatae): their amino acid sequences and
R2 evolutionary rates and a molecular phylogeny for the baboons.";
R3 J. Biochem. 94:1973-1978(1983);
CC - FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC - SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC - MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THIS EXPOSES THEN TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT GEL.
DR F0112954; Unpub.
DR INTERPRO:PRO0111; Fibrinogen_C.
DR PROSITE: PS00514; FIBRIN AGGREGATION; PARTIAL.
KW Blood Coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1076 MW; DCFE6409C7287H06 CRC64;

Query Match 30.8%; Score 16; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QCG 7
DB 2 QCG 4

RESULT 6
ID FIBB JAPHA STANDARD; PRT; 9 AA.
AC P19347;
DT 01-NOV-1990 (Rel. 16, Created);
DT 01-NOV-1990 (Rel. 16, Last sequence update);
DT 26-FEB-2003 (Rel. 41, Last annotation update);
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment);
OS FGR;
CC Papio hamadryas Hamadryas baboon;
CC Sukaryata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

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CC Cercarial dermatitis; Papio.  
OX NCBI TaxID 5557;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=64161822; PubMed=6423621;  
RA Nakamura S., Takenaka C., Takahashi K.;  
RT "Fibrinogen A and B of baboon (Papio anubis, Papio anubis) and  
PT and Theropithecus gelada: their amino acid sequences and  
RT evolutionary rates and a molecular phylogeny for the hominids".  
RJ Biochem. 94:193-197 (1993).  
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
CC AGGREGATION.  
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOGEN AT A AND B EX ALPHA & BETA  
CC CHAINS, AND THIS EXPOSES THE N TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
DR PIR: F08954; E08954;  
DR INTERPRO: IPR002181; Fibrinogen C.  
DR PROSITE: PS03514; FIBRIN AG\_C DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma.  
KW PEPTIDE : 9 FIBRINOPEPTIDE B.  
FT NCN TER : 9  
FT NCN TER : 9  
SQ SEQUENCE 9 AA; 1057 MW; DDFE7879C7287B06 CRC64;  
  
Query Match 30.8%; Score 16; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 QES 7  
DB 3 QES 4  
  
RESULT 7  
FIBR-THRO  
ID FIBR-THRO STANDARD; PRT: 9 AA.  
AC P19142;  
DT 01-NOV-1990 (Rel. 16, Created);  
DT 01-NOV-1990 (Rel. 16, Last sequence update);  
DT 28-FEB-2003 (Rel. 41, Last annotation update);  
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment);  
OS Theropithecus gelada (Gelada baboon);  
OC Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominoidea;  
OC Mammalia; Eutheria; Platyrrhini; Catarrhini; Hominoidea; Homosapiens; Homo;  
OC Cercarial dermatitis; Theropithecus;  
OX NCBI TaxID=5557;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=64161822; PubMed=6423621;  
RA Nakamura S., Takenaka C., Takahashi K.;  
RT "Fibrinogen A and B of baboon (Papio anubis, Papio anubis) and  
PT and Theropithecus gelada: their amino acid sequences and  
RT evolutionary rates and a molecular phylogeny for the hominids".  
RJ Biochem. 94:193-197 (1993).  
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
CC AGGREGATION.  
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOGEN AT A AND B EX ALPHA & BETA  
CC CHAINS, AND THIS EXPOSES THE N TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
DR PIR: F08954; E08954;  
DR INTERPRO: IPR002181; Fibrinogen C.  
DR PROSITE: PS03514; FIBRIN AG\_C DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma.  
KW PEPTIDE : 9 FIBRIN PEPTIDE B.  
FT NCN TER : 9  
FT NCN TER : 9  
SQ SEQUENCE 9 AA; 1057 MW; DDFE7879C7287B06 CRC64;

CC Cercarial dermatitis; Papio.  
OX NCBI TaxID 5557;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=64161822; PubMed=6423621;  
RA Nakamura S., Takenaka C., Takahashi K.;  
RT "Fibrinogen A and B of baboon (Papio anubis, Papio anubis) and  
PT and Theropithecus gelada: their amino acid sequences and  
RT evolutionary rates and a molecular phylogeny for the hominids".  
RJ Biochem. 94:193-197 (1993).  
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
CC AGGREGATION.  
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOGEN AT A AND B EX ALPHA & BETA  
CC CHAINS, AND THIS EXPOSES THE N TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
DR PIR: F08954; E08954;  
DR INTERPRO: IPR002181; Fibrinogen C.  
DR PROSITE: PS03514; FIBRIN AG\_C DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma.  
KW PEPTIDE : 9 FIBRINOPEPTIDE B.  
FT NCN TER : 9  
FT NCN TER : 9  
SQ SEQUENCE 9 AA; 1057 MW; DDFE7879C7287B06 CRC64;  
  
Query Match 30.8%; Score 16; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 QES 7  
DB 3 QES 4  
  
RESULT 5  
AYPN-HELM  
ID AYPN-HELM STANDARD; PRT: 10 AA.  
AC P21731;  
DT 30-MAY-2000 (Rel. 39, Created);  
DT 30-MAY-2000 (Rel. 39, Last sequence update);  
DT 28-FEB-2003 (Rel. 41, Last annotation update);  
DE Aminopeptidase N (EC 3.4.11.2) (CryIA(C) receptor) (Fragment);  
OS Helicoverpa armigera (Cotton bollworm);  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Noctuidae; Heliothinae; Helicoverpa;  
OX NCBI TaxID=29059;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Midgut;  
RA Ingle S.S., Trivedi N., Prasad R., Rao K.K., Chatpar H.S.;  
RT "Aminopeptidase-N as a receptor for Bacillus thuringiensis CryIAC  
RT toxin from Helicoverpa armigera";  
RL Submitted (MAR-1999) to the SWISS-PROT data bank.  
CC -1- FUNCTION: ACTS AS A RECEPTOR FOR B. THURINGIENSIS TOXIN CRYIAC.  
CC -1- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-[-  
CC Xaa- from a peptide, amide or arylamide. Xaa is preferably Ala, but  
CC may be most amino acids including pro (slow action). When a  
CC terminal hydrophobic residue is followed by a prolyl residue, the  
CC two may be released as an intact Xaa-Pro dipeptide.  
CC -1- COFACTOR: Binds; zinc ion (by similarity).  
CC -1- SIMILARITY: Belongs to peptidase family M1.  
DR INTERPRO: IPR006055; Zn\_MpPeptidase.  
DR PROSITE: PS0142; ZINC\_PROTEASE; PARTIAL.  
KW Hydrolyase; Metalloprotease; Aminopeptidase; Zinc.  
FT NCN TER : 10  
FT NCN TER : 10  
SQ SEQUENCE 10 AA; 1033 MW; 050434B87B11F1BB CRC64;  
  
Query Match 30.8%; Score 16; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 QES 7  
DB 4 QES 7  
  
RESULT 9  
USAL-HUMAN  
ID USAL-HUMAN STANDARD; PRT: 10 AA.  
AC P22118;  
DT 01-OCT-1993 (Rel. 27, Created);  
DT 01-OCT-1993 (Rel. 27, Last sequence update);  
DT 16-OCT-2001 (Rel. 40, Last annotation update);  
DE Unknown protein from 2D-page of red blood cells (Spot 1) (Fragment);  
OS Homo sapiens (Human);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;  
OX NCBI TaxID=9606;  
RN [1]  
RP SEQUENCE  
RC TISSUE Erythrocyte;  
RX MEDLINE=94147970; PubMed=8313871;  
RA Gelaz G., Hughes G., Prutiger S., Paquet N., Bairoch A.,  
RA Pasquini C., Sanchez C., Tissot J.-D., Appel R.D., Walzer C.,  
RA Balazs L., HANSEN L.S.S. D.F.;

RT "Plasma and red blood cell protein maps: update (1991);  
 RL Electrophoresis 14:1223-1231(1993);  
 CC "MUSCLE PROTEIN MAPS: ON THE 2D-GEL THE DETERMINED P1 (P-THS UNK) AND  
 CC "PROTEIN IS: 5.4, ITS MW IS: 23 KDa.  
 DR SWISS-2D PAGE: P31118; HUMAN.  
 FT NON-TER 1 1  
 FT NON-TER 10 10  
 SQ SEQUENCE 10 AA: 979 MW: 721065P1ADU05825 QB-04;  
 Query Match 30.8%; Score 16; DB 1; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 TQSG ?  
 DB 1 TQSG 4  
 RESULT 10  
 ID TALL PICCA STANDARD; PRT; 9 AA.  
 AC P17441;  
 DT 01-AUG-1990 (Rel. 15, Created;  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-FEB-2004 (Rel. 41, Last annotation update)  
 DE Transaldolase III (EC 2.2.1.2) (Fragment)  
 OS Pichia jadinii (Yeast) (Candida utilis)  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Pichia.  
 CX NCBI\_TAXID:4903;  
 RN 1;  
 RP SEQUENCE.  
 RX MEDLINE:75145197; PubMed:1032248;  
 RA Tsolis C, Sun S, G;  
 RT Isolation of a peptide containing a binding site for the active center of transaldolase;  
 RL Arch. Biochem. Biophys. 167:525-533(1980);  
 CC "FUNCTION: TRANSALDOOLASE IS IMPORTANT FOR THE BALANCE OF  
 CC METABOLITES IN THE PENTOSE PHOSPHATE PATHWAY  
 CC CATALYTIC ACTIVITY: Sedheptulose 7-phosphate + D-glyceraldehyde  
 CC 3-phosphate + D-erythrose 4-phosphate + D-fructose 6-phosphate.  
 CC "PATHWAY: Pentose phosphate pathway; non-oxidative part  
 CC "SIMILARITY: BELONGS TO THE TRANSALDOOLASE FAMILY. SUBFAMILY 1;  
 CC "ALZ499; A11497;  
 DR InterPro: IPR001457; Transaldolase.  
 DR PROSITE: PS00958; TRANSALDOOLASE 2; PARTIAL.  
 CR PROSITE: PS01054; TRANSALDOOLASE 1; PARTIAL.  
 KW Transferrase; Pentose shunt.  
 FT NON-TER 1 1  
 FT NON-TER 3 3  
 FT NON-TER 9 9  
 SQ SEQUENCE 9 AA: 1033 MW: 725333A1ADU05825 QB-04;  
 Query Match 28.8%; Score 15; DB 1; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CST ?  
 DB 5 CST ?  
 RESULT 11  
 ID EGCELTRE STANDARD; PRT; 7 AA.  
 AC P42111;  
 DT 28-FEB-2004 (Rel. 41, Created;  
 DT 28-FEB-2004 (Rel. 41, Last sequence update)  
 DT 16-SEP-2004 (Rel. 42, Last annotation update)  
 DE Electrolin 5;  
 OS Bacteroides fragilis (Bacteroides fragilis) (Bacteroides fragilis)  
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Vertebrata; Mammalia; Primates;  
 CC Apellidae; Bacteroidia; Anaerobacteria; Bacteroidia; Bacteroidia; Bacteroidia;  
 CC Polychaetidae; Bacteria.

CX NCBI\_TaxID:104895;  
 RN 1;  
 RP SEQUENCE  
 RC TISSUE: Skin secretion;  
 RA Wannitz P.A., Bowie J.H., Tyler M., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litor: electrical comparison with the skin peptides from Litoria  
 RT rubella".  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC "SUBCELLULAR LOCATION: Secreted.  
 CC "TISSUE SPECIFICITY: Skin  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 7  
 FT MOD\_RES 7  
 SQ SEQUENCE 7 AA: 834 MW: 8005807683C5030 CRC64;  
 Query Match 26.9%; Score 14; DB 1; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 EGEL 10  
 DB 5 EGEL 7  
 RESULT 12  
 ID TALL PICCA STANDARD; PRT; 9 AA.  
 AC P17441;  
 DT 01-AUG-1990 (Rel. 15, Created;  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-FEB-2004 (Rel. 41, Last annotation update)  
 DE Transaldolase I (EC 2.2.1.2) (Fragment)  
 OS Pichia jadinii (Yeast) (Candida utilis)  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Pichia.  
 CX NCBI\_TAXID:4903;  
 RN 1;  
 RP SEQUENCE.  
 RX MEDLINE:77110644; PubMed:556324;  
 RA Sun S, G, Tsolis C, G;  
 RT Purification of crystallization of transaldolase isozyme I and  
 RT evidence for different genetic origin of isozymes I and II in  
 RT Candida utilis;  
 RL Arch. Biochem. Biophys. 178:64-78(1977);  
 CC "FUNCTION: TRANSALDOOLASE IS IMPORTANT FOR THE BALANCE OF  
 CC METABOLITES IN THE PENTOSE PHOSPHATE PATHWAY  
 CC CATALYTIC ACTIVITY: Sedheptulose 7-phosphate + D-glyceraldehyde  
 CC 3-phosphate + D-erythrose 4-phosphate + D-fructose 6-phosphate.  
 CC "PATHWAY: Pentose phosphate pathway; non-oxidative part  
 CC "SIMILARITY: BELONGS TO THE TRANSALDOOLASE FAMILY. SUBFAMILY 1;  
 DR InterPro: IPR001457; Transaldolase.  
 DR PROSITE: PS00958; TRANSALDOOLASE 2; PARTIAL.  
 CR PROSITE: PS01054; TRANSALDOOLASE 1; PARTIAL.  
 KW Transferrase; Pentose shunt.  
 FT NON-TER 1 1  
 FT NON-TER 9 9  
 FT NON-TER 9 9  
 SQ SEQUENCE 9 AA: 1008 MW: 274F1AF0E81E058 CRC64;  
 Query Match 26.9%; Score 14; DB 1; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CST 3  
 DB 5 CST 7  
 RESULT 13  
 XNP1: E81E  
 ID XNP1: E81E STANDARD; PRT; 7 AA.  
 AC P41784;  
 DT 01-AUG-1990 (Rel. 15, Created;  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DE Electrolin 5;  
 OS Bacteroides fragilis (Bacteroides fragilis) (Bacteroides fragilis)  
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Vertebrata; Mammalia; Primates;  
 CC Apellidae; Bacteroidia; Anaerobacteria; Bacteroidia; Bacteroidia; Bacteroidia;  
 CC Polychaetidae; Bacteria.



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CM protein: Protein search, using sw model

Run on: November 5, 2003, 17:29:05 : Search time 46 seconds

(without alignment)  
49,251 Million full gaps/score

Title: US-09-914-088-24

Perfect score: 52

Sequence: 1: CSTTGCELA 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 430525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1349

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL.23:  
1: sp.archaea:  
2: sp.bacteria:  
3: sp.fungi:  
4: sp.human:  
5: sp.invertebrate:  
6: sp.mammal:  
7: sp.mic:  
8: sp.organelle:  
9: sp.phage:  
10: sp.plant:  
11: sp.rodent:  
12: sp.virus:  
13: sp.vertebrate:  
14: sp.unclassified:  
15: sp.virus:  
16: sp.bacterioph:  
17: sp.archaea:

Pred. No. is the number of results predicted by BLAST to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID
1	17	32.7	10	15 Q85598
2	17	32.7	10	15 Q85563
3	17	32.7	10	15 Q85619
4	16	30.8	8	5 Q94695
5	16	30.8	10	4 Q9JNG2
6	16	30.8	10	6 Q87342
7	16	30.8	10	11 Q9JL15
8	15	28.6	8	11 P70243
9	15	28.8	9	4 Q9UG34
10	15	28.8	9	12 Q9Q150
11	15	28.8	9	13 Q8ALV2
12	15	28.8	10	2 Q50032
13	15	28.8	10	4 Q60493
14	15	28.6	10	8 Q9G362
15	15	28.6	10	10 Q94158
16	15	28.8	10	11 Q9QVK9

(continued)

# ALIGNMENTS

RESULT 1  
Q85598  
ID Q85598 PRELIM:NARY; PRT; 10 AA.  
AC Q85598; (TrEMBLrel. 01, Created:  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC 2001 (TrEMBLrel. 19, Last annotation update)  
DE Moloney murine sarcoma virus (Strain HT) env/mos 5' junction  
(Fragment)  
OS Moloney murine leukemia virus  
OC Viruses, Retroviruses, Retroviridae, Gamma-retrovirus.  
CX NCBI:TaxId:11801  
RN 11  
PP SEQUENCE FROM N.A.  
RX MEDLINE:91164305; PubMed:6300424;  
FA Donoghue D, Hunter T.  
RT "Recombination functions of variants of Moloney murine sarcoma virus:  
Generation and divergence of a mammalian transforming gene."  
J. Virol. 45:607-617(1983).  
RL EMBL: K01067; AAA46492.1; .  
DR EMBL: K01067  
FT NCN TER 10  
SQ SEQUENCE 10 AA; 1081 MW; 736CFCEBEA77185A4 CRC64;  
Query Match 32.7% Score 17; DB 15; Length 10;  
Best Local Similarity 75.0%; Pred. No. 7.6e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY : CSTT 4  
Db 7 CSOT 10  
RESULT 2  
Q85563  
ID Q85563 PRELIM:NARY; PRT; 10 AA.  
AC Q85563; (TrEMBLrel. 01, Created:  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC 2001 (TrEMBLrel. 19, Last annotation update)  
DE Moloney murine sarcoma virus (Strain HT) env/mos 5' junction  
(Fragment)  
OS Moloney murine leukemia virus  
OC Viruses, Retroviruses, Retroviridae, Gamma-retrovirus.  
CX NCBI:TaxId:11801  
RN 11  
PP SEQUENCE FROM N.A.  
RX MEDLINE:91164305; PubMed:6300424;  
FA Donoghue D, Hunter T.  
RT "Recombination functions of variants of Moloney murine sarcoma virus:  
Generation and divergence of a mammalian transforming gene."  
J. Virol. 45:607-617(1983).  
RL EMBL: K01067; AAA46492.1; .  
DR EMBL: K01067  
FT NCN TER 10  
SQ SEQUENCE 10 AA; 1081 MW; 736CFCEBEA77185A4 CRC64;

Q8120 gallus gali  
Q16428 homo sapien  
Q94516 perimeris  
Q9my15 pongo pygma  
Q8mjt7 eulemur ful  
Q8mjt8 eulemur ful  
Q9qzab mus musculu  
Q9r5n1 cistridium  
Q9r7j9 helicobacte  
Q8nerc homo sapien  
Q8m78 bos mutus g  
Q96kf9 homo sapien  
Q15890 homo sapien  
Q90zvs fulica leuc  
Q85562 moloney mur  
Q51349 pseudomonas  
Q8r514 rattus norv  
Q99j14 mus musculu  
Q85723 simian sarc  
Q47475 escherichia  
Q9r47 bos taurus  
Q81715 hevea bras  
Q83480 rattus norv  
Q9r9e0 bacillus su  
Q29810 homo sapien  
Q47556 escherichia  
Q96p97 homo sapien  
Q8hzy2 canis fami

17 14 26.9 7 13 Q8JC20  
18 14 26.9 8 4 Q16428  
19 14 26.9 8 5 Q9MWH6  
20 14 26.9 8 6 Q9MJD5  
21 14 26.9 9 6 Q8MCT7  
22 14 26.9 9 6 Q8MCT8  
23 14 26.9 9 11 Q9CZAR  
24 14 26.9 10 2 Q8R5N1  
25 14 26.9 10 2 Q8R7J9  
26 14 26.9 10 4 Q8NERC  
27 14 26.9 10 6 Q8M78  
28 14 26.9 10 15 Q9QKJ0  
29 13 25.0 8 4 Q96KF9  
30 13 25.0 8 4 Q15890  
31 13 25.0 8 13 Q90ZVS  
32 13 25.0 8 15 Q85562  
33 13 25.0 9 2 Q51349  
34 13 25.0 9 11 Q8R514  
35 13 25.0 9 11 Q99J14  
36 13 25.0 9 15 Q85723  
37 13 25.0 10 2 Q47475  
38 13 25.0 10 6 Q9R47  
39 13 25.0 10 10 Q81715  
40 12 23.1 7 11 Q83480  
41 12 23.1 8 2 Q9R9E0  
42 12 23.1 8 7 Q29810  
43 12 23.1 9 2 Q47556  
44 12 23.1 9 4 Q96P97  
45 12 23.1 9 6 Q8HZY2

```

DE Env mms fusion protein (fragment)
OS Moloney murine leukemia virus.
OC Viruses; Retroviruses; Retroviridae; Gammaretrovirinae.
CX NCBI_TaxID:11831;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE:82196991; PubMed:6251735;
RA Denegheue D.J., Hunter T.;
RT "A generalized method of subcloning DNA fragments by restriction site
RT recombination. Application to sequencing the amino-terminal region of
RT the transforming gene of Gaidar murine sarcoma virus."
RL J. Virol. 45:607-617(1983).
DR EMBL: K01155; AAA46491.1;
FT NNN TER
SQ SEQUENCE 10 AA; 1062 MW; 196CF3BA771B5H4 CRC64;

Query Match 32.7%; Score 17; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. No. 7 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUST 4
DB 7 CUST 10

RESULT 3
Q95619 PRELIMINARY; PRT; 10 AA.
AC Q95619;
DT 01-MAY-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DT 01-FEB-2003 (TrEMBLrel. 19; Last annotation update)
DE Moloney murine sarcoma virus (strain 10) encodes an oncogene
DE (fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retroviruses; Retroviridae; Gammaretrovirinae.
CX NCBI_TaxID:11831;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE:84144404; PubMed:6103414;
RA Denegheue D.J., Hunter T.;
RT "Recombination functions of various strains of Moloney murine sarcoma virus:
RT generation and divergence of a mammalian transforming gene."
RL J. Virol. 45:607-617(1983).
DR EMBL: K01155; AAA46491.1;
FT NNN TER
SQ SEQUENCE 10 AA; 1062 MW; 196CF3BA771B5H4 CRC64;

Query Match 32.7%; Score 17; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. No. 7 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUST 4
DB 7 CUST 10

RESULT 4
Q94495 PRELIMINARY; PRT; 4 AA.
AC Q94495;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02; Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 08; Last annotation update)
DE Adip. fragment.
OS Adip.
OC
CX NCBI_TaxID:9623;
RN 1;
RP SEQUENCE FROM N.A.

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OS Physatum polycephalum (slime mold).
OC Eukaryota; Mycetozoa; Myxogastromycetidae; Physarida;
OC Physarum.
CX NCBI_TaxID:5791;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE:96182101; PubMed:9622702;
RA Benard M., Laguerre G., Pallotta D., Pierron G.;
RT "Mapping of a replication origin within the promoter region of two
RT unlinked, abundantly transcribed actin genes of Physarum
RT polycephalum."
PL Mol. Cell. Biol. 16:968-976(1996).
DR EMBL: M73459; AAC03706.1;
FT NNN TER
SQ SEQUENCE 8 AA; 878 MW; F406C2CA8187B16 CRC64;

Query Match 30.8%; Score 16; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CUST 8
DB 2 CUST 4

RESULT 5
Q9C950 PRELIMINARY; PRT; 10 AA.
AC Q9C950;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13; Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13; Last annotation update)
DE Canalicular multispecific organic anion transporter (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI_TaxID:2606;
RN 1;
RP SEQUENCE FROM N.A.
RA Tanaka T., Uchiumi T., Hinochita E., Inokuchi A., Toh S., Wada Y.,
RA Nomoto M., Kondo K., Kuwano M.;
RT "Sequence analysis and functional characterization of the 5' flanking
RT region of the human canalicular multispecific organic anion
RT transporter mediating resistance protein 2 (CMOAT/MRP2) gene."
RL Submitted (APR1999) to the EMBL/GenBank/CCDS databases.
DR EMBL: AF144410; AA447499.1;
FT NNN TER
SQ SEQUENCE 10 AA; 1219 MW; 76F14944B39C18R CRC64;

Query Match 30.8%; Score 16; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 12e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUST 4
DB 9 CUST 9

RESULT 6
Q9TS42 PRELIMINARY; PRT; 10 AA.
AC Q9TS42;
DT 01-MAY-2003 (TrEMBLrel. 13, Created)
DT 01-MAY-2003 (TrEMBLrel. 13; Last sequence update)
DT 01-COR-2003 (TrEMBLrel. 21; Last annotation update)
DE CESTRACOL PEPTIDE-1 peptide (fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Artiodactyla; Suidae; Sus.
CX NCBI_TaxID:9623;
RN 1;
RP SEQUENCE FROM N.A.

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RX MEMO: E-91291128; PubMed:2064608;  
 RA Thiele H R, Campbell P W, Jakob T;  
 RT "The protein driven dissociation of oestradiol-receptor stress as a  
 PT preparative tool: Isolation of a 32 KDa fragment for positive when  
 RD Bloch- G. 276:159-174(1991).  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 992 MW; D95E047B1451B7D CRC64;

Query Match 30.8%; Score 16; DB 1; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TQSG 7  
 DB 5 TNEG 8

RESULT 7  
 QY0015 PRELIMINARY; PRT; 10 AA.  
 AC QY0115  
 DT 01-OCT-2000 (TREMUREL: 15, Created)  
 DT 01-OCT-2000 (TREMUREL: 15, Last sequence update)  
 DT 01-OCT-2000 (TREMUREL: 15, Last annotation update)  
 DE Melanocortin type 1 receptor MOP (Fragment)  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI TAXID:10090;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J  
 EX XREF: 20050376; PubMed:1042181;  
 RA Adachi S, Morita K, Kim D K, Ohtsuka H, Iijima T, Ito A, Ito Y M,  
 RA Kikuchi Y;  
 FT "Involvement of mit-transcription factor in expression of alpha  
 FT melanocyte-stimulating hormone receptor in cultured mast cells of  
 KC mice".  
 RL J Biol Chem 270:16418-16425(2000);  
 DR EMBL: AF174316; AF373231;  
 KW Receptor  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1148 MW; 9AB-AAC774B07175 CRC64;

Query Match 30.8%; Score 16; DB 1; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TQSG 6  
 DB 2 STOR 5

RESULT 8  
 P00243 PRELIMINARY; PRT; 4 AA  
 AC P00243  
 DT 01-FEB-1997 (TREMUREL: 02, Created)  
 DT 01-FEB-1997 (TREMUREL: 02, Last sequence update)  
 DT 01-DEC-2001 (TREMUREL: 19, Last annotation update)  
 DE Skeletal muscle specific calcium channel (Fragment)  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI TAXID:10090;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:129;  
 EX XREF: 129;  
 RA Ohtsuka Y A;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: X65725; X65696.1;  
 KW

Query Match 28.3%; Score 15; DB 12; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TQSG 4  
 DB 1

FT NON TER 1  
 SQ SEQUENCE 8 AA; 865 MW; D9C37DD81861ADDE CRC64;

Query Match 28.8%; Score 15; DB 11; Length 8;  
 Best Local Similarity 46.1%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CST 3  
 DB 1 CAT 3

RESULT 9  
 QY0064 PRELIMINARY; PRT; 9 AA.  
 AC QY0064  
 DT 01-MAY-2000 (TREMUREL: 13, Created)  
 DT 01-MAY-2000 (TREMUREL: 13, Last sequence update)  
 DT 01-MAY-2000 (TREMUREL: 13, Last annotation update)  
 DE D334105.1 (Remainder of gene in sequence ALC23513) (Fragment).  
 GN SEZ6L.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI TAXID:9606;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RA Lloyd D J;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AL078460; CAB5175.1;  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 1125 MW; 8154A2CB0B5E0411 CRC64;

Query Match 28.8%; Score 15; DB 4; Length 9;  
 Best Local Similarity 42.3%; Pred. No. 6.3e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 TQSG 10  
 DB 2 TREYEV 8

RESULT 10  
 QY0350 PRELIMINARY; PRT; 9 AA.  
 AC QY0350  
 DT 01-NOV-1998 (TREMUREL: 02, Created)  
 DT 01-NOV-1998 (TREMUREL: 02, Last sequence update)  
 DT 01-DEC-2001 (TREMUREL: 19, Last annotation update)  
 DE Polyprotein (Fragment)  
 OS Hepatitis G virus  
 CC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae;  
 CC GBV-C/HGV group  
 OX NCBI TAXID:45255;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SG3419;  
 RX MEDLINE=99266893; PubMed=10345862;  
 RA Wong S B C, Chan S H, Ren S C;  
 RT "Diversity of GB virus C/hepatitis G virus isolates in Singapore:  
 RT predominance of group 2a and the Asian group 3 variant".  
 RL J Med Virol 69:145-153(1999).  
 DR EMBL: AF076065; AAC1217.1;  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 489 MW; D95CA5A5BEB9CDDC CRC64;

Query Match 28.3%; Score 15; DB 12; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TQSG 4  
 DB 1



Best Loc.: Similarity 75.0%; Pred. No. 26-04,  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STTC 5  
Db 2 SSTR 5

RESULT 15

Q941S6 PRELIMINARY; PRT; 10 AA.  
AC Q941S6: 2001 (TEMUREL.19, Created)  
DT 01-DEC-2001 (TEMUREL.19, Last sequence update)  
DT 01-DEC-2001 (TEMUREL.19, Last annotation update)  
DE Nonspecific lipid transfer protein (Fragment)  
OS Pinus taeda (loblolly pine)  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferales; Pinaceae; Pinus  
CX NCBI\_TaxID 33527  
RN 1;  
RF SEQUENCE FROM N.A.  
RC STRAIN PTL94 1305;  
RA Jones D.F.;  
RT "Genetic mapping of the lipid transfer protein gene family in Pinus  
radiata and Pinus taeda";  
RL Submitted (MAR-2001) to the EMBL/GenBank/CCP databases.  
DR EMBL; AY029012; AAC40261.1;  
FT NON-TER 10  
SQ SEQUENCE 10 AA; 1099 MW; 282C1E3B4H1AEV (P0664).

Query Match: 28.8%; Score 15; DB 10; Length 10  
Best Local Similarity 66.7%; Pred. No. 26-04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 COT 3  
Db 4 OTT 6

Search completed: November 5, 2003, 17:34:39  
Job time: 1.19 secs

GenCore version 5.1.6  
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ON protein: protein search, using sw model

Run on: November 5, 2003, 17:41:00, Search time 17.411 seconds  
with-out alignment  
40 618 Million cell updates/sec

Title: US-09-914-088-24

Perfect score: 52

Sequence: 1 GSTTGEGELA 10

Scoring table: BLOSUM62

Gapop 12.0, Gapext 2.5

Searched: 1107861 segs, 158726573 residues

Total number of hits satisfying chosen parameters: 101420

Maximum DB seq length: 2

Maximum DB seq length: 10

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A Geneseg 19Jun03:  
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22: /SIDSI/gcgdata/geneseq/genesegp emb: AA109-1AT.  
23: /SIDSI/gcgdata/geneseq/genesegp emb: AA109-1AT.  
24: /SIDSI/gcgdata/geneseq/genesegp emb: AA109-1AT.

pred. No. is the number of resular predicted-ly char. to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	21	Antibody pepoid
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3	52	100.0	10	21	Antibody pepoid
4	52	100.0	10	21	Antibody pepoid
5	52	100.0	10	21	Antibody pepoid
6	52	100.0	10	21	Antibody pepoid
7	52	100.0	10	21	Antibody pepoid
8	52	100.0	10	21	Antibody pepoid
9	52	100.0	10	21	Antibody pepoid

10	39	75.0	8	23	ABJ00218	Human IgE immunoge
11	31	59.6	6	21	ABJ05931	P2 mimotope peptid
12	31	59.6	6	22	AAJ16456	Peptide P2sh deriv
13	31	59.6	6	23	ABJ00230	Human IgE immunoge
14	27	51.9	9	24	ABP84333	HLA protein 121P2A
15	27	51.9	9	24	ABP84560	HLA protein 121P2A
16	27	51.9	9	24	ABP85788	HLA protein 121P2A
17	27	51.9	9	24	ABP85838	HLA protein 121P2A
18	27	51.9	9	24	ABP85855	HLA protein 121P2A
19	27	51.9	9	24	ABP86135	HLA protein 121P2A
20	27	51.9	9	24	ABP86502	HLA protein 121P2A
21	27	51.9	9	24	ABP86568	HLA protein 121P2A
22	27	51.9	9	24	ABP86784	HLA protein 121P2A
23	27	51.9	9	24	ABP86859	HLA protein 121P2A
24	27	51.9	9	24	ABP86895	HLA protein 121P2A
25	27	51.9	9	24	ABP87052	HLA protein 121P2A
26	27	51.9	9	24	ABP87155	HLA protein 121P2A
27	27	51.9	9	24	ABP87223	HLA protein 121P2A
28	27	51.9	9	24	ABP87334	HLA protein 121P2A
29	27	51.9	9	24	ABP87527	HLA protein 121P2A
30	27	51.9	9	24	ABP87867	HLA protein 121P2A
31	27	51.9	9	24	ABP87868	HLA protein 121P2A
32	27	51.9	9	24	ABP87940	HLA protein 121P2A
33	27	51.9	9	24	ABP87941	HLA protein 121P2A
34	27	51.9	9	24	ABP88162	HLA protein 121P2A
35	27	51.9	9	24	ABP88228	HLA protein 121P2A
36	27	51.9	9	24	ABP88335	HLA protein 121P2A
37	27	51.9	9	24	ABP88558	HLA protein 121P2A
38	27	51.9	9	24	ABP88635	HLA protein 121P2A
39	27	51.9	9	24	ABP88721	HLA protein 121P2A
40	27	51.9	9	24	ABP88722	HLA protein 121P2A
41	27	51.9	9	24	ABP89053	HLA protein 121P2A
42	27	51.9	9	24	ABP89102	HLA protein 121P2A
43	27	51.9	9	24	ABP89230	HLA protein 121P2A
44	27	51.9	9	24	ABP89273	HLA protein 121P2A
45	27	51.9	9	24	ABP89745	HLA protein 121P2A

ALIGNMENTS

RESULT 1

AAB20873

ID AAB20873 standard, peptide; 10 AA.

AC AAB20873

XX AAB20873

DT 01 FEB 2001 (first entry)

XX Antiallergy peptide: mimotope sequence SEQ ID NO:11.

DE Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier.

PA (SMIR) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
 XX Dyson M, Friede M, Greenwood J, Hewitt B, Laroont A, Mason S,  
 PI Randall R, Turnell WJ, Van Mechelen MP, Virals De Bassols Y,  
 XX WPI, 2000-072033/54.  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX Claim 15, page 9, 123pp; English.  
 XX The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (II) of C-epsilon2 domain (D) of  
 CC immunoglobulin E (IgE), or its macrope. Also described are: (1) an  
 CC immunogen (III) for treating allergy comprising (I); (2) a vaccine (III)  
 CC for treating allergies comprising (I); (3) a ligand (IV) capable of  
 CC recognising E; (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
 CC (IIa) comprising (Ia); and (7) producing (Ia) by producing (II), (I)  
 CC can have anti-allergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (I), (II) and (III) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (IV) is useful for identifying macrope of P1,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (II) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (I), (II) and (III) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AA825907 to AA826099 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX Sequence 10 AA;  
 SQ

Query Match 100.0% Score 52; DB 21; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0024;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSTTGSELA 10  
 DB 1 CSTTGSELA 10  
 RESULT 1  
 AA026435  
 ID AA026435 standard; Peptide; 10 AA.  
 AC AA026435.  
 XX 07 NOV 2001 (first entry)  
 XX Peptide P16 derived as macrope of Cepsilon2 region of human IgE.  
 XX Human linkage technology; conjugated compound; carrier vehicle;  
 XX epitope; Cepsilon2; Cepsilon2; Cepsilon2; Cepsilon2; Cepsilon2; Cepsilon2;  
 XX 15E mediated disease; antibody response.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WT200145745.A2.  
 XX 28-JUN-2001.  
 XX 21-DEC-2001; 2000WQ-0504935.  
 XX 21-DEC-2001; 980P-0140233.  
 XX 22-FEB-2001; 2000WQ-0504935.  
 XX 22-APR-2001; 2000WQ-0504935.  
 XX 22-APR-2001; 2000WQ-0504935.  
 XX 22-APR-2001; 2000WQ-0504935.

PA (SMIR) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT) PEPTIDE THERAPEUTICS LTD.  
 XX Dyson M, Friede M, Greenwood J, Hewitt B, Laroont A, Mason S,  
 PI Randall R, Turnell WJ, Van Mechelen MP, Virals De Bassols Y,  
 XX WPI, 2000-072033/54.  
 XX Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX Claim 15, page 9, 123pp; English.  
 XX The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (II) of C-epsilon2 domain (D) of  
 CC immunoglobulin E (IgE), or its macrope. Also described are: (1) an  
 CC immunogen (III) for treating allergy comprising (I); (2) a vaccine (III)  
 CC for treating allergies comprising (I); (3) a ligand (IV) capable of  
 CC recognising E; (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
 CC (IIa) comprising (Ia); and (7) producing (Ia) by producing (II), (I)  
 CC can have anti-allergic and immunosuppressive activities, and can be used  
 CC as a vaccine and histamine release inhibitor. (I), (II) and (III) are  
 CC useful in medicine and in the manufacture of medicaments for treating  
 CC and preventing allergies. (IV) is useful for identifying macrope of P1,  
 CC in medicine and also in manufacturing medicaments for treating  
 CC allergies. (II) is useful in diagnostics and in the affinity purification  
 CC of circulating anti-IgE antibodies from blood. (I), (II) and (III) are  
 CC useful for treating a patient susceptible to or suffering from allergies.  
 CC (IV) is also useful in diagnosing atopy. AA825907 to AA826099 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention.  
 XX Sequence 10 AA;  
 SQ

Query Match 100.0% Score 52; DB 21; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0024;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSTTGSELA 10  
 DB 1 CSTTGSELA 10  
 RESULT 1  
 AA026435  
 ID AA026435 standard; Peptide; 10 AA.  
 AC AA026435.  
 XX 07 NOV 2001 (first entry)  
 XX Peptide P16 derived as macrope of Cepsilon2 region of human IgE.  
 XX Human linkage technology; conjugated compound; carrier vehicle;  
 XX epitope; Cepsilon2; Cepsilon2; Cepsilon2; Cepsilon2; Cepsilon2; Cepsilon2;  
 XX 15E mediated disease; antibody response.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WT200145745.A2.  
 XX 28-JUN-2001.  
 XX 21-DEC-2001; 2000WQ-0504935.  
 XX 21-DEC-2001; 980P-0140233.  
 XX 22-FEB-2001; 2000WQ-0504935.  
 XX 22-APR-2001; 2000WQ-0504935.  
 XX 22-APR-2001; 2000WQ-0504935.





```

AAU:6633
ID AAU:6633 standard; Peptide: 8 AA.
AC AAU16533,
XX
XX
XX 07 NOV-2001 (first entry)
XX
XX Peptide P2 derived from Cepsilon2 region of human IgE.
XX
XX Human linkage technology; conjugated compound; carrier vehicle;
XX epitope; Cepsilon3; Cepsilon4; immunoglobulin E;
XX IgE mediated disease; antibody response.
XX
XX Homo sapiens.
XX
XX WO200145945-A2.
XX
XX 28-JUN 2001.
XX
XX 21-DEC-2000; 2000WO-GB04935.
XX
XX 31-DEC-1999; 99GB-0030233.
XX
XX 22-FEB 2000; 2000GB-0040396.
XX
XX 22-AUG-2000; 2000GB-0029707.
XX
XX 22-AUG 2000; 2000GB-0029708.
XX
XX JACAM ; ACAMIS RES LTD.
XX (SMK ; SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Philip N. Johnson T;
XX
XX WP: 2001-521967/57.
XX
XX A linkage comprising an immunogenic conjugate useful treatment of IgE
XX mediated diseases.
XX
XX Example 4; Page 21; 48pp; English.
XX
XX The present invention relates to linkage methodology for use in the
XX conjugation of compounds (e.g. peptides) to carrier vehicles
XX (e.g. macromolecules, polymers, dendrimers, proteins) to produce
XX biological and immunological constructs. The invention provides a
XX method for linking an epitope (e.g. a peptide) to a carrier using a
XX protein; for use in a pharmaceutical composition of a vaccine. The
XX invention describes peptides derived from or mimetics of the
XX Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E
XX (IgE), which are used to produce conjugated compounds. The compounds or
XX compositions of the invention are useful in the treatment of a
XX condition for the treatment of IgE mediated diseases. The invention
XX allows for controlled conjugation of a peptide epitope attached to a
XX protein so as to form an immunogenic conjugate which may be able to
XX raise a protective antibody response in an animal or human patient.
XX AAU16632 AAU16913 represent peptides derived from or mimetics of
XX the Cepsilon2/Cepsilon3/Cepsilon4 region of human IgE.
XX
XX Sequence 8 AA;
XX
XX Query Match 75.0%; Score 39; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 STTQEGEL 9
XX Db : STTQEGEL 9
XX
XX RESULT 10
XX AAU00219
XX ID AB000219 standard; Peptide: 8 AA.
XX
XX AC AB000219;
XX
XX DT 02 SEP 2002 (first entry)
XX
XX DE Human IgE immunogenic peptide SEQ ID NO: 2.
XX
XX KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;
XX vaccine; antiallergic.
XX
XX OS Homo sapiens.
XX
XX PV WO200216409-A2.
XX
XX 28-FEB 2002.
XX
XX 17-AUG-2001; 2001WO-EP09576.
XX
XX 22-AUG-2000; 2000GB-020717.
XX
XX (SMK ; SMITHKLINE BEECHAM BIOLOGICALS.
XX (PST ; PEPTIDE THERAPEUTICS LTD.
XX
XX Friede M, Mason S, Cornwell WG, Vinals Bassols YC;

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Job time : 33.333 secs

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RESULT 15
ABP#4540
ID  ABP#4540 standard: peptide, 9 AA
XX  ABP#4540
XX
XX  24-MAR 2001 (first entry)
XX
XX  HLA protein L112A1 peptide #915
XX
XX  Human IL12p33A1 cytosolic immunostimulant variant, ASH,
XX  humoral immune response, cellular immune response,
XX  suppression subtractive hybridisation, HLA, human leukocyte antigen,
XX
XX  Homo sapiens.
XX
XX  W52028H3065 A2.
XX
XX  24-OCT 2002.
XX
XX  09-APR 2002; 2002WO-US11359.
XX
XX  10-APR-2001; 2001US-282739P.
XX
XX  26-MAR 2001; 2001US 286610P.
XX
XX  22-JUN 2001; 2001US-300133P.
XX
XX  CAJEN : AGENSYS INC.
XX
XX  Chaitin-Leid IV, Raitano AB, Paris V, Harp P, Mitchell, D,
XX  Atul IER, Saffian D, Morrison K, Morrison KK, de W, Vaccinists A:
XX
XX  WI: 2003-092956/28.
XX
XX  New composition comprising a substance that modulates the status of
XX  IL12p33A1 polypeptides, useful for eliciting humoral or cellular immune
XX  responses or in assessing the status of IL12p33A1 gene products in normal
XX  versus cancerous tissues.
XX
XX  Claim 11, Page 145; 362pp; English.
XX
XX  The invention relates to a novel composition comprising a substance that
XX  modulates the status of a protein, IL12p33A1, the coding region of the
XX  invention has cytostatic and immunomodulatory activity, and is useful as a
XX  vaccine. The IL12p33A1 proteins and polypeptide subunits are useful for
XX  eliciting humoral or cellular immune responses, and the subunits are
XX  useful for characterising cytotoxicity, as well as for identifying a
XX  locus, as tools that can be used in identifying regions of the genome that
XX  are in the chromosomal region that encodes leukocyte antigen, and to
XX  multiplex phenotype, and in assessing the status of IL12p33A1 gene
XX  products in normal versus cancerous tissues. The protein are useful
XX  for generating and characterising domain-specific antibodies, for
XX  identifying agents or cellular factors that bind to IL12p33A1,
XX  particular structure domain, and in various therapeutic and diagnostic
XX  contexts, including cancer vaccines. The antibodies of the invention
XX  with the product are useful in passive or active immunisation, and in
XX  imaging methodologies for the management of cancer. The sequences shown
XX  in ABP#4540 ABP#5595 represent peptides from the IL12p33A1 variants of
XX  the invention.
XX
XX  Sequence 9 AA;
XX
XX  Query Match 51.9%; Score 27, 28.14; 1st hit
XX  Best Local Similarity 83.3%; Pref 10; 5.0000
XX  Matches 5; Conservative 1; Mismatches 1; 1.0000; 0.0000
XX
XX  3 T30005 4
XX  1 1 1
XX  2 T30005 1

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GenCore version 5.1.6  
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OM: protein - protein search, using sw model

Run on: November 5, 2003, 17:34:45 / Search time 21 seconds  
(without alignment)  
81,785 Million cell updates/sec

Title: US-09-914-088-24

Perfect score: 52

Sequence: 1 (NT13EGELA 10

Scoring table: ELOSMAS2

Gapop 12.0, Gapext 0.5

Searched: 644279 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 5116

Minimum DP seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Datacase: 1 Published Applications AA\*

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- 2: /sgn2\_6/prodata/2/pubpaaf/ICT\_NEW\_PUB.ppt
- 3: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
- 4: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
- 5: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
- 6: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
- 7: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
- 8: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
- 9: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
- 10: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
- 11: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
- 12: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
- 13: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
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- 15: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
- 16: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
- 17: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt
- 18: /sgn2\_6/prodata/2/pubpaaf/US04\_PUBCOMB.ppt

Pred. No. is the number of residue probability of the sequence  
score greater than or equal to the score of the sequence listed,  
and is derived by analysis of the total active residues

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Residues
1	39	75.0	8	12	US-10-082-014-274
2	39	75.0	8	12	US-10-082-014-274
3	39	75.0	9	12	US-10-082-014-274
4	39	75.0	9	12	US-10-082-014-274
5	25	48.1	9	9	US-09-812-122-122
6	25	48.1	9	10	US-09-812-122-122
7	23	44.2	9	12	US-10-082-014-274
8	23	44.2	9	12	US-10-082-014-274
9	23	44.2	9	12	US-09-812-122-122
10	23	44.2	9	12	US-10-082-014-274
11	23	44.2	10	12	US-09-812-122-122
12	23	44.2	10	12	US-10-082-014-274
13	23	44.2	10	12	US-10-082-014-274
14	23	44.2	10	12	US-10-082-014-274
15	22	42.3	9	11	US-09-809-638-62

16	22	42.3	9	11	US-09-809-638-62
17	22	42.3	9	11	US-09-809-638-62
18	22	42.3	10	11	US-09-809-638-62
19	22	42.3	10	11	US-09-809-638-62
20	22	42.3	10	11	US-09-809-638-62
21	22	42.3	10	11	US-09-809-638-62
22	21	40.4	7	9	US-09-989-789-1221
23	21	40.4	7	11	US-09-989-789-1221
24	21	40.4	7	11	US-09-989-789-1221
25	21	40.4	7	11	US-09-989-789-1221
26	21	40.4	7	11	US-09-989-789-1221
27	21	40.4	7	11	US-09-989-789-1221
28	21	40.4	9	9	US-09-910-310-58
29	21	40.4	9	12	US-10-271-617-18
30	21	40.4	9	12	US-10-271-617-18
31	21	40.4	9	12	US-09-942-052-5
32	21	40.4	9	12	US-09-942-052-5
33	21	40.4	9	12	US-09-942-052-5
34	21	40.4	10	9	US-09-978-231-8
35	21	40.4	10	10	US-09-978-231-8
36	21	40.4	10	11	US-09-978-231-8
37	21	40.4	10	11	US-09-978-231-8
38	21	40.4	10	11	US-09-978-231-8
39	21	40.4	10	11	US-09-978-231-8
40	21	40.4	10	11	US-09-978-231-8
41	21	40.4	10	11	US-09-978-231-8
42	21	40.4	10	12	US-09-572-404B-2928
43	21	40.4	10	12	US-09-572-404B-2928
44	21	40.4	10	12	US-10-083-768-120
45	21	40.4	10	12	US-09-942-052-80

ALIGNMENTS

RESULT 1

US-10-082-014-274  
; Sequence 274, Application US/10082014  
; Publication No. US2003014856A1  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N TERMINAL C  
; FILE REFERENCE: JCC-130-0-4564/65124  
; CURRENT APPLICATION NUMBER: US/10/082-014  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 09/910,915  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 240  
; SOFTWARE: PatAlign version 3.1  
; SEQ ID NO: 274  
; LENGTH: 8  
; TYPE: PPT  
; ORGANISM: Homo sapiens  
US-10-082-014-274

Query Match: 75.0%, Score 39, DB 12, Length 8;  
Best Local Similarity: 100.0%, Pred No. 5,8e+05;  
Matches: 0, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;

Oy 2 STTGEGEL 9  
Db : STTGEGEL 8

RESULT 2

US-10-372-076-128  
; Sequence 128, Application US/10372076  
; Publication No. US20030198645A1  
; GENERAL INFORMATION:  
; APPLICANT: Papp, Mark  
; APPLICANT: Papp, Mark  
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
; TITLE OF INVENTION: CHRONIC HEPATITIS

FILE REFERENCE: 4564/97179  
CURRENT APPLICATION NUMBER: US/10/372-036  
CURRENT FILING DATE: 2003-02-21  
PRIOR FILING DATE: 10/080,294  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: Patent in version 3.2  
SEQ ID NO: 128  
LENGTH: 8  
TYPE: PAT  
ORGANISM: Homo sapiens  
US-10-372-036-128

Query Match 75.0%, Score 39; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 2 STORED 9  
DB 1 STORED 8

RESULT 3  
US-10-092-014-293  
Sequence 137, Application US/10082076  
Publication No. US20030185859A1  
GENERAL INFORMATION:  
APPLICANT: Biotech, Ashley J.  
TITLE OF INVENTION: IMMUNOGENIC HBC VIRUS PARTICLES STABILIZED WITH AN N-TERMINAL CY  
FILE REFERENCE: 100,036; Pred. No. 5.8e+05;  
CURRENT APPLICATION NUMBER: US/10/372-014  
CURRENT FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 09/930,915  
PRIOR FILING DATE: 2001-08-15  
NUMBER OF SEQ ID NOS: 290  
SOFTWARE: Patent in version 3.1  
SEQ ID NO: 283  
LENGTH: 9  
TYPE: PAT  
ORGANISM: Homo sapiens  
US-10-092-014-293

Query Match 75.0%, Score 40; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 2 STORED 9  
DB 2 STORED 9

RESULT 4  
US-10-372-036-137  
Sequence 137, Application US/10372076  
Publication No. US20030198646A1  
GENERAL INFORMATION:  
APPLICANT: Biotech, Ashley J.  
TITLE OF INVENTION: IMMUNOGENIC HBC VIRUS PARTICLES STABILIZED WITH AN N-TERMINAL CY  
FILE REFERENCE: 100,036; Pred. No. 5.8e+05;  
CURRENT APPLICATION NUMBER: US/10/372-014  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/080,299  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: Patent in version 3.2  
SEQ ID NO: 137  
LENGTH: 9

TYPE: PAT  
ORGANISM: Homo sapiens  
US-10-372-036-137

Query Match 75.0%, Score 39; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 2 STORED 9  
DB 2 STORED 9

RESULT 5  
US-09-932-192-12  
Sequence 12, Application US/09832182  
Patent No. US20030022979A1  
GENERAL INFORMATION:  
APPLICANT: Resnic Baserga, David Abraham, and Mariana Resnicoff  
TITLE OF INVENTION: Method of Inducing Resistance to Tumor Growth  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030022977A1ris LL  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/832,382  
FILING DATE: 11-APR-2001  
CLASSIFICATION: <UNKNOWN>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/664,641  
FILING DATE: <UNKNOWN>  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul K. Legatid  
REGISTRATION NUMBER: 38,534  
REFERENCE/DOCKET NUMBER: T01 2137  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-932-192-12

Query Match 49.1%, Score 25; DB 9; Length 9;  
Best Local Similarity 57.1%; Pred. No. 5.8e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Caps 0;

QY 1 STORED 9  
DB 1 STORED 9

RESULT 6  
US-09-835-853-3  
Sequence 3, Application US/09835853  
Patent No. US20020165136A1  
GENERAL INFORMATION:  
APPLICANT: Baserga, Renato L.  
APPLICANT: Resnicoff, Mariana  
APPLICANT: Huang, Zhiwei  
TITLE OF INVENTION: HBC PARTICLES AND METHODS OF USE

1 NUMBER OF SEQUENCES: 23  
 2 CORRESPONDENCE ADDRESS:  
 3 ADDRESSEE: HALE and DGER LLP  
 4 STREET: 1455 Pennsylvania Avenue, N.W.  
 5 CITY: Washington  
 6 STATE: D.C.  
 7 COUNTRY: USA  
 8 ZIP: 20004  
 9 COMPUTER READABLE FORM:  
 10 MEDIUM TYPE: Floppy disk  
 11 COMPUTER: IBM PC compatible  
 12 OPERATING SYSTEM: PC-DOS/MS-DOS  
 13 SOFTWARE: Parent in Release #1, Version #1.0  
 14 CURRENT APPLICATION DATA:  
 15 APPLICATION NUMBER: US/09/835,835  
 16 FILING DATE:  
 17 CLASSIFICATION:  
 18 PRIOR APPLICATION DATA:  
 19 APPLICATION NUMBER: US 08/704,344  
 20 FILING DATE: 28-AUG-1996  
 21 ATTORNEY/AGENT INFORMATION:  
 22 NAME: WIXON, Henry N.  
 23 REGISTRATION NUMBER: 32,273  
 24 REFERENCE/DOCKET NUMBER: 104222-196  
 25 TELECOMMUNICATION INFORMATION:  
 26 TELEPHONE: (202) 942-8459  
 27 TELEFAX: (202) 942-8484  
 28 INFORMATION FOR SEQ ID NO: 3:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 9 amino acids  
 31 TYPE: amino acid  
 32 STRANDEDNESS: single  
 33 TOPOLOGY: linear  
 34 MOLECULE TYPE: peptide  
 35 HYPOTHETICAL: NO  
 36 ANTI-SENSE: NO  
 37 US 09-835 833 3

Query Match: 48.2%, Score 23; DB 9; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5,8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSTT 4  
 DB 1 CSTT 4

RESULT 7  
 US-09-832-703-92  
 1 Sequence 92, Application US/0981273  
 2 Publication No. US2002009524A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Estell, David A.  
 5 APPLICANT: Chen, Yiyou  
 6 APPLICANT: Murray, Christopher J.  
 7 APPLICANT: Tzjelina, Pilar  
 8 TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
 9 FILE REFERENCE: GC617-2  
 10 CURRENT APPLICATION NUMBER: US/09/831,123  
 11 CURRENT FILING DATE: 2001-04-11  
 12 PRIOR APPLICATION NUMBER: US 60/137,149  
 13 PRIOR FILING DATE: 2000-04-14  
 14 NUMBER OF SEQ ID NOS: 117  
 15 SOFTWARE: Pas-SEQ for Windows Version 4.0  
 16 SEQ ID NO 92  
 17 LENGTH: 9  
 18 TYPE: PPT  
 19 ORGANISM: Artificial Sequence  
 20 FEATURE:  
 21 OTHER INFORMATION: peptides screened from a phage display random  
 22 OTHER INFORMATION: peptide library  
 23 US-09-832 703-92

Query Match: 44.2%, Score 23; DB 9; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5,8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSTT 4  
 DB 1 CSTT 4

RESULT 8  
 US-10-303-331-92  
 1 Sequence 92, Application US/1030331  
 2 Publication No. US2003052976A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Janssen, Giselle G.  
 5 APPLICANT: Murray, Christopher J.  
 6 APPLICANT: Kinetzky, Deborah S.  
 7 TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
 8 FILE REFERENCE: GC617-3  
 9 CURRENT APPLICATION NUMBER: US/10/303,231  
 10 CURRENT FILING DATE: 2002-11-25  
 11 PRIOR APPLICATION NUMBER: US 09/842,723  
 12 PRIOR FILING DATE: 2001-04-11  
 13 PRIOR APPLICATION NUMBER: US 60/197,259  
 14 PRIOR FILING DATE: 2000-04-14  
 15 NUMBER OF SEQ ID NOS: 125  
 16 SOFTWARE: PasSEQ for Windows Version 4.0  
 17 SEQ ID NO 92  
 18 LENGTH: 9  
 19 TYPE: PPT  
 20 ORGANISM: Artificial Sequence  
 21 FEATURE:  
 22 OTHER INFORMATION: peptides screened from a phage display random  
 23 OTHER INFORMATION: peptide library  
 24 US-10-303 331-92

Query Match: 44.2%, Score 23; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5,8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSTT 4  
 DB 1 CSTT 4

RESULT 9  
 US-09-833 39-119  
 1 Sequence 119, Application US/0983339  
 2 Publication No. US20030175960A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Tureci, Ozlem  
 5 APPLICANT: Sahin, Ugur  
 6 APPLICANT: Pfreundschuh, Michael  
 7 TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof  
 8 FILE REFERENCE: JUC 5622.1  
 9 CURRENT APPLICATION NUMBER: US/09/833,039  
 10 CURRENT FILING DATE: 2001-04-12  
 11 PRIOR APPLICATION NUMBER: US 09/409,455  
 12 PRIOR FILING DATE: 1999-09-30  
 13 PRIOR APPLICATION NUMBER: US 09/344,340  
 14 PRIOR FILING DATE: 1999-06-25  
 15 PRIOR APPLICATION NUMBER: US 09/105,839  
 16 PRIOR FILING DATE: 1999-06-26  
 17 PRIOR APPLICATION NUMBER: US 08/851,130  
 18 PRIOR FILING DATE: 1997-05-05  
 19 NUMBER OF SEQ ID NOS: 143  
 20 SEQ ID NO 119  
 21 LENGTH: 9  
 22 TYPE: PPT  
 23 ORGANISM: Homo sapiens  
 24 OTHER INFORMATION: Hom sapiens  
 25 US-09-833 39-119

Query Match: 44.2%, Score 23; DB 12; Length 9;



1 SOFTWARE: Patent in version 3.2  
2 SEQ ID NO: 12  
3 LENGTH: 10  
4 TYPE: PRT  
5 ORGANISM: Homo sapiens  
6 US 10-164 614-12

Query Match: 44.2% Score 21; DB 12; Length 10;  
Best local similarity: 55.6% Pred. No. 5, 60, 52;  
Matches: 5; Conservative 1; Mismatches 3; In-bits 3; Gaps 0;

QY 2 STQCEHLE 10  
DB : ATPMEAFLE 9

RESULT 15  
US-09-909-618-61  
1 Sequence 61; Application US/0909549  
2 Publication No. US2003059895A;  
3 GENERAL INFORMATION:  
4 APPLICANT: Maty Paris  
5 APPLICANT: Via M. Chailita-Bid  
6 APPLICANT: Steve Chappell Mitchell;  
7 APPLICANT: Camille E.H. Atar  
8 APPLICANT: Arthur R. Raitano  
9 APPLICANT: Ava Jakobovits  
10 TITLE OF INVENTION: 124P508: A TISSUE SPECIFIC PROTEIN  
11 TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANTERS  
12 FILE REFERENCE: 124-35USC2  
13 CURRENT APPLICATION NUMBER: US/09/603,618  
14 CURRENT FILING DATE: 2001-03-14  
15 NUMBER OF SEQ ID NOS: 746  
16 SOFTWARE: FastSeq for Windows Version 4.0  
17 SEQ ID NO: 61  
18 LENGTH: 9  
19 TYPE: PRT  
20 ORGANISM: Homo sapiens  
US-09-909-618-61

Query Match: 42.3% Score 20; DB 11; Length 10;  
Best local similarity: 80.0% Pred. No. 5, 80, 59;  
Matches: 4; Conservative 1; Mismatches 3; In-bits 3; Gaps 0;

QY 1 EUEIA 10  
DB : EUEIA 9

Search completed: November 5, 2003, 10:14:27  
Job time: 24 secs



Alt	Score	Query	Match	Length	DB	ID	Description
1	24	49	1	9	3	US-08-704-341-3	Sequence 1, Appl
2	25	49	1	9	4	US-08-643-141A-12	Sequence 1, Appl
3	25	49	1	9	4	US-09-431-341-12	Sequence 1, Appl
4	26	49	1	9	4	US-09-343-341-12	Sequence 1, Appl
5	27	44	2	10	4	US-09-144-341-12	Sequence 1, Appl
6	27	44	2	10	4	US-08-444-511A-9	Sequence 19, Appl
7	27	44	2	10	3	US-08-532-662-29	Sequence 29, Appl
8	27	44	2	10	4	US-09-664-235-49	Sequence 29, Appl
9	27	44	2	10	4	US-08-734-043B-9	Sequence 9, Appl
10	27	42	3	9	3	US-09-254-354-143	Sequence 143, Appl
11	27	42	3	9	3	US-09-342-17-343	Sequence 43, Appl
12	27	40	4	7	2	US-08-369-54-9	Sequence 9, Appl
13	27	40	4	7	3	US-09-128-47-9	Sequence 12, Appl
14	27	40	4	9	1	US-08-615-141-13	Sequence 15, Appl
15	27	40	4	9	1	US-08-193-143A-13	Sequence 16, Appl
16	27	40	4	9	2	US-08-290-268-19	Sequence 19, Appl
17	27	40	4	9	2	US-08-386-233-26	Sequence 19, Appl
18	27	40	4	9	4	US-09-163-740-18	Sequence 18, Appl
19	27	40	4	10	2	US-08-764-643-12	Sequence 120, Appl
20	27	40	4	10	3	US-08-573-235-120	Sequence 120, Appl
21	27	40	4	10	3	US-08-373-325-104	Sequence 108, Appl
22	27	40	4	10	3	US-09-244-238A-12	Sequence 120, Appl
23	27	40	4	10	3	US-09-331-364-11	Sequence 41, Appl
24	27	40	4	10	3	US-09-143-728A-8	Sequence 42, Appl
25	27	40	4	10	3	US-09-5461-637-115	Sequence 120, Appl
26	27	40	4	10	4	US-09-540-390-120	Sequence 120, Appl
27	27	40	4	10	4	US-09-540-390-120	Sequence 120, Appl



NUMBER OF SEQ ID NOS: 132  
 SEQ ID NO: 119  
 LENGTH: 9  
 TYPE: PAT  
 ORGANISM: Homo sapiens  
 US-09-914-088-24

Query Match 44.2% Score 23 DB 4 Length 9  
 Best Local Similarity 55.6% Pred No. 2.3e+02  
 Matches 5 Conservative 1 Mismatches 1 Indels 0 Gaps 0

QY 2 STTQELIA 10  
 | | | | |  
 Db 1 ATNPAELA 9

RESULT 6  
 US-08-441-513A-9  
 Sequence 9, Application US/08441513A  
 Patent No. 5981480  
 GENERAL INFORMATION:  
 APPLICANT: Utef, Roman  
 APPLICANT: Presta, Leonard G.  
 APPLICANT: Winslow, John W.  
 TITLE OF INVENTION: Patropic Neurotrophic Factors  
 NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Genetech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 SEQID TYPE: 1.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winntatic (Genetech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/441-513A  
 FILING DATE: 15-May-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/25917  
 FILING DATE: 01-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: TURNER, P.D., T-0001  
 REGISTRATION NUMBER: 36,700  
 REFERENCE NUMBER: 802000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-225-8674  
 TELEFAX: 650-225-9881  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-441-513A-9

Query Match 44.2% Score 23 DB 4 Length 9  
 Best Local Similarity 55.6% Pred No. 2.3e+02  
 Matches 5 Conservative 1 Mismatches 1 Indels 0 Gaps 0

QY 2 STTQELIA 10  
 | | | | |  
 Db 1 ATNPAELA 9

RESULT 7  
 US-08-581-662-29  
 Sequence 29, Application US/08581662  
 Patent No. 6101215  
 GENERAL INFORMATION:

APPLICANT: Gao, Wei-Qiang  
 TITLE OF INVENTION: Treatment of Balance Impairments  
 FILE REFERENCE: P09F1  
 CURRENT APPLICATION NUMBER: US/08/581,662  
 CURRENT FILING DATE: 1995 12 29  
 NUMBER OF SEQ ID NOS: 36  
 SEQ ID NO: 29  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-08-581-662-29

Query Match 44.2% Score 23 DB 3 Length 10  
 Best Local Similarity 40.3% Pred No. 2.3e+02  
 Matches 4 Conservative 0 Mismatches 1 Indels 0 Gaps 0

QY 1 CSTTQ 5  
 | | | | |  
 Db 2 CRTTQ 6

RESULT 8  
 US-09-664-295-29  
 Sequence 29, Application US/09664295  
 Patent No. 6429196  
 GENERAL INFORMATION:  
 APPLICANT: Gao, Wei-Qiang  
 TITLE OF INVENTION: Treatment of Balance Impairments  
 FILE REFERENCE: GENENT.051C1  
 CURRENT APPLICATION NUMBER: US/09/664,295  
 CURRENT FILING DATE: 2000-09-18  
 PRIOR APPLICATION NUMBER: US 08/581,662  
 PRIOR FILING DATE: 1995 12-29  
 NUMBER OF SEQ ID NOS: 37  
 SEQ ID NO: 29  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-664-295-29

Query Match 44.2% Score 23 DB 4 Length 10  
 Best Local Similarity 80.3% Pred No. 2.3e+02  
 Matches 4 Conservative 0 Mismatches 1 Indels 0 Gaps 0

QY 1 CSTTQ 5  
 | | | | |  
 Db 2 CRTTQ 6

RESULT 9  
 US-08-794-049-7  
 Sequence 7, Application US/08794049  
 Patent No. 6503728  
 GENERAL INFORMATION:  
 APPLICANT: Utef, Roman  
 APPLICANT: Presta, Leonard G.  
 APPLICANT: Winslow, John W.  
 TITLE OF INVENTION: Patropic Neurotrophic Factors  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Genetech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 SEQID TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winntatic (Genetech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/794,049

? FILING DATE: 01-Feb-1997  
 ? CLASSIFICATION: 435  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: 08/253939  
 ? FILING DATE: 03 JUN 1994  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: TORCHIA, PH.D., Timothy E.  
 ? REGISTRATION NUMBER: 36,700  
 ? REFERENCE/DOCKET NUMBER: P09080  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: 650/225-8674  
 ? TELEFAX: 650/302-9891  
 ? INFORMATION FOR SEQ ID NO: 9:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 10 amino acids  
 ? TYPE: Amino Acid  
 ? TOPOLOGY: linear  
 ?  
 US 09-914-088-24

Query Match 44.2% Score 23; DB 4; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDTQ 5  
 Db 2 CDTQ 4

RESULT 12  
 US 09-914-088-24  
 ? Sequence 143, Application US/032554-4  
 ? Patent No. 6174687  
 ? GENERAL INFORMATION:  
 ? APPLICANT: RUSGALLI, EKKI  
 ? APPLICANT: PASQUALINI, RENAUD  
 ? APPLICANT: RAJOTTE, DAVID  
 ? TITLE OF INVENTION: Methods of identifying and removing nucleic acids using  
 ? TITLE OF INVENTION: Membrane Disposition  
 ? FILE REFERENCE: P. 1, 343  
 ? CURRENT APPLICATION NUMBER: US/09-914-088-24  
 ? FILING DATE: 1999-02-26  
 ? EARLIER APPLICATION NUMBER: 09/145,111  
 ? EARLIER FILING DATE: 1998-03-13  
 ? NUMBER OF SEQ ID NOS: 452  
 ? SOFTWARE: Patent In Ver. 2.0  
 ? SEQ ID NO: 143  
 ? LENGTH: 9  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence  
 ?  
 US-09-914-088-24

Query Match 42.3% Score 22; DB 4; Length 9;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDTQ 5  
 Db 1 CDTQ 4

RESULT 11  
 US 09-914-088-24  
 ? Sequence 143, Application US/090421-2  
 ? Patent No. 6232187  
 ? GENERAL INFORMATION:  
 ? APPLICANT: RUSGALLI, EKKI  
 ? APPLICANT: PASQUALINI, RENAUD  
 ? TITLE OF INVENTION: Molecules that bind to and inhibit the function of  
 ? TITLE OF INVENTION: Tissues  
 ? FILE REFERENCE: P. 1, 2842  
 ? CURRENT APPLICATION NUMBER: US/09-914-088-24

? CURRENT FILING DATE: 1998-03-13  
 ? NUMBER OF SEQ ID NOS: 436  
 ? SOFTWARE: Patent In Ver. 2.0  
 ? SEQ ID NO: 143  
 ? LENGTH: 9  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ?  
 US-09-914-088-24

Query Match 42.3% Score 22; DB 4; Length 9;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CDTQ 5  
 Db 1 CDTQ 5

RESULT 12  
 US-08-869-506-9  
 ? Sequence 9, Application US/08869506  
 ? Patent No. 5827710  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Uchida, Kohji  
 ? APPLICANT: Matsukawa, Hirokazu  
 ? APPLICANT: Matsuo, Yushi  
 ? APPLICANT: Furuta, Teyosi  
 ? TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN  
 ? TITLE OF INVENTION: LACTATE DEHYDROGENASE  
 ? NUMBER OF SEQUENCES: 11  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: NIXON S VANDERHAYE P.C.  
 ? STREET: 1100 N. 5827710th Glete Rd. 8th floor  
 ? CITY: Arlington  
 ? STATE: VA  
 ? COUNTRY: USA  
 ? ZIP: 22201-4741  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent In Release #1.0, Version #1.30  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/869,506  
 ? FILING DATE: 05-JUN-1997  
 ? CLASSIFICATION: 435  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: JP 7397/1994  
 ? FILING DATE: 29 MAR 1996  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Crawford, Arthur R.  
 ? REGISTRATION NUMBER: 25,327  
 ? REFERENCE/DOCKET NUMBER: 159-41  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: 703-816-4000  
 ? TELEFAX: 703-816-4100  
 ? INFORMATION FOR SEQ ID NO: 9:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 7 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS:  
 ? TOPOLOGY: linear  
 ?  
 US-08-869-506-9

Query Match 40.4% Score 21; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CDTQ 5  
 Db 1 CDTQ 4

RESULT 11  
 US-08-869-506-9  
 ? Sequence 9, Application US/08869506  
 ? Patent No. 5827710  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Uchida, Kohji  
 ? APPLICANT: Matsukawa, Hirokazu  
 ? APPLICANT: Matsuo, Yushi  
 ? APPLICANT: Furuta, Teyosi  
 ? TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN  
 ? TITLE OF INVENTION: LACTATE DEHYDROGENASE  
 ? NUMBER OF SEQUENCES: 11  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: NIXON S VANDERHAYE P.C.  
 ? STREET: 1100 N. 5827710th Glete Rd. 8th floor  
 ? CITY: Arlington  
 ? STATE: VA  
 ? COUNTRY: USA  
 ? ZIP: 22201-4741  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent In Release #1.0, Version #1.30  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/869,506  
 ? FILING DATE: 05-JUN-1997  
 ? CLASSIFICATION: 435  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: JP 7397/1994  
 ? FILING DATE: 29 MAR 1996  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Crawford, Arthur R.  
 ? REGISTRATION NUMBER: 25,327  
 ? REFERENCE/DOCKET NUMBER: 159-41  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: 703-816-4000  
 ? TELEFAX: 703-816-4100  
 ? INFORMATION FOR SEQ ID NO: 9:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 7 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS:  
 ? TOPOLOGY: linear  
 ?  
 US-08-869-506-9

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DB      1 3 PAGE 6
RESULT 13
US-09-128-967 9
Sequence 9, Application US/09128967
Patent No. 605/141
GENERAL INFORMATION:
APPLICANT: Uchida, Kohji
APPLICANT: Matsukawa, Hirokazu
APPLICANT: Matsuo, Yusei
APPLICANT: Fujita, Tetsuo
TITLE OF INVENTION: DNA ENCODING THE SUBUNIT P AND Q
NUMBER OF INVENTION: 1
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKUN & VANDERHYE P.C.
STREET: 1100 No. 605/141th Glens Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09128-967
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/869,576
FILING DATE: 05-JUN-1997
APPLICATION NUMBER: JP 73797/1996
FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,317
REFERENCE/DOCKET NUMBER: 159 4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLGY: linear
MODEM TYPE: 10-Base
US-09-128-967 9
Query Match 40.4% Score 21, DB 1, Length 9;
Best Local Similarity 100.0% Prod. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;
CY 5 QSEQ 6
DB 3 QSEQ 6
RESULT 14
US 08-615-181-10
Sequence 10, Application US/08615181
Patent No. 5756666
GENERAL INFORMATION:
APPLICANT: MASAFUMI, TAKIUCHI
APPLICANT: MIWA, KIYOSHI
TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING AN ANTI-
TITLE OF INVENTION: RESPONSE TO HIV AND AIDS ALONE FROM HIV PREVENTING AND
TITLE OF INVENTION: CURING AIDS
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 576/164th Clark Street, Suite 800
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,338A
FILING DATE: 11 JAN 1994
US-08-615-181-10
Query Match 40.4% Score 21, DB 1, Length 9;
Best Local Similarity 66.7% Prod. No. 2.5e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CY 4 TSEQEL 9
DB 4 TSEQEL 9
RESULT 15
US-08-615-181-10
Sequence 15, Application US/08191338A
Patent No. 5761164
GENERAL INFORMATION:
APPLICANT: Galenoff, Emanuel
TITLE OF INVENTION: Immunogenic Cancer Proteins and Peptides
TITLE OF INVENTION: and Method of Use
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 576/164th Clark Street, Suite 800
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,338A
FILING DATE: 11 JAN 1994

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1 CLASSIFICATION: 436
2 ATTORNEY/AGENT INFORMATION:
3 NAME: No. 5763164thrup, Thomas E.
4 REGISTRATION NUMBER: 33,268
5 REFERENCE/DOCKET NUMBER: 04-10-02
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: 312-744-0090
8 TELEFAX: 312-755-4499
9 INFORMATION FOR SEQ ID NO: 36:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 3 amino acids
12 TYPE: amino acid
13 STRANDEDNESS: single
14 TOPOLOGY: linear
15 MOLECULE TYPE: peptide
16 FEATURE:
17 NAME/KEY: Xaa
18 LOCATION: 5
19 IDENTIFICATION METHOD: Phosphorylated Threonine
20 US-08-191338A-36

Query Match 40.4% Score 217 DB 11 Length 91
Post Local Similarity 57.1% Prol No. 2 Sequences
Matches 4, Conservative 2, Mismatches 11 Indels 0 Gaps 0

CY 3 TPOGRL 9
IR 1 STEEXL 7

Search completed: November 5, 2003, 11:36:12
Seq ID# 36: 123333 3025

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GenCore version: 5.1.6  
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OX protein - protein search, using SW model

Run on: November 5, 2003, 18:41:05, Search time: 0 seconds  
(without alignment)  
02:09:44 Mapped cell updated

Title: US 09 914-088-26

Perfect score: 66

Sequence: 1 CSQKWLSDPT 11

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 28108 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 1106

Minimum DB seq length: 0

Maximum DB seq length: 11

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 751

1: PIR1

2: PIR2

3: PIR3

4: PIR4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	34.8	10	2 A49187	gonadotropin-releasing hormone
2	21	31.8	11	2 PT0273	lg heavy chain CRD
3	20	30.3	10	1 RH503	penicillin
4	20	30.3	10	1 RH503	penicillin
5	20	30.3	10	1 RH503	penicillin
6	20	30.3	10	1 RH503	penicillin
7	20	30.3	10	1 A6174	gonadotropin-releasing hormone
8	20	30.3	10	2 B46510	gonadotropin-releasing hormone
9	20	30.3	10	2 A46316	gonadotropin-releasing hormone
10	20	30.3	10	2 A21114	gonadotropin-releasing hormone
11	19	28.8	10	2 PQ0177	gonadotropin-releasing hormone
12	19	28.8	10	2 A60547	gonadotropin-releasing hormone
13	19	28.8	11	2 C59111	protein tyrosine kinase
14	19	28.8	11	2 T17041	cytochrome-c oxidase
15	18	27.3	6	2 S29881	Na/K-exchanging
16	18	27.3	7	2 PH602	lg heavy chain V-D-Jr
17	18	27.3	10	2 PT0289	lg heavy chain CRD
18	18	27.3	11	2 S32575	intracellular protein
19	17	25.8	8	2 XGH02U	the glycoprotein
20	16	24.2	7	2 PT0576	T-cell receptor beta
21	16	24.2	8	2 T14524	hypothetical protein
22	16	24.2	9	2 A43843	cell surface adhesion
23	16	24.2	9	2 PT0211	lg heavy chain CRD
24	16	24.2	10	2 S27573	cytochrome-c oxidase
25	16	24.2	10	2 T17054	cytochrome-c oxidase
26	16	24.2	11	2 T17018	cytochrome-c oxidase
27	15	22.7	5	2 PT0672	T-cell receptor beta
28	15	22.7	7	2 S33567	tubulin beta-3 chain
29	15	22.7	7	4 A58725	viridoxin - dextran

30	15	22.7	8	2 S59622	metallothionein is
31	15	22.7	9	2 A60108	exotoxin A - Strept
32	15	22.7	9	2 PT0324	lg heavy chain CRD
33	15	22.7	9	2 A37227	macrophage chemotax
34	15	22.7	9	2 PT0562	T-cell receptor be
35	15	22.7	10	2 T40332	trpE protein - Bac
36	15	22.7	10	2 T17075	cytochrome-c oxidase
37	15	22.7	10	2 T17563	cytochrome-c oxidase
38	15	22.7	10	2 T12325	cytochrome-c oxidase
39	15	22.7	10	2 T12329	cytochrome-c oxidase
40	15	22.7	10	2 T14212	cytochrome-c oxidase
41	15	22.7	10	2 T14215	cytochrome-c oxidase
42	15	22.7	10	2 T14223	cytochrome-c oxidase
43	15	22.7	11	2 A31571	follicle-stimulating h
44	15	22.7	11	2 B41946	T-cell receptor ga
45	15	22.7	11	2 S53436	beta-D-galactosidase

ALIGNMENTS

RESULT 1

A49187  
gonadotropin-releasing hormone 11: sea lamprey  
C:Species: Petromyzon marinus (sea lamprey)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 03-Mar-1995  
C:Accession: A49187  
R:Swier, S.A.; Chiang, Y.C.; Lomas, S.; Conlon, J.M.  
Endocrinology 132, 1125-1131, 1993  
A:Title: Primary structure and biological activity of a third gonadotropin-releasing hormone  
A:Reference number: A49187; MUI:9178316; PMID:8440174  
A:Accession: A49187  
A:Status: preliminary  
A:Molecule type: Protein  
A:Residues: 1-10 <SOW>  
A:Experimental source: brain  
A:Note: sequence extracted from NCB: backbone (NCBI:126381)

Query Match: 34.8%; Score 23; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 6.9e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KHWLSD 9  
DB 1 EHWSD 6

RESULT 2

PT0273  
lg heavy chain CRD region (clone 1-109A) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0273  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Share, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: PT0273; MUI:91108137; PMID:1895102  
A:Accession: PT0273  
A:Molecule type: DNA  
A:Residues: 1-11 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match: 31.8%; Score 21; DB 2; Length 11;  
Best Local Similarity 37.5%; Pred. No. 1.6e+03;  
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 QKWLSDR 10  
DB 1 ESRKSPDF 8

RESULT 3

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Query Map: DB 17 Length 10;
Best fit found at position 16.38 Prog No. 2,24+01;
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Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KHW 6  
DB 1 QHW 3

RESULT 8  
gonadoliberin 11 - spiny dogfish  
N/A: alternate names: gonadotropin-releasing hormone  
C: Species: *Squalus acanthias* (spiny dogfish)  
C: Date: 06 Jan 1999 #sequence\_revision 02 Jan 1999 #text\_change 14 Jan 2003  
C: Accession: B46030  
R: Lovejoy, D.A.; Fischer, W.H.; Nganvorachon, S.; Chang, A.C.; Nukushnik, C.S.; Peter, R.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992  
A: Title: Distinct sequence of gonadotropin releasing hormone (GHRH) in dogfish brain pro  
A: Reference number: A46030; MUID:92335360; PMID:1631133  
A: Accession: B46030  
A: Status: Preliminary  
A: Molecule type: protein  
A: Residues: 1-10 <CON>  
A: Superfamily: gonadoliberin  
C: Keywords: hormone; pyroglutamic acid  
F:10/Modified site: pyroglutamate carboxylic acid (pin) #status experimental

Query Match 30.3%; Score 20; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.2e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KHW 6  
DB 1 QHW 3

RESULT 9  
gonadoliberin 1 - spiny dogfish  
N/A: alternate names: gonadotropin-releasing hormone  
C: Species: *Squalus acanthias* (spiny dogfish)  
C: Date: 06 Jan 1999 #sequence\_revision 06 Jan 1999 #text\_change 14 Dec 1998  
C: Accession: A46030  
R: Lovejoy, D.A.; Fischer, W.H.; Nganvorachon, S.; Chang, A.C.; Nukushnik, C.S.; Peter, R.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992  
A: Title: Distinct sequence of gonadotropin releasing hormone (GHRH) in dogfish brain pro  
A: Reference number: A46030; MUID:92335360; PMID:1631133  
A: Accession: A46030  
A: Status: Preliminary  
A: Molecule type: protein  
A: Residues: 1-10 <CON>  
C: Keywords: hormone; pyroglutamic acid  
F:10/Modified site: pyroglutamate carboxylic acid (pin) #status experimental

Query Match 30.3%; Score 20; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.2e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KHW 6  
DB 1 QHW 3

RESULT 10  
gonadoliberin - chum salmon  
C: Species: *Oncorhynchus keta* (chum salmon)  
C: Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 14 Jan 1999  
C: Accession: A21114  
R: Sherwood, N.J.; Eiden, L.; Brownstein, W.J.; Brownstein, M.J.; Vale, W.  
Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983  
A: Title: Characterization of a teleost gonadotropin releasing hormone  
A: Reference number: A21114; MUID:8319-143; PMID:641367  
A: Accession: A21114

A: Status: Preliminary  
A: Molecule type: protein  
A: Residues: 1-10 <SHE>

Query Match 30.3%; Score 20; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.2e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KHW 6  
DB 1 QHW 3

RESULT 11  
PQ0177  
neuroedin 1 - laughing frog  
C: Species: *Rana ridibunda* (laughing frog)  
C: Date: 23 Nov 1991 #sequence\_revision 23 Nov 1991 #text\_change 11-Jan-2003  
C: Accession: PQ0177  
R: Conlon, J.M.; O'Hare, F.; Vaudry, H.  
Biochem. Biophys. Res. Commun. 178, 526-530, 1991  
A: Title: Primary structures of the bombesin-like neuropeptides in frog brain show that  
A: Reference number: PQ0177; MUID:91315477; PMID:1859413  
A: Accession: PQ0177  
A: Molecule type: protein  
A: Residues: 1-10 <CON>  
A: Experimental source: brain  
C: Superfamily: gastrin releasing peptide  
C: Keywords: amidated carboxyl end  
F:10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 28.8%; Score 19; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KHW 6  
DB 3 KHW 4

RESULT 12  
A60647  
neuroedin 1 - bovine  
C: Species: *Bos primigenius taurus* (cattle)  
C: Date: 14 May 1993 #sequence\_revision 14-May-1993 #text\_change 07-May-1999  
C: Accession: A60647  
R: Demaire, S.; Trifalco, E.M.; Chouinard, L.; Cecyre, D.; Dessureault, J.; Metcalf, P.J.  
Peptides 17, 355-360, 1999  
A: Title: Structure, identification, subcellular localization and secretion of bovine ad  
A: Reference number: A60647; MUID:9931342; PMID:2755976  
A: Accession: A60647  
A: Molecule type: protein  
A: Residues: 1-10 <CON>  
A: Note: this neuropeptide was purified from secretory granules of cells in the adrenal  
C: Superfamily: gastrin releasing peptide  
C: Keywords: adrenal gland; neuropeptide

Query Match 28.8%; Score 19; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KHW 6  
DB 3 KHW 4

RESULT 13  
C59151  
protein tyrosine kinase (EC 2.7.1.112) - jack bean (fragment)  
C: Species: *Canavalia ensiformis* (jack bean)  
C: Date: 07 Dec 1999 #sequence\_revision 07 Dec 1999 #text\_change 04 Feb-2003  
C: Accession: C59151  
R: Oliveira, A.B.A.; Machado, G.L.T.; Gomes, V.M.; Xavier-Neto, C.; Pereira, A.C.P.; Vie



GenCore version 5.1.6  
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OM protein - protein search, using sw mode.

Run on: November 5, 2003, 18:17:24 ; Search time: 11 seconds  
(without alignment)  
47,027 Million cell updates/sec

Title: US-09-914-088-26

Perfect score: 66

Sequence: 1 CSQHWLSDRF 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 44

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post processing: Minimum Match 3%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41\*

Pred. No. is the number of results predicted by choice to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Length	DB ID	Description
1	23	34.8	10	1 GON3_PETMA	P04546 periplaneta
2	20	30.3	9	1 COW_CONVE	P03047 conus ventr
3	20	30.3	10	1 GON3_ALAY	P00041 alligator m
4	20	30.3	10	1 GON3_CHEP	P03677 cheilosoma
5	20	30.3	10	1 GON3_CUPE	P01749 cupeia pall
6	20	30.3	10	1 GON3_CHEP	P03677 cheilosoma
7	20	30.3	10	1 GON3_CHEP	P03677 cheilosoma
8	20	30.3	10	1 GON3_CHEP	P03677 cheilosoma
9	20	30.3	10	1 GON3_CHEP	P03677 cheilosoma
10	19	28.4	10	1 GON3_CHEP	P03677 cheilosoma
11	18	27.3	11	1 GON3_CHEP	P03677 cheilosoma
12	18	27.3	11	1 GON3_CHEP	P03677 cheilosoma
13	17	25.8	6	1 GLU2_HUMAN	P07100 homo sapien
14	17	25.8	10	1 MP2_MICO	P03004 macropoditis
15	16	24.3	10	1 FAR5_MACH	P03074 macrobrachi
16	15	22.7	8	1 FAR3_HUMAN	P04485 homarus ame
17	14	21.2	7	1 BRP1_HUMAN	P08803 conus imper
18	13	19.7	5	1 UCL1_MOUSE	P08619 mus musculu
19	13	19.7	6	1 E101_HUMAN	P03004 macropoditis
20	13	19.7	7	1 FAR2_ASSEN	P03004 macropoditis
21	13	19.7	8	1 CKN1_MATE	P03004 macropoditis
22	13	19.7	9	1 OXY1_SALU	P03004 macropoditis
23	13	19.7	10	1 BRP2_HUMAN	P08803 conus imper
24	13	19.7	10	1 BRP2_HUMAN	P08803 conus imper
25	13	19.7	10	1 CAER_HUMAN	P03004 macropoditis
26	13	19.7	10	1 URAG_HUMAN	P03004 macropoditis
27	13	19.7	11	1 CAV1_HUMAN	P03004 macropoditis
28	13	19.7	11	1 CEP1_HUMAN	P03004 macropoditis
29	13	19.7	11	1 CXL1_HUMAN	P03004 macropoditis
30	12	18.2	7	1 TFP1_PANCA	P03004 macropoditis
31	12	18.2	8	1 COW2_COW	P03004 macropoditis
32	12	18.2	8	1 FAR2_MACH	P03004 macropoditis
33	12	18.2	8	1 HTP1_PETMA	P04546 periplaneta

34	12	18.2	8	1 HTP2_PETMA	P04549 periplaneta
35	12	18.2	8	1 HTP1_TENNO	P25419 tenebrio mo
36	12	18.2	9	1 LITQ_LITAU	P08945 litorea aur
37	12	18.2	9	1 NEUX_HUMAN	P04277 homo sapien
38	12	18.2	10	1 AEG1_AGRAR	P03465 agriocyba ae
39	12	18.2	10	1 AKW1_LOCM	P01626 locusta mig
40	12	18.2	10	1 APE_CARG	P04474 capnocyph
41	12	18.2	10	1 HTP1_ROMM	P18110 romalea mic
42	12	18.2	10	1 HTP2_CARMO	P11385 carausius m
43	12	18.2	10	1 TKU1_UREUN	P04751 urechis uni
44	12	18.2	10	1 TPIS_NICPL	P19118 nicotiana gl
45	12	18.2	11	1 MGS_THETS	P41989 thecmyzon

#### ALIGNMENTS

RESULT 1  
GON3\_PETMA STANDARD; PRT; 10 AA.  
AC P04546;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update);  
DE 28-FEB-2003 (Rel. 41, Last annotation update);  
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III)  
DE (Mallotian III);  
CS Petromyzon marinus (Sea lamprey);  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
CC Petromyzontiformes; Petromyzontidae; Petromyzon.  
CX NCBI\_TaxID=7757;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=93178316; PubMed=8443174;  
RA Sower S.A., Chiang Y. C., Lovas S., Conlon J.M.;  
RT "Primary structure and biological activity of a third gonadotropin  
releasing hormone from lamprey brain";  
RL Endocrinology 132:125-131(1993);  
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates  
the secretion of both luteinizing and follicle-stimulating  
hormones.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the GNRH family.  
DR InterPro: IPR002012; GNRH.  
DR Pfam: PF00446; GNRH; 1.  
DR PROSITE: PS00473; GNRH; 1.  
KW Hormone; Amidation; Hypothalamus; Pyroglutamate; Pyroglutamate carboxylic acid.  
FT MISC\_FEATURE 1..13 PYROGLUTAMATE CARBOXYLIC ACID.  
FT MISC\_FEATURE 10..13 AMIDATION.  
SQ SEQUENCE (10 AA): 1277 MW: 284536237AAIF5A3 CRC64:  
Query Match 34.8% Score 23; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2; E+02;  
Matches 3; Conservative 1; Mismatches 2; Index 0; Gaps 0;

QY 4 KHWLSD 9  
DB 1 QHWSHD 6  
RESULT 2  
COW\_CONVE STANDARD; PRT; 9 AA.  
AC P03047;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update);  
DE Contryphan-Vn.  
CS Conus ventricosus (Mediterranean cone);  
CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
CC Apogastropoda; Caenogastropoda; Sericoconcha; Hypsogastropoda;  
CC Neogastropoda; Conus; Conidae; Conus.  
CX NCBI\_TaxID=117762;

```

BN SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RP TISSUE VENDOR:
RX MEDLINE 21547783; PubMed:1688955;
RA Yassine G.B., Schenina M.B., Ascerzi P., Pollicella P.,
RT "Contryphan-Vn: a novel peptide from the venom of the Western blue
RT scorpion Centruroides vittosus."
RP Biochem. Biophys. Res. Commun. 289:908-913(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1038.6; METHOD: MALDI
CC -1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Amidation; Diamine acid.
FT DISULFID 1 9
FT MOD RES 5 3 D-TRYPTOPHAN.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1091 MW; 803867612367686A C5664.

Query Match 10.3%; Score 20; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1; Gaps 0;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 1 CSCREW 6
DB 3 CPKREW 9

RESULT 3
CONS ALIMI
ID GONI ALIMI STANDARD; PRT; 10 AA.
AC P23411 P23407.
DT 01 FEB 1991 (Rev. 17, Last sequence update).
DT 24 FEB 2003 (Rev. 41, Last annotation update).
DE Gonadoliberin 1: Gonadotropin-releasing hormone 1 (GNRH-1);
DE GnRH.
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Cyprinodontiformes; Poeciliidae; Poeciliinae;
OX NCBI_TaxID 8445;
RN 1;
PF SEQUENCE.
RP TISSUE Brain;
RX MEDLINE 9152138; PubMed:182082;
RA Laverney D.A., Fischer W.H., Parker D.B., McVey J.E., Park M.,
RA Lavoie N., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator Alligator mississippiensis."
RP J. Neuroendocrinol. 16:119-125(2004).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
CC -1- MASS SPECTROMETRY: MW=1246.56; METHOD: MALDI.
CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
KW Peptide; Amidation; Pyroglutamate; Carboxylic acid.
FT MOD RES 1 1 PYROGLUTAMINE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 10 AA; 1264 MW; 284B3639DB5A5A3 CRC64;

Query Match 10.3%; Score 20; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 6; Gaps 0;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 4 KRW 6
DB 1 QHW 3

RESULT 5
CONS CLUPA
ID GONI CLUPA STANDARD; PRT; 10 AA.
AC P87347 P87347.
DT 16 OCT 2001 (Rev. 41, Last sequence update).
DT 28 FEB 2003 (Rev. 41, Last annotation update).
DE Gonadoliberin 1: Gonadotropin-releasing hormone 1 (GNRH-1) (LR RH);
DE GnRH.
OS Clupea pallasi (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neocyprinidae; Teleostei; Clupeomorpha; Clupeidae;
CC Clupea;
OX NCBI_TaxID=10724;
RN 1;
PF SEQUENCE, AND FUNCTION.
RP TISSUE Brain, and pituitary;
RX MEDLINE 2011435; PubMed:1065929;
RA Carlsfeld J., Powell J.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring."
RP Endocrinology 141:525-532(2002).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
OR InterPro: IPR005512; GNRH;
OR Pfam: PF00446; GNRH;

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AC P80677;
DT 01 NOV 1997 (Rev. 35, Created);
DT 01 NOV 1997 (Rev. 35, Last sequence update);
DT 28 FEB 2003 (Rev. 41, Last annotation update);
DE Gonadoliberin 1: Gonadotropin-releasing hormone 1 (GNRH-1);
DE GnRH.
OS Chelysoma productum.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Ascidacea; Enterozoa;
OC Phlebobranchia; Corellidae; Chelyosoma.
OX NCBI_TaxID=71177;
RN 1;
PF SEQUENCE.
RX MEDLINE=6411567; PubMed=8814821;
RA Powell J.F.F., Reska Skinner S.M., Prakash M.C., Fischer W.H.,
RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;
RT "Two new forms of gonadotropin-releasing hormone in a protochordate
RT and the evolutionary implications."
RP Proc Natl Acad Sci USA 93:10461-10464(1996).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: GNRH NEURONS LIE WITHIN BLOOD SINUSES CLOSE TO
CC THE GONADS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING
CC THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.
CC -1- MASS SPECTROMETRY: MW=1246.56; METHOD: MALDI.
CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
DR InterPro: IPR02012; GNRH.
DR Pfam: PF00446; GNRH;
DR PROSITE: PS00473; GNRH;
KW Hormone; Amidation; Pyroglutamate; Carboxylic acid.
FT MOD RES 1 1 PYROGLUTAMINE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 10 AA; 1264 MW; 284B3639DB5A5A3 CRC64;

Query Match 10.3%; Score 20; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 6; Gaps 0;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 4 KRW 6
DB 1 QHW 3

RESULT 5
CONS CLUPA
ID GONI CLUPA STANDARD; PRT; 10 AA.
AC P87347 P87347.
DT 16 OCT 2001 (Rev. 41, Last sequence update).
DT 28 FEB 2003 (Rev. 41, Last annotation update).
DE Gonadoliberin 1: Gonadotropin-releasing hormone 1 (GNRH-1) (LR RH);
DE GnRH.
OS Clupea pallasi (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neocyprinidae; Teleostei; Clupeomorpha; Clupeidae;
CC Clupea;
OX NCBI_TaxID=10724;
RN 1;
PF SEQUENCE, AND FUNCTION.
RP TISSUE Brain, and pituitary;
RX MEDLINE 2011435; PubMed:1065929;
RA Carlsfeld J., Powell J.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring."
RP Endocrinology 141:525-532(2002).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
OR InterPro: IPR005512; GNRH;
OR Pfam: PF00446; GNRH;

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OM protein - protein search, using sw model

Run on: November 5, 2003, 12:41:29 / Search time: 19 seconds  
(without alignment)  
#6,016 Million cell updates/sec

Title: US-09-914-088 26

Perfect score: 66

Sequence: 1 CSQKWSERT 11

Scoring table: ELKSJMa2

Gapop 10.0 , Gapext 0.5

Searched: 810525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1748

Maximum DB seq length: 0

Maximum DB seq length: 11

Post processing: Minimum Match 3%

Maximum Match 100%

Listing first 45 summaries

Database :

```
SPRMBL 231*
1: sp.archaea*
2: sp.bacteria*
3: sp.fungi*
4: sp.human*
5: sp.invertebrate*
6: sp.mammal*
7: sp.mice*
8: sp.organalle*
9: sp.prage*
10: sp.plant*
11: sp.todent*
12: sp.virus*
13: sp.vvertebrate*
14: sp.unclassified*
15: sp.vvirus*
16: sp.bacteriap*
17: sp.archeap*
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Pred. No. is the number of results for identity that have a score greater than or equal to the value of the pred. no. printed, and is derived by analysis of the full database.

SUMMARY

Result	No.	Score	Query Match	Length DB	ID	Description
1	21	31.8	9	8	QW8X4	QW8X4 diadema mex
2	21	31.8	11	8	Q8SKP8	Q8SKP8 streptophorus
3	21	31.8	11	13	Q9C238	Q9C238 gallus gall
4	21	31.8	11	15	Q81410	Q81410 fouse mamma
5	20	30.3	8	8	Q8WGT0	Q8WGT0 lemis haita
6	20	30.3	9	8	Q8WGE6	Q8WGE6 helicobacter
7	20	30.3	10	2	Q9F9H5	Q9F9H5 cyctolatus
8	19	29.8	8	6	Q02831	Q02831 varanus gig
9	19	29.8	9	8	Q94V10	Q94V10 varanus gig
10	19	29.8	10	8	Q94V35	Q94V35 varanus gig
11	19	29.8	10	8	Q8SHN1	Q8SHN1 bradypodion
12	19	29.8	10	8	Q95878	Q95878 rata muscus
13	19	29.8	10	11	Q7C184	Q7C184 mus musculus
14	19	29.8	11	7	Q77844	Q77844 mesochorus
15	19	29.8	11	7	Q77844	Q77844 mesochorus
16	19	29.8	11	7	Q77914	Q77914 mesochorus

17	19	29.8	11	8	Q79921	Q79921 phrynoscepha
18	18	27.3	8	4	Q1589C	Q1589C homo sapien
19	18	27.3	9	2	Q937C8	Q937C8 escherichia
20	18	27.3	9	2	Q937H9	Q937H9 enterobacte
21	18	27.3	10	2	Q937J5	Q937J5 acinetobact
22	18	27.3	10	8	Q79915	Q79915 leiotelepis b
23	18	27.3	10	8	Q8SHQ2	Q8SHQ2 charaalep j
24	18	27.3	10	8	Q9G694	Q9G694 leiotelepis g
25	18	27.3	10	15	Q85598	Q85598 moloney mur
26	18	27.3	10	15	Q85563	Q85563 moloney mur
27	18	27.3	10	15	Q85619	Q85619 moloney mur
28	17	25.8	8	11	Q99MNC	Q99MNC mus musculu
29	17	25.8	9	4	Q9H1Z6	Q9H1Z6 homo sapien
30	17	25.8	9	12	P90159	P90159 barley mild
31	17	25.8	10	2	Q47561	Q47561 escherichia
32	17	25.8	10	8	Q9XMB4	Q9XMB4 aegilops ta
33	17	25.8	10	8	Q94V26	Q94V26 varanus cil
34	17	25.8	10	8	Q9G362	Q9G362 acanthosaur
35	17	25.8	11	2	Q47626	Q47626 escherichia
36	16	24.2	8	6	Q95M23	Q95M23 sus scrofa
37	16	24.2	9	2	Q9R3M1	Q9R3M1 staphylococ
38	16	24.2	10	3	Q8TGB8	Q8TGB8 pleurotus o
39	16	24.2	10	6	Q9TU33	Q9TU33 canis famli
40	16	24.2	10	6	Q9TAP3	Q9TAP3 liolaemus a
41	16	24.2	10	8	Q9T829	Q9T829 liolaemus f
42	16	24.2	10	8	Q9T8W5	Q9T8W5 liolaemus r
43	16	24.2	10	8	Q8W916	Q8W916 liolaemus m
44	16	24.2	10	8	Q9TAN7	Q9TAN7 liolaemus o
45	16	24.2	10	8	Q79888	Q79888 basilliscus

# ALIGNMENTS

## RESULT 1

QW8X4 100% PRELIMINARY: PR7 9 AA.

AC QW8X4, 20, Created  
BT 01-MAR-2002 (TREVURE), 20, Last sequence update)  
DT 01-MAR-2002 (TREVURE), 20, Last sequence update)  
DE Cytochrome oxidase subunit 1 (Fragment).  
GN C011.  
OS Diadema mexicanum.  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinzoidea; Euechinzoidea; Diadematacea; Diadematoida; Diadematidae;  
CX NCBI TaxID=105356;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN:Q70, and C0117;  
RX MEDLINE=21123357; PubMed=1430656;  
RA Lessios H.A., Kessing B.D., Pearse J.S.;  
RT "Population structure and speciation in tropical seas: global  
physogeography of the sea urchin Diadema";  
RL Evolution 55:1965-1975(2001).  
[2].  
RN SEQUENCE FROM N.A.  
RC STRAIN:Q70, and C0117;  
RX MEDLINE=21123357; PubMed=11703875;  
RA Lessios H.A., Garrido M.J., Kessing B.D.;  
RT "Demographic history of Diadema antillarum, a keystone herbivore on  
Caribbean reefs";  
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).  
DR EMBL: AY012920; AAL33843.1;  
DR EMBL: AY012921; AAL33844.1;  
KW Mitochondrion.  
FT NON TIR  
SQ SEQUENCE 9 AA: 1174 MW: 2571173B46DC2D3 CRC64;

Query Match: 51.8%; Score 21; DB 9; Length 9;  
Best local similarity: 50.3%; Pred. No. 8.3e+05;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY 5 HWL5 8
DB 1 HWVA 4

RESULT 2
Q8341C PRELIMINARY; PRT; 11 AA.
AC Q8341C
DT 01-NOV-1996 (TREMUREL. 01, Created)
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)
DT 01-JUN-2002 (TREMUREL. 21, Last annotation update)
DE Superantigen (Fragment)
GN SAG.
OS Mouse mammary tumor virus.
OC Viruses; Retroviruses; Retroviridae; Betaretrovirus.
OX NCBI TaxID:11757.
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=Mtv-6;
RX MEDLINE=9533174; PubMed=7811795;
RA Cho K., Ferrick C.A., Morris D.W.;
RT "Structure and biological activity of the subgenomic Mtv-6 endogenous
RT provirus."
RL Virology 206:395-403 (1995).
DR EXBL: L37518; A246363.1;
DR InterPro: IPR01213; MMTV_SAG.
DR Pfam: PF01054; MMTV_SAG.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1401 MW; 5E6B080A7326C6D7 CRC64;

Query Match 31.8%; Score 21; DB 15; Length 11;
Best Local Similarity 50.0%; Pred. No. 3e-03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

QY 3 QKHWLS 8  
DB 5 QCKWLN 10

```

RESULT 5
Q8WGU7 PRELIMINARY; PRT; 8 AA.
AC Q8WGU7
DT 01-MAR-2002 (TREMUREL. 20, Created)
DT 01-MAR-2002 (TREMUREL. 20, Last sequence update)
DT 01-MAR-2002 (TREMUREL. 20, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
OS Lomus birra.
CG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Decapoda; Decapoda; Anomura; Lomoridae;
OC Lomidae; Lomus.
CX NCBI TaxID:177234;
RN 11
RP SEQUENCE FROM N.A.
RA Morrison G.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
RA Cunningham C.W.;
RT "Mitochondria: gene rearrangements support a hypothesis of parallel
RT evolution to the crab-like form."
RL Submitted (0CT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF436035; AAL31611.1;
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1038 MW; C5B599C733640321 CRC64;

Query Match 30.3%; Score 20; DB 8; Length 8;
Best Local Similarity 75.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 4 KHWL 7  
DB 2 KRWL 5

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY 5 HWL5 8
DB 1 HWVA 4

RESULT 2
Q8341C PRELIMINARY; PRT; 11 AA.
AC Q8341C
DT 01-NOV-1996 (TREMUREL. 01, Created)
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)
DT 01-JUN-2002 (TREMUREL. 21, Last annotation update)
DE Superantigen (Fragment)
GN SAG.
OS Mouse mammary tumor virus.
OC Viruses; Retroviruses; Retroviridae; Betaretrovirus.
OX NCBI TaxID:11757.
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=Mtv-6;
RX MEDLINE=9533174; PubMed=7811795;
RA Cho K., Ferrick C.A., Morris D.W.;
RT "Structure and biological activity of the subgenomic Mtv-6 endogenous
RT provirus."
RL Virology 206:395-403 (1995).
DR EXBL: L37518; A246363.1;
DR InterPro: IPR01213; MMTV_SAG.
DR Pfam: PF01054; MMTV_SAG.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1401 MW; 5E6B080A7326C6D7 CRC64;

Query Match 31.8%; Score 21; DB 15; Length 11;
Best Local Similarity 50.0%; Pred. No. 3e-03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

QY 3 QKHWLS 8  
DB 5 QCKWLN 10

```

RESULT 5
Q8WGU7 PRELIMINARY; PRT; 8 AA.
AC Q8WGU7
DT 01-MAR-2002 (TREMUREL. 20, Created)
DT 01-MAR-2002 (TREMUREL. 20, Last sequence update)
DT 01-MAR-2002 (TREMUREL. 20, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
OS Lomus birra.
CG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Decapoda; Decapoda; Anomura; Lomoridae;
OC Lomidae; Lomus.
CX NCBI TaxID:177234;
RN 11
RP SEQUENCE FROM N.A.
RA Morrison G.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
RA Cunningham C.W.;
RT "Mitochondria: gene rearrangements support a hypothesis of parallel
RT evolution to the crab-like form."
RL Submitted (0CT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF436035; AAL31611.1;
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1038 MW; C5B599C733640321 CRC64;

Query Match 30.3%; Score 20; DB 8; Length 8;
Best Local Similarity 75.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 4 KHWL 7  
DB 2 KRWL 5



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AC Q04035.1
BT C1-DEC-2001 (TREMUREL.19, Created)
DT 01-DEC-2001 (TREMUREL.19, Last sequence update)
DE Cytoschrome c oxidase subunit 1 (fragment)
GN COL
OS Varanus griseus griseus
OG Mitochondrion
OC Eukaryota; Metazoa; Chordata; Vertebrata; Squamata;
OC Lepidosauria; Squamata; Scleroglossa; Anguilliformes; Varanus
OX NCBI_TaxID=69628;
KN [1]_TaxID=69628;
RP SEQUENCE FROM N.A.
RA Ast J. J.
RT "Mitochondrial DNA evidence and evolution in Varanus (Squamata:
RL Chelonios 1710-672011)
DR EMBL AF437501; AAL10063.1;
KW Mitochondrion;
FT NCR TER
SQ SEQUENCE 10 AA; 1215 MW; 0576687636411275 YA;

Query Match 28.8%; Score 19; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 WWS 8
DB 5 WWS 8

RESULT 13
Q05580 PRELIMINARY; PRT; 10 AA.
AC Q05580
DT 01-AUG-1998 (TREMUREL.07, Created)
DT 01-AUG-1998 (TREMUREL.07, Last sequence update)
DE Cytoschrome c oxidase subunit 1 (fragment)
GN CARS (CARS OR C4)
OS Mus musculus "Musset"
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Mus
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Sowden J., Smith E., Morrison K., Edwards Y.
RT "Sequence comparisons and functional studies of the proximal promoter
RC of the carbonic anhydrase 3 (CA3) gene";
RL Gene 14:157-165 (1991)
DR EMBL AF066404; GZAG757.1;
DR X07311.48257; GZ11;
DR M07311.48257; GZ11;
FT NCR TER
SQ SEQUENCE 10 AA; 1135 MW; 56F8E71A0C37B13 CRC64;

Query Match 28.8%; Score 19; DB 11; Length 10;
Best Local Similarity 37.5%; Pred. No. 6.1e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 KMWSCRT 11
DB 3 KMWATPAT 10

RESULT 14
Q77895 PRELIMINARY; PRT; 11 AA.
AC Q77895
DT 01-NOV-1998 (TREMUREL.08, Created)
DT 01-NOV-1998 (TREMUREL.08, Last sequence update)
DE MHC class II B (class 4 fragment)
OS Oryzomys palustris (Mile tilapia; Tilapia nilotica)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Cyprinodontiformes; Neoteleostei;

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```

GN COL
OS Rana muscosa
OG Mitochondrion
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Anura; Neobatrachia; Ranidae; Rana
OX NCBI_TaxID=65556;
KN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE 21184282; PubMed 11286498;
RA Macy J.R., Strasburg C.L., Riessen J.A., Vredenburg V.T.,
RA Jennings M., Larson A.
RT "Molecular Phylogenetics of Western North American Frogs of the Rana
RT boylii Species Group";
RC Mol. Phylogenet. Evol. 19:131-143 (2001);
DR EMBL AF314024; AAK56906.1;
KW Mitochondrion;
FT NCR TER
SQ SEQUENCE 10 AA; 1335 MW; CDD480C9D371F1A9 CRC64;

Query Match 25.8%; Score 19; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WWS 8
DB 5 WWS 8

RESULT 13
Q05580 PRELIMINARY; PRT; 10 AA.
AC Q05580
DT 01-AUG-1998 (TREMUREL.07, Created)
DT 01-AUG-1998 (TREMUREL.07, Last sequence update)
DE Cytoschrome c oxidase subunit 1 (fragment)
GN CARS (CARS OR C4)
OS Mus musculus "Musset"
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Mus
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Sowden J., Smith E., Morrison K., Edwards Y.
RT "Sequence comparisons and functional studies of the proximal promoter
RC of the carbonic anhydrase 3 (CA3) gene";
RL Gene 14:157-165 (1991)
DR EMBL AF066404; GZAG757.1;
DR X07311.48257; GZ11;
DR M07311.48257; GZ11;
FT NCR TER
SQ SEQUENCE 10 AA; 1135 MW; 56F8E71A0C37B13 CRC64;

Query Match 28.8%; Score 19; DB 11; Length 10;
Best Local Similarity 37.5%; Pred. No. 6.1e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 KMWSCRT 11
DB 3 KMWATPAT 10

RESULT 14
Q77895 PRELIMINARY; PRT; 11 AA.
AC Q77895
DT 01-NOV-1998 (TREMUREL.08, Created)
DT 01-NOV-1998 (TREMUREL.08, Last sequence update)
DE MHC class II B (class 4 fragment)
OS Oryzomys palustris (Mile tilapia; Tilapia nilotica)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Cyprinodontiformes; Neoteleostei;

```

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
 CC Cichlidae; Oreochromis.

XX NCBI TaxID=8128;

RY [1]

RP SEQUENCE FROM N.A.

RX XEGLINE98315113; PubMed=9649539;

RA Maiga-Trillo E., Zaleska-Rutczynska Z., McAndrew R., Vinces V.

RA Figueroa F., Sultmann H., Klein C.

RT "Linkage relationships and haplotype polymorphism among cichlid mhc

RT class II B loci."

RT Genetics 149:1527-1537(1998).

RL ENBEL AF049994; AAC4133317

DR NON-TER

FT NON-TER

SQ SEQUENCE 11 AA; 1253 YW; 72449701849878 CR0047

Query Match: 28.8%; Score 19; 18 31; Length 11;

Best Local Similarity 50.0%; P-adj. No. 6; 100.00;

Matches 2; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 6 WISC 4

DB 1 WISE 4

RESULT 15

Q77884

ID Q77884 PRELIMINARY; FR1 11 AA;

AC Q77884;

DT 01-NOV-1998 (TrEMBL); 38, Created;

DT 01-NOV-1998 (TrEMBL); 38, Last sequence updated;

DT 01-DEC-2001 (TrEMBL); 19, Last annotation update;

DE MHC class II B locus 4 (Fragment).

CS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).

OC Fungi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Eucaryotia; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;

CC Cichlidae; Oreochromis.

XX NCBI TaxID=8128;

RY [1]

RP SEQUENCE FROM N.A.

RX XEGLINE98315113; PubMed=9649539;

RA Maiga-Trillo E., Zaleska-Rutczynska Z., McAndrew R., Vinces V.

RA Figueroa F., Sultmann H., Klein C.

RT "Linkage relationships and haplotype polymorphism among cichlid mhc

RT class II B loci."

RT Genetics 149:1527-1537(1998).

RL ENBEL AF049994; AAC4133317

DR NON-TER

FT NON-TER

SQ SEQUENCE 11 AA; 1253 YW; 72449701849878 CR0047

Query Match: 28.8%; Score 19; 18 31; Length 11;

Best Local Similarity 50.0%; P-adj. No. 6; 100.00;

Matches 2; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 6 WISC 9

DB 1 WISE 4

Search completed: November 5, 2003, 16:44:47

Job time: 31 secs

GenCore version: 5.1.6  
Copyright (c) 1993-2003 CompuGen, Ltd.

(M) proteins - protein search, using sw tool

Run on: November 5, 2003, 18:10:49 / Search time: 49 seconds  
(without database)  
43.66 Million cell updates

Title: JS-09-014-088-26

10-10-68

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Sequence : accordeon
; OSKFWLSORT ;
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Scoring table: BCSMe2

Gap: 0.0, Gap: 0.0

Searched: 110863 seqs, 15872653 residues

Total number of girls satisfying closed parentage condition

Mr. William D. B. Smith, Esq. - 0

Max: min DB seq	length: 11
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Post: - processing: Maximum March 2007

SECRET  
UNCLASSIFIED

Listing first 45 summaries

Catlabase : A Geneset : 193003 : •

11	/SID1/cgdata/geneseq/geneseq-ent/AA-981.DAT
12	/SID1/cgdata/geneseq/geneseq-ent/AA-981.DAT
13	/SID1/cgdata/geneseq/geneseq-ent/AA-982.DAT
14	/SID1/cgdata/geneseq/geneseq-ent/AA-983.DAT
15	/SID1/cgdata/geneseq/geneseq-ent/AA-984.DAT
16	/SID1/cgdata/geneseq/geneseq-ent/AA-985.DAT
17	/SID1/cgdata/geneseq/geneseq-ent/AA-986.DAT
18	/SID1/cgdata/geneseq/geneseq-ent/AA-987.DAT
19	/SID1/cgdata/geneseq/geneseq-ent/AA-988.DAT
20	/SID1/cgdata/geneseq/geneseq-ent/AA-989.DAT
21	/SID1/cgdata/geneseq/geneseq-ent/AA-990.DAT
22	/SID1/cgdata/geneseq/geneseq-ent/AA-991.DAT
23	/SID1/cgdata/geneseq/geneseq-ent/AA-992.DAT
24	/SID1/cgdata/geneseq/geneseq-ent/AA-993.DAT

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	11	21	AAB3C474
2	66	100.0	11	21	AAB3E932
3	66	100.0	11	22	AAB3E677
4	66	100.0	11	22	AAB3A130
5	66	100.0	11	23	AEB3C225
6	57	86.4	10	21	AAB3E479
7	57	86.4	10	21	AAB3E479
8	57	86.4	10	22	AAB3E654
9	57	86.4	10	22	AAB3E135
					Aggallatey peptid
					P3 minotape peptid
					Peptide 117 derive
					155 peptide #8 M
					Human IgE minotape
					I-mnoglobulin E
					IgE Cephalon 2 do
					Peptide P3 derived
					IgE peptide #3. M

## ALIGNMENTS

RESULT :

AA820974

ID AAB20874 standard; peptide; 11 AA.

XX  
XX

AC AAE26974;

[illegible]

XX  
JAN 20 1951  
LIBRARY

DEPARTMENT OF AGRICULTURE

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
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KW Immunoglobulin E; IgE; immunogenic

KW prostate cancer; Haemophilus influ

KW malaria; cytostatic; antiallergic;

protozoa; Alzheimer's disease;

H  
C  
O  
S

CX CX

XX  
CC  
00:00:00

Key  
Qualification/Qualification

17 015 p. 11 p. 11

13 "people" = 3000  
14 "people" = 3000

XX  
XX

WC200(5037)-A1.

(SMIK) SYNTHKLONE BEECHAM BIOLOGICALS.

PA (SMIK) SYNTHKLONE BEECHAM BIOLOGICALS.  
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
PI Dyson M, Friede M, Greenwood C, Hewitt E, Laront A, Mason S;  
XX Randall R, Turnell WG, Van Vechelen MP, Virals De Bassols YC;  
XX WPI: 2000-57240/53.  
XX Immunogens and vaccine comprising the immunised antigen for preventing  
PT and treating infectious diseases such as malaria and chronic disease e.g.  
PT cancer, comprises peptide and carrier from protein B of influenza  
XX Patent, comprises peptide and carrier from protein B of influenza  
XX Claim 10, Page 18, 53pp; English.  
XX The present invention describes an immunogen (I) comprising a peptide  
XX (Ia) and a carrier (Ib) derived from protein B of Hemagglutinin influenza  
XX or its fragment. Also described are (ii) a vaccine comprising (I), and  
XX an excipient; (2) preparation of (I), comprising conjugating a peptide  
XX to protein B or its fragment; and (3) preparation of a vaccine of (I),  
XX comprising formulating (I) with an excipient. (I) has cytostatic,  
XX antiallergic, neotropic, neuroprotective and protease-inhibitory  
XX (ii) and the vaccine are useful for the manufacture of a medicament for  
XX preventing and treating infectious diseases such as malaria or chronic  
XX disease such as cancer. Alzheimer's disease or HIV-1 in a patient.  
XX Unlike prior art immunogens, (I) induces high levels of anti-peptide  
XX immune responses while inducing a moderate humoral response against the  
XX carrier. The present sequence represents a specifically claimed  
XX epitope peptide sequence, which can be used in an immunogen of the  
XX present invention.

XX Sequence 1: AA:

Query Match 100.0%; Score 66; DB 21; Length 11;

Best local similarity 100.0%; Pred. NO. 0.0022;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQKHWLSORT 11

DB 1 CSQKHWLSORT 11

RESULT 1

AAB25902

10 AAB25902 Standard; Peptide; 11 AA

XX AAB25902

XX AAB25902

XX DB 25902 (first entry)

XX Peptide P17 derived as mimotope of P17 SEQ ID NO. 1

XX Epitope mimotope human, immunoglobulin G, carrier vehicle; treating

XX allergic disease, immunoglobulin G, carrier vehicle; treating

XX immunosuppressive; vaccine; histamine release inhibitory; treating

XX allergy; atopy.

XX Homo sapiens.

XX W02060145745-A2

XX 21 AUG 2001

XX 22 FEB 1999; 2006WO-EP01455.

XX 25 FEB 1999; 99GB-0004405.

XX 29-MAR-1999; 99GB-0007151.

XX 03-MAY-1999; 99GB-0010637.

XX 03-MAY-1999; 99GB-0010638.

XX 07-AUG-1999; 99GB-0018594.

XX 07-AUG-1999; 99GB-0018603.

XX 07-SEP-1999; 99GB-0021046.

XX 07-SEP-1999; 99GB-0021047.

XX 23-OCT-1999; 99GB-0025619.

XX 23 NOV 1999; 99GB-0027698.

(SMIK) SYNTHKLONE BEECHAM BIOLOGICALS.

(PEPT-) PEPTIDE THERAPEUTICS LTD.

Dyson M, Friede M, Greenwood C, Hewitt E, Laront A, Mason S;

Randall R, Turnell WG, Van Vechelen MP, Virals De Bassols YC;

WPI: 2000-572071/53.

Peptides useful for treating, preventing and ameliorating allergic  
diseases, comprising an isolated surface exposed group of a specific  
domain from immunoglobulin E.

Claim 16; Page 9; 12pp; English.

The present invention describes a peptide (I) comprising an isolated  
surface exposed group/epitope (E) of C-epsilon-2 domain (D) of  
immunoglobulin E (IgE), or its mimotope. Also described are: (1) an  
immunogen (ii) for treating allergy comprising (I); (2) a vaccine (iii)  
for treating allergies comprising (II); (3) a ligand (IV) capable of  
recognising E; (4) a pharmaceutical composition (PC) comprising (IV),  
(5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
(Ia) comprising (Ia); and (7) producing (II) by producing (II); (II)  
can have antiallergic and immunosuppressive activities, and can be used  
as a vaccine and histamine release inhibitor. (I), (II) and (III) are  
useful in medicine and in the manufacture of medicaments for treating  
and preventing allergies. (IV) is useful for identifying mimotopes of E.  
In medicine and also in manufacturing medicaments for treating  
allergies. (I) is useful in diagnostics and in the affinity purification  
of circulating anti-IgE antibodies from blood. (2) (III) and (IV) are  
useful for treating a patient susceptible to or suffering from allergies.  
(IV) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
peptide sequences which are used in the exemplification of the present  
invention.

XX Sequence 1: AA:

Query Match 100.0%; Score 66; DB 21; Length 11;

Best local similarity 100.0%; Pred. NO. 0.0022;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQKHWLSORT 11

DB 1 CSQKHWLSORT 11

RESULT 1

AAB25902

10 AAB25902 Standard; Peptide; 11 AA

XX AAB25902

XX AAB25902

XX DB 25902 (first entry)

XX Peptide P17 derived as mimotope of Cepsilon2 region of human IgE.

XX Human, linkage technology; conjugated compound; carrier vehicle;

XX epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;

XX IgE mediated disease; antibody response.

XX Homo sapiens.

XX Synthesis.

XX W02060145745-A2

XX 28 DEC 2001

XX 21 DEC 2000; 2006WO-GB04935.

XX 21 DEC 1999; 99GB-0003233.

XX 22-FEB-2000; 2006GB-0004596.

XX 22-AUG-2000; 2006GB-0002707.

XX 22 AUG 2001; 2006GB-002708.









XX WF1: 2002-489648/52.  
 XX  
 XX  
 PT Conjugate for use in vaccine for treatment of allergy, comprises  
 PT disulfide bridge cyclized peptide and immunogenic carrier.  
 XX  
 XX  
 PS Claim 4: Page 9, 45pp; English.  
 XX  
 XX The present invention relates to conjugates suitable for use in vaccines,  
 CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
 CC immunogenic carrier. The vaccine can be used in the treatment of  
 CC allergies. The present sequence is a peptide immunogen derived from human  
 CC immunoglobulin E (IgE) suitable to be cyclized and used in the invention.  
 XX  
 XX Sequence 10 AA,  
 SQ  
 Query Match 86.4%, Score 57, DB 20, Length 1;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SQKHWLSRDT 11  
 DB : SQKHWLSRDT 10  
 RESULT 11  
 AAAY4260E  
 LC AAY4260E standard; peptide; 8 AA  
 AC AAY4260E,  
 XX  
 XX 10 JAN 2000 (first entry)  
 XX  
 XX Human IgE peptide fragment.  
 XX  
 XX Immunoglobulin E (IgE) antagonist; FrepsilonR1 receptor; human; pds;  
 KW receptor binding; binding determinant sequence; anti-IgE antibody;  
 KW Allergic disease.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US596579-A.  
 XX  
 XX 12-06-1999.  
 XX  
 XX 21 APR 1994; 94US-032639.  
 XX  
 XX 14 AUG 1991; 91US-0744768.  
 XX  
 XX 26 JAN 1994; 94US 0179483.  
 XX  
 XX GENE I GENENTECH INC.  
 XX  
 XX Jardieu RM, Presta LG;  
 XX WPI: 1999-079941/49.  
 XX  
 XX Immunoglobulin E variants as peptide antigens suitable for raising and  
 PT screening anti-immunoglobulin E (IgE) antibodies; the isolation and  
 PT purification of FrepsilonR1 receptor and in the treatment of allergic  
 PT diseases  
 PT  
 XX Example 1: Column 37-38; 37pp; English.  
 XX  
 XX The invention provides immunoglobulin E (IgE) and IgE variants comprising one  
 CC or more of the FrepsilonR1 receptor binding determinant sites of human  
 CC IgE. The antagonists include IgE variants comprising immunoglobulin  
 CC complete and binding determinant sequences. The FrepsilonR1 and the  
 CC sequence shown in AAY42581. The FrepsilonR1 binding determinant  
 CC sequence are selected from the sequences shown in AAY42577 and  
 CC the FrepsilonR1 loop binding determinant sequences are selected from  
 CC sequences shown in AAY42575-Y42581. The variants are used in raising  
 CC and screening anti-IgE antibodies, in the isolation and purification of  
 CC FrepsilonR1 receptor and in the treatment and prevention of allergic

CC diseases.  
 XX  
 XX Sequence 8 AA;  
 Query Match 72.7%, Score 48; DB 20; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QKHWLSR 10  
 DB 1 QKHWLSR 8  
 RESULT 12  
 AAAY95217  
 ID AAY95217 standard; protein; 8 AA.  
 XX  
 XX AAY95217;  
 AC AAY95217;  
 XX  
 XX 29 JUN 2000 (first entry)  
 XX  
 XX Human IgE mutant #15 fragment amino acid sequence.  
 XX  
 XX Immunoglobulin E (IgE); anti-human IgE; bispecific antibody; FcEL; FcEL;  
 KW low affinity binding receptor; high affinity binding receptor; allergy;  
 KW diagnosis; treatment; histamine release; heavy chain; prevent.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US633453-A.  
 XX  
 XX 14 MAR 2000.  
 XX  
 XX 06-JUN 1995; 95US 0466151.  
 XX  
 XX 15 MAR 1995; 95US-045617.  
 XX  
 XX 14 AUG 1992; 92WO-US6860.  
 XX  
 XX 26 JAN 1994; 94US-0185899.  
 XX  
 XX GENE I GENENTECH INC.  
 XX  
 XX Presta LG, Jardieu RM;  
 XX WPI: 2000-269913/23.  
 XX  
 XX New bispecific antibodies, useful for treating immunoglobulin  
 PT E mediated disease, binds to IgE, but only when on the low affinity  
 PT receptor, and to an antigen other than IgE.  
 XX  
 XX Example 4: Column 33; 45pp; English.  
 XX  
 XX This sequence represents a fragment of an amino acid sequence encoding a  
 CC mutant human immunoglobulin E (IgE). The mutant IgE is used to test the  
 CC binding of IgE to its receptors. The invention relates to a bispecific  
 CC antibody that binds specifically to IgE when IgE is bound to its low  
 CC affinity receptor (FcEL), but does not bind to IgE when IgE is bound to  
 CC its high affinity receptor (FcEH). The bispecific antibody comprises an  
 CC IgE-binding arm with human framework residues of a recipient human  
 CC antibody and donor murine CDR (complementarity determining region)  
 CC residues, but with at least one human CDR residue replacing the analogous  
 CC murine residue. The antibody also comprises an Fv that is specific for a  
 CC predetermined antigen other than IgE. The antibodies work by displacing  
 CC bound IgE from its receptor, or via competitive inhibition of its  
 CC binding. The bispecific antibodies are used for diagnosis, treatment and  
 CC prevention of allergy and other IgE-mediated diseases. Also, when  
 CC immobilised, for the isolation of FcEL from cells (for research or  
 CC therapy); the bispecific antibodies of the invention do not cause  
 CC granulation or release of histamine from mast cells.  
 XX  
 XX Sequence 8 AA;  
 Query Match 72.7%, Score 48; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;



Job time : 4. secs

DT 28 MAY 2001 (first entry)  
XX  
DE Human immunoglobulin E related peptide SEQ ID NO:107  
XX  
KW Immunoglobulin E, vaccine; IgE; cytotoxic T lymphocyte response;  
KW immune response; major histocompatibility complex; MHC; immunoregulation;  
KW antiallergic; antihistamine; immunosuppressive; vasopressin; cytostatic;  
KW dermatological; antiinflammatory; IgE-mediated reaction; food allergy;  
KW atopic hypersensitivity conditions; allergic rhinitis; allergic asthma;  
KW atopic dermatitis; non-atopic hypersensitivity conditions; anaphylaxis;  
KW urticaria hives;  
XX  
CS Homo sapiens  
CS Synthetic  
XX  
PN WC000365716-A2  
XX  
FD 27 FEB 2003  
XX  
PI CB AUG 2001; 2002WO US26986  
XX  
PI 13 AUG 2001; 2001US 312129  
XX  
PI (05ET) AGS THERAPEUTICS INC.  
XX  
PI Chen SA, Yang Y, Batankiewicz T, Chen Z  
XX  
PI WPI; 2001 264242/26  
XX  
PI Identifying peptides that induce cytotoxic T lymphocyte (CTL) response  
XX  
PI against IgE, by identifying peptide eliciting CTL response to IgE  
XX  
PI peptides naturally presented by major histocompatibility complex class  
XX  
PI I protein  
XX  
PI Example 5, Page 20; 18pp; English  
XX  
XX The present invention describes a method for identifying peptides  
XX that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
XX E (IgE), comprising providing a test peptide, the selected of being able  
XX to bind to major histocompatibility complex (MHC) and T-cell, and  
XX evaluating it for ability to elicit in a mammal a CTL response to  
XX naturally processed and presented for peptides, where a peptide that  
XX induces such a response is identified. Also described are compositions,  
XX (a) comprising at least one recombinant peptide (a) identified by (MHC),  
XX (b) comprising at least one isolated polypeptide (a) and (b), and  
XX (c) comprising antigen-presenting cells that recognize at least one (a).  
XX Where (a) are able to bind to at least one MHC class I molecule and to  
XX elicit in a mammal a CTL response, naturally processed and presented  
XX for peptides (a) have utility in immunotherapy, immunosuppression,  
XX vaccination, dermatological, anti-infective, anti-inflammatory,  
XX and can be used as inducers of CTL response in a mammal.  
XX Variations of (a) can be used for vaccination, immunosuppression, and  
XX normal, (b) are useful for modulation of immune response, such as  
XX IgE-mediated atopic hypersensitivity conditions, and (c) are useful for atopic  
XX hypersensitivity conditions. IgE myeloma in a mammal, identified by (a) are  
XX useful for treating atopic hypersensitivity conditions, such as allergic  
XX rhinitis, allergic asthma, food allergy, food intolerance, non-  
XX atopic hypersensitivity conditions, such as anaphylaxis and urticaria  
XX hives. The present sequence represents a peptide which is used in an  
XX example from the present invention.  
XX  
XX Sequence 5 AA:  
XX  
XX Query Match 56 18; Score 15; E=0.4; Pos=100  
XX Best Local Similarity 100%; Pos=100; Score=15; E=0.4  
XX Matches 6; Conservative 0; Mismatches 0; Pos=100; Score=15; E=0.4  
XX  
XX 2 SEQID 7  
XX 4 SEQID 9  
XX

GenCore version 5.1.6  
Copyright (c) 1993-2003 CompuGen Ltd.

Protein - protein search, using sw model

Run on: November 5, 2004, 19:43:55 / Search time 23 seconds  
Without alignment  
65,142 Million pairs of bases/sec

Title: US 09 914-088-26

Perfect score: 66  
Sequence: 1 GQKHWLSRP 11

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 644079 seqs, 171749232 residues

Total number of hits satisfying chosen parameters: 1848

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 04  
Maximum Match 1004  
Listing first 45 summaries

Database: Published Applications AA\*

- 1 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 2 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 3 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 4 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 5 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 6 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 7 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 8 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 9 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 10 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 11 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 12 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 13 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 14 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 15 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 16 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 17 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb
- 18 /cgn2\_6/prodata2/pubpaai/US09\_PUB0006.rapb

Pred. No. is the number of residues in the predicted sequence.  
score greater than or equal to the score of the best hit found.  
and is derived by analysis of the total score of the hit.

SW0005100

Result No.	Score	Query Match	Length DB	ID	Accession
1	48	72.7	8	US 09 914-088-26	Sequence 24, Appl
2	48	72.7	8	US 09 914-088-26	Sequence 57, Appl
3	48	72.7	8	US 09 914-088-26	Sequence 24, Appl
4	48	72.7	8	US 09 914-088-26	Sequence 57, Appl
5	48	72.7	8	US 09 914-088-26	Sequence 24, Appl
6	48	72.7	8	US 09 914-088-26	Sequence 57, Appl
7	37	42.1	9	US 10 083-768-112	Sequence 57, Appl
8	35	53.0	9	US 10 083-768-112	Sequence 52, Appl
9	35	53.0	9	US 10 083-768-112	Sequence 61, Appl
10	30	43.5	9	US 10 083-768-112	Sequence 21, Appl
11	29	43.9	10	US 10 083-768-112	Sequence 128, Appl
12	28	43.9	11	US 10 083-768-112	Sequence 45, Appl
13	28	42.4	7	US 10 083-768-112	Sequence 141, Appl
14	28	42.4	10	US 10 083-768-112	Sequence 141, Appl
15	26	39.4	7	US 10 083-768-112	Sequence 45, Appl

16	26	39.4	10	US 09 914-088-26	Sequence 455, Appl
17	26	39.4	10	US 09 914-088-26	Sequence 193, Appl
18	26	39.4	10	US 10 083-768-112	Sequence 73, Appl
19	26	39.4	10	US 10 083-768-112	Sequence 112, Appl
20	25	37.9	9	US 10 083-768-112	Sequence 24, Appl
21	25	37.9	9	US 10 083-768-112	Sequence 9, Appl
22	25	37.9	10	US 10 083-768-112	Sequence 63, Appl
23	25	37.9	10	US 10 083-768-112	Sequence 68, Appl
24	25	37.9	10	US 10 083-768-112	Sequence 122, Appl
25	25	37.9	11	US 10 083-768-112	Sequence 10, Appl
26	25	37.9	11	US 10 083-768-112	Sequence 35, Appl
27	24	36.4	5	US 09 914-088-26	Sequence 34, Appl
28	24	36.4	7	US 10 083-768-112	Sequence 20, Appl
29	24	36.4	9	US 09 914-088-26	Sequence 78, Appl
30	24	36.4	9	US 09 914-088-26	Sequence 86, Appl
31	24	36.4	8	US 09 914-088-26	Sequence 75, Appl
32	24	36.4	8	US 09 914-088-26	Sequence 86, Appl
33	24	36.4	9	US 10 083-768-112	Sequence 112, Appl
34	24	36.4	9	US 10 083-768-112	Sequence 4, Appl
35	24	36.4	9	US 10 083-768-112	Sequence 440, Appl
36	24	36.4	9	US 10 083-768-112	Sequence 53, Appl
37	24	36.4	10	US 09 914-088-26	Sequence 7, Appl
38	24	36.4	10	US 09 914-088-26	Sequence 8, Appl
39	24	36.4	10	US 10 083-768-112	Sequence 565, Appl
40	24	36.4	10	US 10 083-768-112	Sequence 62, Appl
41	24	36.4	10	US 10 083-768-112	Sequence 120, Appl
42	24	36.4	10	US 10 083-768-112	Sequence 208, Appl
43	24	36.4	10	US 10 083-768-112	Sequence 142, Appl
44	24	36.4	10	US 10 083-768-112	Sequence 154, Appl
45	24	36.4	10	US 10 083-768-112	Sequence 260, Appl

ALIGNMENTS

RESULT:  
US-09-914-088-26  
; Sequence 24, Application: US/09020277  
; Patent No. US20010033542A1  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Paul M.  
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)  
; FILE REFERENCE: PCT/EP2002/05  
; CURRENT APPLICATION NUMBER: US/09/020277  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: US 08/455,417  
; PRIOR FILING DATE: 1995-02-15  
; PRIOR APPLICATION NUMBER: US 08/186,493  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/04660  
; PRIOR FILING DATE: 1992-09-14  
; PRIOR APPLICATION NUMBER: US 07/879,435  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-09-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 24  
; LENGTH: 8  
; TYPE: PPT  
; ORGANISM: Homo sapiens  
US-09-914-088-26

Query Match: 72.7% Score 48; DB 9; Length 8;  
Best local Similarity: 100.0%; Pred. No. 5, Re-05;  
Matches: 6; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY: 1 GQKHWLSRP 10  
DP: 1 GQKHWLSRP 4

RESULT:

```

US 09-902-096-57
Sequence 57, Application US/9902077
Patent No. US2001003849A
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Gardier, Paula M.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
FILE REFERENCE: P018202US
CURRENT APPLICATION NUMBER: US/99-096-57
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 08/744,495
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/06660
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO: 57
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US 09-922-079-57

```

```

Query Match 72.7% Score 48: DB 11: Length 8;
Best Local Similarity 100.0%; Pct 100.0%; Pct 100.0%;
Matches 87 Conservative 0; Mismatches 0; Gaps 0;

```

```

CY 3 QKHWLSR 10
DB 1 QKHWLSR 8

```

```

RESULT 3
US 09-902-096-57
Sequence 57, Application US/9902077
Patent No. US2001003849A
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Gardier, Paula M.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
FILE REFERENCE: P018202US
CURRENT APPLICATION NUMBER: US/99-096-57
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 08/744,495
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/06660
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO: 57
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US 09-902-096-57

```

```

Query Match 72.7% Score 48: DB 11: Length 8;
Best Local Similarity 100.0%; Pct 100.0%; Pct 100.0%;
Matches 87 Conservative 0; Mismatches 0; Gaps 0;

```

```

CY 3 QKHWLSR 10
DB 1 QKHWLSR 8

```

```

RESULT 4
US 09-902-096-57
Sequence 57, Application US/9902077
Patent No. US2001003849A
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Gardier, Paula M.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
FILE REFERENCE: P018202US
CURRENT APPLICATION NUMBER: US/99-096-57
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 08/744,495
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/06660
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO: 57
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US 09-902-096-57

```

```

Query Match 72.7% Score 48: DB 11: Length 8;
Best Local Similarity 100.0%; Pct 100.0%; Pct 100.0%;
Matches 87 Conservative 0; Mismatches 0; Gaps 0;

```

```

CY 3 QKHWLSR 10
DB 1 QKHWLSR 8

```

```

RESULT 5
US 09-925-179-24
Sequence 54, Application US/99925179
Publication No. US20010044858A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Gardier, Paula M.
TITLE OF INVENTION: Anti-IL-6 Antibodies (as amended)
FILE REFERENCE: P0192010US
CURRENT APPLICATION NUMBER: US/99-925,179
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 08/744,495
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/06660
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 69
SEQ ID NO: 24
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US 09-925-179-24

```

```

Query Match 72.7% Score 48: DB 11: Length 8;
Best Local Similarity 100.0%; Pct 100.0%; Pct 100.0%;
Matches 87 Conservative 0; Mismatches 0; Gaps 0;

```

```

CY 3 QKHWLSR 10
DB 1 QKHWLSR 8

```

Db 1 QKHWLSDR 2

```

RESULT 6
US-10-214-524-57
; Sequence 57, Application US/09925174
; Publication No. US2003034468A1
; GENERAL INFORMATION:
; APPLICANT: Cardieu, Paula M.
; APPLICANT: Prestia, Leonard G.
; TITLE OF INVENTION: Anti-IGF Antibodies and analogs
; FILE REFERENCE: P018P22C1C1US
; CURRENT APPLICATION NUMBER: US/09925174
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/454,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/455,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/195,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06960
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,764
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 57
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-174-57

```

```

Query Match 72.7% Score 48; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

CY 3 QKHWLSDR 13

```

Db 1 QKHWLSDR 8
RESULT 7
US-10-214-524-17
; Sequence 17, Application US/10214524
; Publication No. US2003037142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IFE 00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10214524
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human (Homo sapiens)
US-10-214-524-17

```

```

Query Match 56.1% Score 37; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

CY 2 SQKHWL 7

Db 4 SQKHWL 9

```

RESULT 8
US-10-144-188-52
; Sequence 52, Application US/10144188
; Publication No. US20030370212A1
; GENERAL INFORMATION:
; APPLICANT: Cai, Zeling
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; APPLICANT: Shi, Weixing
; APPLICANT: Kong, Yan
; APPLICANT: Degraw, Juli
; TITLE OF INVENTION: Ex Vivo Panning For Generating Cytotoxic T Lymphocytes Specific
; FILE REFERENCE: P10010 OPT-1627
; CURRENT APPLICATION NUMBER: US/10144188
; PRIOR FILING DATE: 2002-05-11
; PRIOR APPLICATION NUMBER: 60/291,380
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide antigen
US-10-144-188-52

```

```

Query Match 53.0% Score 35; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

CY 6 WLSDR 11

Db 1 WLSDR 6

```

RESULT 9
US-10-214-524-6
; Sequence 6, Application US/10214524
; Publication No. US2003037142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zheng
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10214524
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human (Homo sapiens)
US-10-214-524-6

```

```

Query Match 53.0% Score 35; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

CY 6 WLSDR 11

Db 1 WLSDR 6

```

RESULT 10
US-10-214-524-11
; Sequence 11, Application US/10014974

```



Publication No. US20030143156A1

GENERAL INFORMATION:

APPLICANT: DYAX CORP.

INVENTOR: Reitzel, James P.

APPLICANT: Wescott, Charles R.

APPLICANT: Satoh, Aakon K.

TITLE OF INVENTION: FIBRIN BINDING PROPERTIES USEFUL AS IMAGING AGENTS

FILE REFERENCE: DEX-224.1 PCT: DEX 224.1 DE

CURRENT APPLICATION NUMBER: US/09/094,994

CURRENT FILING DATE: 2001-12-27

PRIOR APPLICATION NUMBER: US 09/742,419

PRIOR FILING DATE: 2000-12-23

NUMBER OF SEQ TO NOS: 56

SOFTWARE: Patent in version 3.1

SEQ ID NO: 1

LENGTH: 9

TYPE: 157

ORGANISM: Artificial Sequence

FEATURES:

OTHER INFORMATION: fibrin binding loop

US 10 034-914 21

Query Match 45.58; Score 10; DB 12; Length 9;

Best Local Similarity 57.18; Pred No 5.6e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 CSQKHWL 7

DB 1 CSQHWL 7

RESULT 11

US-10 053-768-118

Sequence 118, Application US/08450842

Publication No. US2003015916A1

GENERAL INFORMATION:

APPLICANT: Dower, William J.

INVENTOR: Bartlett, Ronald W.

INVENTOR: Swick, Steven E.

INVENTOR: Jeffin, David J.

INVENTOR: Gates, Christian

INVENTOR: Haselden, Sherill S.

INVENTOR: Mattheakis, Jerry A.

INVENTOR: Schatz, Peter J.

INVENTOR: Weystrom, Christopher R.

INVENTOR: Wiegman, Nicholas J.

INVENTOR: STREET: Five Moore Drive, P.O. Box 1000

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patent in Release #100, Wisconsin

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/094,994

FILING DATE: 27-Feb-2002

ATTORNEY/AGENT INFORMATION:

NAME: Rubric, Robert T.

REGISTRATION NUMBER: 16,492

REFERENCE/DOCKET NUMBER: 1K04515W

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 118:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 118:

US-10 053-768-118

Query Match 43.9%; Score 29; DB 12; Length 10;

Best Local Similarity 44.4%; Pred No 2.4e+02;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 CSQKHWL 9

DB 1 CSQKHWL 9

RESULT 12

US 08-450-842-45

Sequence 45, Application US/08450842

Publication No. US20020045576A1

GENERAL INFORMATION:

APPLICANT: GENENTECH, INC.

INVENTOR: ROSENTHAL, ARNON

TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kt floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,842

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/456419

FILING DATE: 19-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/040013

FILING DATE: 23-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/649482

FILING DATE: 31-JAN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/587707

FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 16,700

REFERENCE/DOCKET NUMBER: 666201D3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

US 08-450-842-45

Query Match 43.9%; Score 29; DB 8; Length 11;

Best Local Similarity 42.9%; Pred No 2.6e+02;

Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Cy 1 QRMWLD 9





```

11111
: QKHWLSR 8

RESULT 2
: US-08-466-151-57
: Sequence 57, Application US/08466151
: Patent No. 6037453
: GENERAL INFORMATION:
: APPLICANT: Gardiner, Paula M.
: APPLICANT: Fresco, Leonard G.
: TITLE OF INVENTION: Immunoglobulin Variants
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466,151
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/466163
: FILING DATE: 06-Jun-1995
: APPLICATION NUMBER: 08/405617
: FILING DATE: 14-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 05/185899
: FILING DATE: 26 JAN-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/879495
: FILING DATE: 07 MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/744768
: FILING DATE: 14-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Svoboda, Craig G.
: REGISTRATION NUMBER: 39,044
: REFERENCE/DOCKET NUMBER: P07-9P2C1D1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-1489
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: US-08-466-151-24

Query Match 72.7% Score 48; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY ? QKHWLSR 10
DB 1 QKHWLSR 8

RESULT 4
US-08-466-151-57
: Sequence 57, Application US/08466151
: Patent No. 6037453
: GENERAL INFORMATION:
: APPLICANT: Gardiner, Paula M.
: APPLICANT: Fresco, Leonard G.
: TITLE OF INVENTION: Immunoglobulin Variants
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466,151
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/466163
: FILING DATE: 06-Jun-1995
: APPLICATION NUMBER: 08/405617
: FILING DATE: 14-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/185899
: FILING DATE: 27 JAN 1994

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1 PRIOR APPLICATION DATA:  
 2 APPLICATION NUMBER: 07/879495  
 3 FILING DATE: 07-MAY-1992  
 4 PRIOR APPLICATION DATA:  
 5 APPLICATION NUMBER: 07/744765  
 6 FILING DATE: 14-AUG-1991  
 7 ATTORNEY/AGENT INFORMATION:  
 8 NAME: Svoboda, Craig G.  
 9 REGISTRATION NUMBER: 19,044  
 10 REFERENCE/DOCKET NUMBER: PG148,110  
 11 TELECOMMUNICATION INFORMATION:  
 12 TELEPHONE: 650/226-1489  
 13 TELEFAX: 650/952-9861  
 14 INFORMATION FOR SEQ ID NO: 57:  
 15 SEQUENCE CHARACTERISTICS:  
 16 LENGTH: 8 amino acids  
 17 TYPE: Amino Acid  
 18 TOPOLOGY: Linear  
 19 US 08-466-163B-57

Query Match 72.7% Score 497 DB 1, Length 8;  
 Best Local Similarity 100.0%, Pred. No. 2.5e-05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QKWLSCR 10  
 DB 1 QKWLSCR 8

RESULT 5  
 US-08-466-163B-54  
 1 Sequence 57, Application US/08466163  
 2 Patent No. 6329509  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Jaidieu, Paula M.  
 5 APPLICANT: Presta, Leonard G.  
 6 TITLE OF INVENTION: Immunoglobulin Variants  
 7 FILE REFERENCE: P0718P2C1D  
 8 CURRENT APPLICATION NUMBER: US/08/466163B  
 9 PRIOR FILING DATE: 1995-06-06  
 10 PRIOR APPLICATION NUMBER: US 08/405,617  
 11 PRIOR FILING DATE: 1995-03-15  
 12 PRIOR APPLICATION NUMBER: US 08/185,499  
 13 PRIOR FILING DATE: 1994-01-26  
 14 PRIOR APPLICATION NUMBER: US 07/879,495  
 15 PRIOR FILING DATE: 1992-05-07  
 16 PRIOR APPLICATION NUMBER: US 07/744,765  
 17 PRIOR FILING DATE: 1991-08-14  
 18 NUMBER OF SEQ ID NOS: 44  
 19 SEQ ID NO: 54  
 20 LENGTH: 8  
 21 TYPE: PRT  
 22 ORGANISM: Homo sapiens  
 23 US-08-466-163B-54

Query Match 72.7% Score 497 DB 1, Length 8;  
 Best Local Similarity 100.0%, Pred. No. 2.5e-05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QKWLSCR 10  
 DB 1 QKWLSCR 8

RESULT 6  
 US-08-466-163B-57  
 1 Sequence 57, Application US/08466163B  
 2 Patent No. 6329509  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Jaidieu, Paula M.  
 5 APPLICANT: Presta, Leonard G.  
 6 TITLE OF INVENTION: Immunoglobulin Variants  
 7 FILE REFERENCE: P0718P2C1D

1 CURRENT APPLICATION NUMBER: US/08/466,163B  
 2 CURRENT FILING DATE: 1995-06-06  
 3 PRIOR APPLICATION NUMBER: US 08/405,617  
 4 PRIOR FILING DATE: 1995-03-15  
 5 PRIOR APPLICATION NUMBER: US 08/185,899  
 6 PRIOR FILING DATE: 1994-01-26  
 7 PRIOR APPLICATION NUMBER: US 07/879,495  
 8 PRIOR FILING DATE: 1992-05-07  
 9 PRIOR APPLICATION NUMBER: US 07/744,768  
 10 PRIOR FILING DATE: 1991-08-14  
 11 NUMBER OF SEQ ID NOS: 64  
 12 SEQ ID NO: 57  
 13 LENGTH: 8  
 14 TYPE: PRT  
 15 ORGANISM: Homo sapiens  
 16 US-08-466-163B-57

Query Match 72.7% Score 487 DB 4, Length 8;  
 Best Local Similarity 100.0%, Pred. No. 2.5e-05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QKWLSCR 10  
 DB 1 QKWLSCR 8

RESULT 7  
 US 08-764-640-118  
 1 Sequence 118, Application US/C8764640  
 2 Patent No. 5869451  
 3 Patent No. 5869451 5837683  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Dower, William J.  
 6 APPLICANT: Barrett, Ronald W.  
 7 APPLICANT: Cutilia, Steven E.  
 8 APPLICANT: Gates, Christian  
 9 APPLICANT: Schatz, Peter J.  
 10 APPLICANT: Balasubramanian, Palaniappan  
 11 APPLICANT: Wagstrom, Christopher R.  
 12 APPLICANT: Hendrix, Richard W.  
 13 APPLICANT: Depierre, Randolph B.  
 14 APPLICANT: Podduluri, Surekha  
 15 APPLICANT: Yin, Qun  
 16 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
 17 TITLE OF INVENTION: RECEPTOR  
 18 NUMBER OF SEQUENCES: 244  
 19 CORRESPONDENCE ADDRESS:  
 20 ADDRESSEE: Glaxo Wellcome  
 21 STREET: Five Moore Drive, P.O. Box 13398  
 22 CITY: Research Triangle Park  
 23 STATE: NC  
 24 COUNTRY: USA  
 25 ZIP: 27709  
 26 COMPUTER READABLE FORM:  
 27 MEDIUM TYPE: Floppy disk  
 28 COMPUTER: IBM PC compatible  
 29 OPERATING SYSTEM: PC-DOS/MS-DOS  
 30 SOFTWARE: Patent In Release #1.0, Version #1.30  
 31 CURRENT APPLICATION DATA:  
 32 APPLICATION NUMBER: US/08/764,640  
 33 FILING DATE: 11-DEC-1996  
 34 CLASSIFICATION: 514  
 35 ATTORNEY/AGENT INFORMATION:  
 36 NAME: Hrubiec, Robert T.  
 37 REGISTRATION NUMBER: 36,392  
 38 REFERENCE/DOCKET NUMBER: PK3281  
 39 TELECOMMUNICATION INFORMATION:  
 40 TELEPHONE: 919-248-1000  
 41 INFORMATION FOR SEQ ID NO: 118:  
 42 SEQUENCE CHARACTERISTICS:  
 43 LENGTH: 13 amino acids  
 44 TYPE: amino acid  
 45 STRANDEDNESS:

1 TOPOLOGY: linear  
2 MOLECULE TYPE: peptide  
3 US-08 764-640-118

Query Match 43.9% Score 29, DR 1 Length 10  
Best Local Similarity 44.4% Prev. No. 75  
Matches 4: Conservative 2; Mismatches 0; Gaps 0

QY : CSQKHWLSL 9  
DB : CTRTOWLE 9

RESULT 1

US-08-973 225-118

1 Sequence 118, Application US/0897328A

2 Patent No. 6041913

3 GENERAL INFORMATION:

4 APPLICANT: Lower, William J.

5 APPLICANT: Barrett, Ronald W.

6 APPLICANT: Cwirla, Steven E.

7 APPLICANT: Duffin, David C.

8 APPLICANT: Gates, Christian

9 APPLICANT: Haselden, Sherill S.

10 APPLICANT: Mathiak, Sally J.

11 APPLICANT: Magstrom, Christopher R.

12 APPLICANT: Reichen, Richard W.

13 APPLICANT: Depina, Hansclm B.

14 APPLICANT: Podsutari, Suresha

15 APPLICANT: Yin, Qun

16 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

17 NUMBER OF SEQUENCES: 232

18 CORRESPONDENCE ADDRESS:

19 ADDRESSEE: Glaxo Wellcome

20 STREET: Five Moore Drive, P.O. Box 1338

21 CITY: Research Triangle Park

22 STATE: NC

23 COUNTRY: USA

24 ZIP: 27709

25 COMPUTER READABLE FORM:

26 MEDIUM TYPE: Floppy disk

27 COMPUTER: IBM PC compatible

28 OPERATING SYSTEM: PC-DOS/MS-DOS

29 SOFTWARE: Patent in Release #1.0, Version #1.30

30 CURRENT APPLICATION DATA:

31 APPLICATION NUMBER: US/09/244,298A

32 FILING DATE: 11 DEC-1996

33 CLASSIFICATION: 514

34 ATTORNEY/AGENT INFORMATION:

35 NAME: Hrabiec, Robert T.

36 REGISTRATION NUMBER: 36,392

37 REFERENCE/DOCKET NUMBER: PK328:

38 TELECOMMUNICATION INFORMATION:

39 TELEPHONE: 919-248-1000

40 INFORMATION FOR SEQ ID NO: 118:

41 SEQUENCE CHARACTERISTICS:

42 LENGTH: 10 amino acids

43 TYPE: amino acid

44 STRADEDNESS:

45 TOPOLOGY: linear

46 MOLECULE TYPE: peptide

47 SEQUENCE DESCRIPTION: SEQ ID NO: 118

48 US-08-973 225-118

Query Match 43.9% Score 29, DR 1 Length 10

Best Local Similarity 44.4% Prev. No. 75

Matches 4: Conservative 2; Mismatches 0; Gaps 0

QY : CSQKHWLSL 9

DB : CTRTOWLE 9

RESULT 1

US-09-914 26A-118

1 Sequence 118, Application US/0916794

2 Patent No. 6251864

3 GENERAL INFORMATION:

4 APPLICANT: Lower, William J.

5 APPLICANT: Barrett, Ronald W.

6 APPLICANT: Cwirla, Steven E.

7 APPLICANT: Gates, Christian

8 APPLICANT: Haselden, Sherill S.

9 APPLICANT: Mathiak, Sally J.

10 APPLICANT: Magstrom, Christopher R.

11 APPLICANT: Reichen, Richard W.

12 APPLICANT: Depina, Hansclm B.

13 APPLICANT: Podsutari, Suresha

14 APPLICANT: Yin, Qun

15 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

16 NUMBER OF SEQUENCES: 232

17 CORRESPONDENCE ADDRESS:

18 ADDRESSEE: Glaxo Wellcome

19 STREET: Five Moore Drive, P.O. Box 1338

20 CITY: Research Triangle Park

21 STATE: NC

22 COUNTRY: USA

23 ZIP: 27709

24 COMPUTER READABLE FORM:

25 MEDIUM TYPE: Floppy disk

26 COMPUTER: IBM PC compatible

27 OPERATING SYSTEM: PC-DOS/MS-DOS

28 SOFTWARE: Patent in Release #1.0, Version #1.30

29 CURRENT APPLICATION DATA:

30 APPLICATION NUMBER: US/09/244,298A

31 FILING DATE: 11 DEC-1996

32 CLASSIFICATION: 514

33 ATTORNEY/AGENT INFORMATION:

34 NAME: Hrabiec, Robert T.

35 REGISTRATION NUMBER: 36,392

36 REFERENCE/DOCKET NUMBER: PK328:

37 TELECOMMUNICATION INFORMATION:

38 TELEPHONE: 919-248-1000

39 INFORMATION FOR SEQ ID NO: 118:

40 SEQUENCE CHARACTERISTICS:

41 LENGTH: 10 amino acids

42 TYPE: amino acid

43 STRADEDNESS:

44 TOPOLOGY: linear

45 MOLECULE TYPE: peptide

46 SEQUENCE DESCRIPTION: SEQ ID NO: 118

47 US-09-914 26A-118

Query Match 43.9% Score 29, DR 1 Length 10

Best Local Similarity 44.4% Prev. No. 75

Matches 4: Conservative 2; Mismatches 0; Gaps 0

QY : CSQKHWLSL 9

DB : CTRTOWLE 9

RESULT 1

US-09-914 26A-118

1 Sequence 118, Application US/0916794

2 Patent No. 6251864

3 GENERAL INFORMATION:

4 APPLICANT: Lower, William J.

5 APPLICANT: Barrett, Ronald W.

6 APPLICANT: Cwirla, Steven E.

7 APPLICANT: Gates, Christian

8 APPLICANT: Haselden, Sherill S.

9 APPLICANT: Mathiak, Sally J.

10 APPLICANT: Magstrom, Christopher R.

11 APPLICANT: Reichen, Richard W.

12 APPLICANT: Depina, Hansclm B.

13 APPLICANT: Podsutari, Suresha

14 APPLICANT: Yin, Qun

15 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

16 NUMBER OF SEQUENCES: 232

17 CORRESPONDENCE ADDRESS:

18 ADDRESSEE: Glaxo Wellcome

19 STREET: Five Moore Drive, P.O. Box 1338

20 CITY: Research Triangle Park

21 STATE: NC

22 COUNTRY: USA

23 ZIP: 27709

24 COMPUTER READABLE FORM:

25 MEDIUM TYPE: Floppy disk

26 COMPUTER: IBM PC compatible

27 OPERATING SYSTEM: PC-DOS/MS-DOS

28 SOFTWARE: Patent in Release #1.0, Version #1.30

29 CURRENT APPLICATION DATA:

30 APPLICATION NUMBER: US/09/244,298A

31 FILING DATE: 11 DEC-1996

32 CLASSIFICATION: 514

33 ATTORNEY/AGENT INFORMATION:

34 NAME: Hrabiec, Robert T.

35 REGISTRATION NUMBER: 36,392

36 REFERENCE/DOCKET NUMBER: PK328:

37 TELECOMMUNICATION INFORMATION:

38 TELEPHONE: 919-248-1000

39 INFORMATION FOR SEQ ID NO: 118:

40 SEQUENCE CHARACTERISTICS:

41 LENGTH: 10 amino acids

42 TYPE: amino acid

43 STRADEDNESS:

44 TOPOLOGY: linear

45 MOLECULE TYPE: peptide

46 SEQUENCE DESCRIPTION: SEQ ID NO: 118

47 US-09-914 26A-118

Query Match 43.9% Score 29, DR 1 Length 10

Best Local Similarity 44.4% Prev. No. 75

Matches 4: Conservative 2; Mismatches 0; Gaps 0

QY : CSQKHWLSL 9

DB : CTRTOWLE 9

RESULT 1

US-09-914 26A-118

1 Sequence 118, Application US/0916794

2 Patent No. 6251864

3 GENERAL INFORMATION:

4 APPLICANT: Lower, William J.

5 APPLICANT: Barrett, Ronald W.

6 APPLICANT: Cwirla, Steven E.

7 APPLICANT: Gates, Christian

8 APPLICANT: Haselden, Sherill S.

9 APPLICANT: Mathiak, Sally J.

10 APPLICANT: Magstrom, Christopher R.

11 APPLICANT: Reichen, Richard W.

12 APPLICANT: Depina, Hansclm B.

13 APPLICANT: Podsutari, Suresha

14 APPLICANT: Yin, Qun

15 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

16 NUMBER OF SEQUENCES: 232

17 CORRESPONDENCE ADDRESS:

18 ADDRESSEE: Glaxo Wellcome

19 STREET: Five Moore Drive, P.O. Box 1338

20 CITY: Research Triangle Park

21 STATE: NC

22 COUNTRY: USA

23 ZIP: 27709

24 COMPUTER READABLE FORM:

25 MEDIUM TYPE: Floppy disk

26 COMPUTER: IBM PC compatible

27 OPERATING SYSTEM: PC-DOS/MS-DOS

28 SOFTWARE: Patent in Release #1.0, Version #1.30

29 CURRENT APPLICATION DATA:

30 APPLICATION NUMBER: US/09/244,298A

31 FILING DATE: 11 DEC-1996

32 CLASSIFICATION: 514

33 ATTORNEY/AGENT INFORMATION:

34 NAME: Hrabiec, Robert T.

35 REGISTRATION NUMBER: 36,392

36 REFERENCE/DOCKET NUMBER: PK328:

37 TELECOMMUNICATION INFORMATION:

38 TELEPHONE: 919-248-1000

39 INFORMATION FOR SEQ ID NO: 118:

40 SEQUENCE CHARACTERISTICS:

41 LENGTH: 10 amino acids

42 TYPE: amino acid

43 STRADEDNESS:

44 TOPOLOGY: linear

45 MOLECULE TYPE: peptide

46 SEQUENCE DESCRIPTION: SEQ ID NO: 118

47 US-09-914 26A-118

Query Match 43.9% Score 29, DR 1 Length 10

Best Local Similarity 44.4% Prev. No. 75

Matches 4: Conservative 2; Mismatches 0; Gaps 0

QY : CSQKHWLSL 9

DB : CTRTOWLE 9

RESULT 1

US-09-914 26A-118

1 Sequence 118, Application US/0916794

2 Patent No. 6251864

3 GENERAL INFORMATION:

4 APPLICANT: Lower, William J.

5 APPLICANT: Barrett, Ronald W.

6 APPLICANT: Cwirla, Steven E.

7 APPLICANT: Gates, Christian

8 APPLICANT: Haselden, Sherill S.

9 APPLICANT: Mathiak, Sally J.

10 APPLICANT: Magstrom, Christopher R.

11 APPLICANT: Reichen, Richard W.

12 APPLICANT: Depina, Hansclm B.

13 APPLICANT: Podsutari, Suresha

14 APPLICANT: Yin, Qun

15 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

16 NUMBER OF SEQUENCES: 232

17 CORRESPONDENCE ADDRESS:

18 ADDRESSEE: Glaxo Wellcome

19 STREET: Five Moore Drive, P.O. Box 1338

20 CITY: Research Triangle Park

21 STATE: NC

22 COUNTRY: USA

23 ZIP: 27709

24 COMPUTER READABLE FORM:

25 MEDIUM TYPE: Floppy disk

26 COMPUTER: IBM PC compatible

27 OPERATING SYSTEM: PC-DOS/MS-DOS

28 SOFTWARE: Patent in Release #1.0, Version #1.30



Best Local Similarity 44.4%; Pref. No. 751  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQVHWLSD 9  
DP 1 STRVWLLD 9

RESULT 14  
US-08-424-45  
Sequence 45, Application US-08451947  
Patent No. 607206  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451947  
FILING DATE: 19-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/426419  
FILING DATE: 19-APR-1995  
PRIOR APPLICATION NUMBER: 06/030614  
FILING DATE: 22-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: TORCHIA, PHD, Timothy E.  
REGISTRATION NUMBER: 36,730  
REFERENCE/DOCKET NUMBER: PG666P1C2  
TELECOMMUNICATIONS INFORMATION:  
TELEPHONE: 415/942-8674  
TELEFAX: 415/942-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 45:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

QY 1 CSQVHWLSD 9  
DP 1 STRVWLLD 9

RESULT 15  
US-08-928-44-45  
Sequence 45, Application US/08928694  
Patent No. 607326  
GENERAL INFORMATION:  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)

GENERAL INFORMATION:  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424-836A  
FILING DATE: 19-APR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240187  
FILING DATE: 10-May-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648482  
FILING DATE: 31-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/587707  
FILING DATE: 25-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: TORCHIA, PHD, Timothy E.  
REGISTRATION NUMBER: 36,730  
REFERENCE/DOCKET NUMBER: PG666P1C2  
TELECOMMUNICATIONS INFORMATION:  
TELEPHONE: 415/925-8674  
TELEFAX: 415/942-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 45:  
LENGTH: 11 amino acids  
TYPE: Amino Acid  
TOP LOGY: Linear  
US-08-424-426A-45

Query Match 42.9%; Score 29; DB 2; Length 11;  
Best Local Similarity 42.9%; Pref. No. 81;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQVHWLSD 9  
DP 1 STRVWLLD 9

RESULT 15  
US-08-928-44-45  
Sequence 45, Application US/08928694  
Patent No. 607326  
GENERAL INFORMATION:  
APPLICANT: ROSENTHAL, ARNON  
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)



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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/528,843
3 FILING DATE: 12-Sep-1997
4 CLASSIFICATION: 424
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 08/451,947
7 FILING DATE: 26-MAY-1995
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: 08/426,619
10 FILING DATE: 19-APR-1995
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: 08/030,016
13 FILING DATE: 22-MAR-1993
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: 07/645,442
16 FILING DATE: 31-JAN
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 07/587,707
19 FILING DATE: 1993
20 ATTORNEY/AGENT INFORMATION:
21 NAME: TORCHIO, PHD., TIMOTHY E
22 REGISTRATION NUMBER: 36,700
23 REFERENCE/DOCKET NUMBER: PC660,001,000
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: 650/225-8674
26 TELEFAX: 650/952-9881
27 INFORMATION FOR SEQ ID NO: 45:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 11 amino acids
30 TYPE: Amino Acid
31 TOPOLOGY: Linear
32 US 08 028 694 45

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Query Match: 43.9% Score: 29; DB: 1; Length: 110
Best Local Similarity: 42.9%; Pos: No. 93
Matches: 3; Conservative: 4; Mismatched: 0; Gaps: 0

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CY 3 OVERLAP 9
DB 1 11111
PRIORWISE 7

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Search completed: November 5, 2003, 10:44:33  
 Job time: 27 secs